Translation suppression promotes stress granule formation and cell survival in response to cold shock

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ABSTRACT
Cells respond to different types of stress by inhibition of protein synthesis and subsequent assembly of stress granules (SGs), cytoplasmic aggregates that contain stalled translation pre-initiation complexes. Global translation is regulated through the translation initiation factor eIF2α and the mTOR pathway. Here we identify cold shock as a novel trigger of SG assembly in yeast and mammals. Whereas cold shock-induced SGs take hours to form, they dissolve within minutes when cells are returned to optimal growth temperatures. Cold shock causes eIF2α phosphorylation through the kinase PERK in mammalian cells, yet this pathway is not alone responsible for translation arrest and SG formation. In addition, cold shock leads to reduced mitochondrial function, energy depletion, concomitant activation of AMP-activated protein kinase (AMPK) and inhibition of mTOR signalling. Compound C, a pharmacological inhibitor of AMPK, prevents the formation of SGs and strongly reduces cellular survival in a translation-dependent manner. Our results demonstrate that cells actively suppress protein synthesis by parallel pathways, which induce SG formation and ensure cellular survival during hypothermia.  
Key words: AMP-activated protein kinase / eIF2α phosphorylation / energy metabolism / hypothermia / protein synthesis

INTRODUCTION
The rate of protein synthesis in cells is tightly regulated. In response to various forms of stress, cells reduce global translation whereby they prevent further protein damage, re-allocate their resources to repair processes and ensure cellular survival. Most types
of stress cause translation inhibition through phosphorylation of the α subunit of the translation initiation factor eIF2, which delivers initiator tRNA\textsubscript{Met} to the small 40S ribosomal subunit (Holcik and Sonenberg, 2005). In mammals, eIF2α phosphorylation is mediated via the four kinases HRI, PERK, GCN2 and PKR, whereas yeast contains only Gcn2. Phosphorylated eIF2 no longer dissociates from its GDP exchange factor eIF2B, which prevents recharging of the eIF2-GTP-tRNA\textsubscript{Met} ternary complex and inhibits translation initiation. As a consequence of polysome disassembly, stalled translation pre-initiation complexes accumulate and aggregate into cytosolic stress granules (SGs) (Kedersha et al., 2002).

In addition to eIF2α phosphorylation, translation is controlled by the mTOR pathway (Wullschleger et al., 2006). When insulin signalling, nutrients or energy availability is low, inhibition of mTOR attenuates translation through the eIF4E-binding proteins (4EBPs) and S6-kinase 1 (S6K1) (Holz et al., 2005; Richter and Sonenberg, 2005). Inhibition of protein synthesis is intimately linked to the assembly of SGs, which contain poly(A)-mRNA, small, but not large ribosomal subunits, as well as translation initiation factors eIF3, eIF4E, eIF4G and the cytoplasmic poly(A)-binding protein (PABP) (Kedersha et al., 2002). RNA-binding SG proteins such as TIA1, TIAR and G3BP participate in the aggregation process driving SG assembly (Kedersha et al., 1999; Kedersha et al., 2002; Tourriere et al., 2003; Gilks et al., 2004). It is important to note that SGs form as a consequence of translation arrest, but they are not required for the arrest of translation (Anderson and Kedersha, 2008). Current thinking is that SGs help keep pre-initiation complexes assembled, and by sequestering specific proteins play a role in cellular survival and signal transduction (Kim et al., 2005; Arimoto et al., 2008). In Saccharomyces cerevisiae, SG-like aggregates, also termed EGP-bodies, were described under conditions of glucose deprivation and heat shock (Hoyle et al., 2007; Buchan et al., 2008; Grousl et al., 2009). Their composition is similar to mammalian SGs, yet yeast SGs lack eIF3 and small ribosomal subunits.

While mechanisms controlling translation have been studied extensively for ER-stress, oxidative stress, heat shock, amino acid starvation and exposure to double stranded RNA (Holcik and Sonenberg, 2005), very little is known about mechanisms controlling translation during temperature downshift. Mammalian cells exposed to hypothermia show a progressive reduction of global translation rates (Roobol et al., 2009). In yeast, factors supporting protein synthesis including ribosomal proteins are downregulated at temperatures below 10°C (Homma et al., 2003; Murata et al., 2006), yet the mechanism responsible for cold shock-induced translation suppression remains largely unexplored. The adaptive response to low temperatures is of preeminent importance in organisms that cannot control body temperature. Even in thermoregulating warm-blooded animals, temperatures in the skin of extremities can drop below 10°C (Heus et al., 1995), and the body temperature in small hibernating mammals reaches 2°C during torpor (Carey et al., 2003).

In this study, we identify cold shock as a condition under which both mammalian cells and \textit{S. cerevisiae} form SGs. Through our analysis of eIF2α phosphorylation, mTOR signalling and AMPK activation, we provide evidence that translation suppression and SG formation promote the survival of mammalian cells at low temperatures.

RESULTS
Cold shock induces SGs, translation arrest and polysome disassembly in mammalian cells

To test whether mammalian cells react to hypothermia with a translation arrest response, we first analyzed African green monkey COS7 kidney cells because of their excellent imaging properties. Upon shift to a range of temperatures below 37°C, immunofluorescence (IF) staining of the translation initiation factor eIF3B revealed extensive formation of cytoplasmic granules after 10 hours at 10°C, whereas granules did not form at 30°C or 20°C (Figure 1A). COS7 cells did not form eIF3B granules at 4°C either (Figure 1A and Supplemental Figure S1A), and in fact detached from the plate after 10 hours at 4°C, indicative of cell death. In contrast, COS7 cells remained adherent up to 24 hours at 10°C. This suggested that cells mount a stress response specific for adaptation to temperatures around 10°C. The eIF3B granules observed at 10°C were distinctly smaller and more numerous than SGs in cells subjected to arsenite-induced oxidative stress (Figure 1B). Poly(A)-mRNA accumulated in the same granules, as determined by colocalization with eIF3B (Figure 1C). Cold shock-induced granules also contain eIF4G (Figure 1D), eIF2α (Figure 1E) and the RNA-binding proteins G3BP (Figure 1F), PABP (Figure 1G), HuR and TIA1 (data not shown), confirming that these are bona-fide SGs. Cold shock-induced SGs were also detected in human Du145, HeLa and Huh7 cells, as well as in mouse embryonic fibroblasts (MEFs; Supplemental Figure S1B), indicating that our observation was not restricted to a particular cell line.

In following the kinetics of SG formation after cold shock, we detected the first granules after 4 hours at 10°C in 26% of COS7 cells (Supplemental Figure S1C; quantification in Figure 1H). This number increased progressively and reached a maximum of 93% SG-positive cells after 10 hours of cold shock. SGs then persisted for 24 hours, the last time point analyzed. Video microscopy showed that SGs remain assembled during 10°C hypothermia (Supplemental Movie S1), which is different from oscillatory SGs induced by virus infection (Ruggieri et al., 2012).

To directly assess translation rates, COS7 cells were labelled with 35S-methionine/cysteine. Incorporation into nascent proteins was reduced to less than 10% already after one hour at 10°C compared to cells grown at 37°C, and remained at this low level during the entire cold shock period (Figure 1I and J). Sucrose gradient density centrifugation showed a progressive loss of polysomes during cold shock (Figure 1K), confirming that protein synthesis is suppressed. The percentage of polysome-associated ribosomes, which reflects the proportion of ribosomes engaged in translation, was found to drop from 67% at 37°C to 8% after 10 hours at 10°C (bar graph in Figure 1K). We concluded that translation inhibition is accompanied by polysome disassembly during cold shock, which leads to the progressive assembly of SGs.

Cold shock induces SGs in S. cerevisiae

Next, we examined whether the translational arrest in response to cold shock is conserved in S. cerevisiae. Using the SG marker Pub1 genomically tagged with GFP, we observed prominent granules when cells were shifted from 30°C to 10°C for 4 hours, but not when shifted to 15°C (Figure 2A, full time course in Supplemental Figure S2A–C). SGs were strongly induced after 4 hours at 0°C, and persisted for at least 24 hours (Figure 2B). The SG markers Pab1-mCherry (Figure 2B) and poly(A)-mRNA (Figure 2C) also localized to these granules.

Time course experiments (Supplemental Figure S2A and B) and automated image analysis (Figure 2D) showed that the earliest SGs were formed after 2 hours of
incubation at 10°C or 0°C, and that their number increased steadily during the first 8 hours. Between 8 and 24 hours of cold shock, the granules became fewer, yet larger and more elongated as Pub1-GFP continued to accumulate in the aggregates. An example of automated cell and foci detection is provided in Supplemental Figure S3. As in mammalian cells, the slow appearance of cold shock-induced SGs in yeast is in stark contrast to other types of stress such as heat shock or glucose deprivation, where SGs are formed within 10 to 20 minutes (Hoyle et al., 2007; Buchan et al., 2008; Grousl et al., 2009).

Given that yeast SGs show a tight connection to processing (P)-bodies (Buchan et al., 2008), cytoplasmic foci at which mRNA decay enzymes are concentrated, we also visualized the P-body markers Dep2 and Pat1 (Supplemental Figure S4A and B). Both Dep2-GFP and Pat1-GFP formed numerous foci after 4 hours at 0°C, yet only some of them colocalized with the SG marker Pab1-mCherry, indicative of physically separated SGs and P-bodies. On the other hand, colocalization became pronounced after 24 hours at 0°C, suggesting that the large aggregates during prolonged hypothermia arise from fusions between SGs and P-bodies.

**Rapid SG disassembly during recovery from cold shock**

Given the unusually slow kinetics of SG assembly during cold shock, we wanted to investigate the fate of these SGs upon return to optimal growth temperatures. First we analyzed a Pub1-GFP expressing *S. cerevisiae* strain in which SGs had been induced by keeping cells for 4 hours at 0°C. Very much to our surprise, SGs disappeared within 2.5 minutes after returning cells to 30°C (Figure 3A and B), and polysomes were fully assembled within 5 minutes (Figure 3C and D). Interestingly, recovery from cold shock occurs faster than recovery from glucose starvation, where it takes about 10 minutes for polysomes to fully re-assemble (Supplemental Figure S5).

In mammalian COS7 cells, SGs disappeared 5–10 minutes after returning from a 10°C cold shock to 37°C (Figure 4A and B), whereas the re-assembly of polysomes was rather slow (Figure 4C). Quantification showed that one hour after return to 37°C, polysomal ribosomes had reached only two thirds of the level in control cells, and full recovery was observed after 6 hours. Thus, while SGs disassemble within minutes in both yeast and mammalian cells during recovery from cold shock, the re-assembly of polysomes occurs within minutes in yeast, yet takes several hours in COS7 cells. This suggested that in COS7 cells, SG disassembly is not the rate-limiting step for the resumption of translation after return to optimal growth temperatures.

**eIF2α phosphorylation alone is not responsible for cold shock-induced translation arrest**

Our next goal was to characterize the signalling pathways that control translation during cold shock. We first tested whether phosphorylation of eIF2α at serine 51 is involved. In COS7 cells and MEFs, we observed an increase in phospho-eIF2α levels 2–4 hours after reducing the temperature to 10°C, and eIF2α phosphorylation persisted until 24 hours (Figure 5A and B). The slow increase in eIF2α phosphorylation paralleled the progressive suppression of translation (Figure 1K) and the slow induction of SGs (Figure 1H). During recovery from cold shock, we found that eIF2α remained highly phosphorylated for 30 minutes, and was fully dephosphorylated only after 2 hours upon return to 37°C (Figure 5C). While SGs disassembled much more rapidly within 5–10 minutes (Figure 4B), the kinetics of translation re-initiation (Figure 4C) appeared to follow eIF2α dephosphorylation.
Four eIF2α kinases, HRI, PERK, GCN2 and PKR, mediate translational arrest in response to different types of stress. By analyzing ko MEFs of each of these kinases, we identified PERK to be responsible for eIF2α phosphorylation during cold shock (Figure 5D, lanes 5 and 6). PERK is known to be activated by endoplasmic reticulum (ER) stress (Harding et al., 1999), and this was confirmed by the failure of PERK ko MEFs to phosphorylate eIF2α in response to treatment with dithiothreitol (DTT, lanes 7 and 8). In contrast to DTT-induced ER stress, cold shock caused SG formation (data not shown) and translation suppression in both wt and PERK ko MEFs (Figure 5E). This suggested that PERK activation is not the only pathway by which translation is inhibited during cold shock.

We further tested knock-in MEFs in which both eIF2α alleles were replaced either with wt eIF2α-SS encoding for serine at position 51, or with mutant eIF2α-AA encoding for non-phosphorylatable alanine at this position (Scheuner et al., 2001). Similar to the PERK MEFs, both eIF2α-SS and -AA MEFs showed massive polysome disassembly (Figure 6A) and SG formation (Figure 6B and C) upon cold shock. As a control, we subjected the cells to oxidative stress induced by arsenite, and observed that the eIF2α-AA MEFs were resistant to translation inhibition and did not form SGs (Figure 6A–C), as reported previously (McEwen et al., 2005).

Given that S. cerevisiae contains a single eIF2α kinase, Gcn2, we then addressed the role of eIF2α phosphorylation in yeast using a gcn2Δ strain. In both wt and gcn2Δ cells, polysomes were disassembled to a similar degree upon cold shock (Figure 7A and B). Also, gcn2Δ cells responded to cold shock by robust induction of SGs, just as wt cells (Figure 7C and D). Hence, eIF2α phosphorylation appears not to be required for cold shock-induced translation arrest, both in yeast and mammalian cells. These data point towards an additional, possibly redundant, pathway that suppresses translation during cold shock.

**mTOR inhibition during cold shock**

Another pathway by which cells attenuate translation occurs through inhibition of mTOR activity (Wullschleger et al., 2006). In the absence of mTOR signalling, translation is inhibited by dephosphorylation of the mTOR targets 4EBP and S6K1. Dephosphorylated 4EBP prevents eIF4E from recruiting 43S pre-initiation complex factors (Richter and Sonenberg, 2005). Upon cold shock, we observed dephosphorylation of 4EBP1 (Figure 8A, lanes 1 and 2) as well as increased binding of 4EBP1 to eIF4E using a cap-sepharose pull-down assay (lanes 4 and 5). At the same time, binding of eIF4AI, eIF3B and PABP was reduced, and equal changes were observed when cells were treated with the mTOR inhibitor rapamycin (lane 6). By recording polysome profiles, we observed that at 37°C, 10 hours of rapamycin treatment reduced polysomal ribosomes moderately from 69% to 41% (Supplemental Figure S6). After 10 hours of 10°C cold shock, translation was suppressed to a much greater extent with only 7% polysomal ribosomes remaining. This fraction was not reduced further by rapamycin, suggesting that mTOR is fully inhibited during cold shock.

mTOR activates translation at least in part through phosphorylation of 4EBP proteins (Richter and Sonenberg, 2005). 4EBP1 and 4EBP2 double ko MEFs lack 4EBP activity since the third member of the family, 4EBP3, is not expressed in these cells (Dowling et al., 2010). The suppressive effect of mTOR inhibition on translation was previously shown to be much weaker in 4EBP1+2 ko MEFs than in wt MEFs (Dowling et al., 2010). During 10°C cold shock, however, translation suppression was
as efficient in 4EBP1+2 ko MEFs as in wt counterparts (Figure 8B). Likewise, SG formation was not affected by deletion of EAP1 and CAF20, the two 4EBP paralogs in yeast (Supplemental Figure S7). These results suggested that 4EBP proteins alone do not account for cold shock-induced repression of translation.

In yeast, eIF4A dissociates from pre-initiation complexes upon glucose starvation and shifts to the free fraction in polysome gradients (Castelli et al., 2011). We therefore asked whether such an alternative mechanism might as well cause translation suppression during cold shock. However, neither eIF4G, eIF4E, eIF4AI nor eIF3B showed a prominent change in their sucrose gradient distribution upon cold shock in mammalian Huh7 cells (Figure 8C). Only PABP and ribosomal protein L7 shifted from polysomal towards lighter fractions, consistent with the disassembly of polysomes. We inferred that pre-initiation complexes, at large, remain assembled during cold shock, while mTOR inhibition reduces the specific association of eIF4E with eIF4AI, eIF3B and PABP.

**Cold shock causes energy depletion and AMPK activation**

Since mTOR is controlled by the nutrient and energy status of the cell (Wullschleger et al., 2006), mTOR inhibition indicated that energy availability might be a critical factor during cold shock. Indeed, we found that ATP levels dropped progressively during cold shock in COS7 cells (Figure 9A). After 8 hours at 10°C, ATP levels were below 60% of those in control cells, and close to the level observed after treating cells for one hour with the mitochondrial uncoupler carbonyl cyanide trifluoromethoxyphenylhydrazone (FCCP).

As the major source of ATP, mitochondria were stained with mitotracker and found to undergo prominent morphological changes in cold shocked COS7 cells. Whereas mitochondria formed an elongated tubular network under control conditions, they were arranged in circular-shaped clumps after 10 hours at 10°C (Figure 9B). These clumps did not colocalize with SGs (data not shown) and may reflect mitochondrial fragmentation. Additionally, we measured a drop in mitotracker staining by flow cytometry in cold shocked cells (Figure 9C). Since mitotracker retention depends on the mitochondrial membrane potential, this suggested that hypothermia causes reduced mitochondrial function.

When ATP levels inside the cell are low, the AMP:ATP ratio rises and stimulates AMPK, whereby its α subunit becomes phosphorylated at threonine 172 (Hardie, 2007). AMPK in turn phosphorylates numerous proteins and thereby orchestrates cellular responses to reduced energy supply. Consistent with reduced ATP levels, we observed strong activation of AMPK in COS7 cells in response to cold shock (Figure 9D). During recovery from cold shock, AMPK was dephosphorylated 15–30 minutes after returning cells to 37°C (Figure 9E), which is after SG disassembly (Figure 4B) yet before eIF2α dephosphorylation (Figure 5C) and full resumption of translation (Figure 4C).

**AMPK inhibition prevents SG formation and attenuates translation repression**

To further address the role of AMPK, we made use of compound C, a cell-permeable inhibitor of AMPK (Zhou et al., 2001). Treatment of COS7 cells with compound C reduced phosphorylation of raptor, an AMPK target and integral component of the TOR complex 1 (TORC1), at both 37°C and 10°C (Supplemental Figure S8A). We found that compound C prevented the formation of SGs at both 4 and 8 hours of cold shock (Figure 10A). Likewise, compound C attenuated cold shock-induced translation
repression (Figure 10B and C). Quantification of the polysome profiles revealed that compound C causes a more than two-fold increase in polysomal ribosomes after both 4 and 8 hours of 10°C cold shock (Figure 10D). These data suggested that activation of AMPK during cold shock contributes to translation suppression. To validate these results, we analyzed MEFs lacking both isoforms of the catalytic α subunit of AMPK (Laderoute et al., 2006) and found a subtle de-repression of translation in these cells (Supplemental Figure S8B). The difference between wt and AMPKα1+2 ko MEFs was weaker than the effect of compound C, suggesting that compound C might exert its effect not only through AMPK inhibition.

Since the kinase Src is also supposed to be inhibited by compound C (Bain et al., 2007), we tested whether a different antagonist, Src inhibitor-1, would affect SG formation as well. Indeed, we found that cold shock-induced SGs were strongly reduced in cells treated with Src inhibitor-1 (Figure 10E). Taken together, these results suggested that different targets of compound C, including AMPK and Src kinase, contribute to translation repression and SG formation in response to cold shock.

SG formation and translation repression are linked to cellular survival during cold shock

Finally, we tested whether formation of SGs and translation arrest are important for cellular survival under cold shock conditions. COS7 cells tolerate hypothermia surprisingly well with less than 10% of damaged or dead cells even after 10 hours of a 10°C cold shock (Figure 10F). In stark contrast, cells showed massive cell death when exposed to the same cold shock in the presence of compound C or Src inhibitor-1, resulting in 86% or 82% dead cells, respectively. Under 37°C control conditions, 10 hours of treatment with compound C or Src inhibitor-1 augmented the percentage of damaged or dead cells only minimally from 4 to 7%. Importantly, the lethal effect of compound C during cold shock was antagonized by simultaneous inhibition of translation with cycloheximide or puromycin (Figure 10G). As expected for a translation elongation inhibitor that prevents ribosome release, cycloheximide blocked the assembly of SGs under cold shock conditions (Supplemental Figure S9). Taken together, these results demonstrate that translation arrest is essential for cellular survival under conditions of cold shock.

DISCUSSION

In this report, we describe an essential stress response pathway by which cells adapt to cold conditions through the repression of global protein synthesis and subsequent formation of SGs. Adaptation to low temperatures is physiologically important to all poikilotherm organisms, which need to adjust their metabolism to ambient temperature. Moreover, the body temperature in some small hibernating mammals drops to 2–10°C (Carey et al., 2003), the range in which we observed translation repression and SG formation. Indeed, translation is strongly attenuated in hibernating animals, and loss of polysomes was observed in corresponding tissue extracts (Carey et al., 2003). AMPK activation also occurs in hibernating animals (Horman et al., 2005), suggesting that the regulatory response we describe at the cellular level might apply to the biology of hibernation. Even in non-hibernating mammals, the skin temperature in extremities can drop below 10°C upon exposure to cold (Heus et al., 1995). In the medical context, cold storage at 4°C is the routine method to preserve organs before transplantation and reduce reperfusion damage. Besides inhibiting tissue-degrading enzymes, there is evidence that AMPK activation contributes to the beneficial effects of cold organ storage (Bouma et al., 2010).
Our study identified cold shock as a novel, evolutionary conserved inducer of SGs in mammalian cells and in yeast. These SGs contain all characteristic components including poly(A)-mRNA, PABP/Pab1 and TIA1/Pub1, and, in mammalian cells, eIF2α, eIF3B and eIF4G (Figures 1 and 2). Cold shock-induced SGs appear only after keeping cells for several hours at low temperatures, yet dissolve very rapidly within minutes of return to optimal growth temperatures (Figures 3 and 4). This is in stark contrast to heat shock or arsenite-induced oxidative stress, where SGs appear after 15–30 minutes, but take 30–90 minutes to disassemble when the stressor is removed (Kedersha et al., 1999; Kedersha et al., 2000). Given that ATP levels drop slowly (Figure 9) and polysomes disassemble progressively during cold shock (Figure 1), it is plausible that the threshold for SG formation is met only after several hours at low temperature. Rapid SG resolution may reflect the fact that nucleic acids and proteins are well preserved in the cold, and that enzymatic activities will increase instantly upon temperature upshift. In contrast, biomolecules suffer considerable damage during oxidative stress or heat shock, where recovery requires repair processes or de novo synthesis, and therefore takes longer.

Our analysis points towards several mechanisms that suppress translation under cold shock conditions (Figure 11). First, every enzymatic process is temperature-dependent, which implies that cold shock will force cellular enzymes, including those involved in translation, to work below their temperature optimum. Second, ATP levels drop during cold shock, presumably because of compromised mitochondrial function (Figure 9). Since protein synthesis is considered to be the single most energy consuming process in the cell, using 22–30% of the cellular energy (Buttgereit and Brand, 1995; Choo et al., 2010), it is particularly sensitive to ATP availability. Importantly, passive mechanisms are not alone responsible for cold shock-induced translation repression. Our findings (I) that cold shock causes eIF2α phosphorylation in a PERK-dependent manner (Figure 5), (II) that the mTOR pathway is inhibited (Figure 8) and (III) that an AMPK inhibitor interferes with translation suppression (Figure 10) demonstrate participation of active mechanisms. While PERK is well established as an ER stress-responsive kinase (Harding et al., 1999), it also activated by hypoxia (Koumenis et al., 2002). Since the secretory pathway is particularly sensitive to low temperatures (Saraste et al., 1986), we speculate that proteins accumulate in the ER and cause activation of PERK under cold shock conditions. The involvement of both eIF2α and TORC1 would further explain why interfering with either of the two pathways in the PERK ko MEFs (Figure 5), the eIF2α-AA knock-in MEFs (Figure 6) or the 4EBP1+2 ko MEFs (Figure 8) did not affect translation suppression during cold shock. AMPK was proposed to activate eEF2 kinase and thereby inhibit translation elongation (Horman et al., 2002), which may add to the redundancy of mechanisms suppressing translation at low temperatures.

Our results indicate that the cold shock response serves to adjust cellular energy consumption. By actively reducing the rate of translation, cells are able to save ATP and thereby improve their capacity to survive. In line with this idea, pharmacological inhibition of AMPK and Src kinase caused massive cell death during cold shock (Figure 10). Importantly, blocking translation with cycloheximide or puromycin strongly reduced the lethal effect of compound C. Under glucose starvation, translation inhibitors were also found to enhance survival by reducing ATP consumption (Choo et al., 2010).

We further noticed that cell death induced by compound C and Src inhibitor-1 at 10°C correlated with lack of SG formation (Figure 10), which may suggest that SGs play a role in cell survival. Indeed, SGs were previously found to serve an anti-apoptotic
function by sequestering RACK1 after DNA damage, which prevents RACK1 from activating the pro-apoptotic MTK1 kinase (Arimoto et al., 2008). Under cold shock conditions, however, cycloheximide treatment did not only save cells from compound C-induced cell death, but also prevented the assembly of SGs (Supplemental Figure S9). We concluded that cold shock-induced SGs are not required for survival, whereas translation suppression is critical for cells to adapt their energy metabolism and ensure survival under conditions of low temperatures.

MATERIALS AND METHODS

Yeast strains and culture

*S. cerevisiae* strains used in this study are listed in Supplemental Table S1. Standard yeast genetic techniques were applied throughout this study. Genomic tagging with mCherry and yEGFP was carried out as described (Janke et al., 2004), and transformations were performed using the lithium acetate method (Schiestl and Gietz, 1989). For all experiments, cells were grown to OD$_{600}$ 0.4–0.6 in synthetic complete dextrose (SCD) medium containing 2% glucose at 30°C. To induce cold shock, cells were harvested by centrifugation, resuspended in fresh, ice-cold medium and incubated on ice with continuous shaking for different time periods. For recovery experiments, cells were directly transferred from ice to a shaking waterbath prewarmed to 30°C. For glucose depletion experiments, cells were grown to exponential phase, filtered using a vacuum pump, washed and resuspended in in SC medium lacking glucose, and incubated at 30°C for 10 min. For recovery experiments, glucose was added to starved cells to a final concentration of 2%.

Mammalian cell culture

HeLa, Huh7 and COS7 cells as well as MEFs were cultured in Dulbecco’s Modified Eagle Medium (DMEM) containing 10% fetal bovine serum (PAA Laboratories), 2 mM L-glutamine, 100 U/ml penicillin and 0.1 mg/ml streptomycin (all PAN Biotech) at 37°C in 5% CO$_2$. DU145 cells were maintained in RPMI 1640 medium supplemented with 10% FBS, L-glutamine, penicillin and streptomycin. eIF2α-SS and -AA MEFs (Scheuner et al., 2001) were a kind gift from R.J. Kaufman (Ann Arbor, Michigan, USA). 4EBP1+2 ko MEFs (Dowling et al., 2010) were kindly provided by Nahum Sonenberg (Montreal, Canada), AMPKα1+2 ko MEFs (Laderoute et al., 2006) were a kind gift from Benoit Viollet (Paris, France), and PERK ko MEFs (Harding et al., 2003) were kindly provided by David Ron (New York, USA). Plasmid pSRα-HA-GFP-PABP (p2024) has been described previously (Kedersha et al., 2000), and was transfected into COS7 cells using polyethyleneimine (Polysciences Europe, 1 mg/ml, pH 7.0). Cells were replated onto glass coverslips 12 hours prior to cold shock.

IF microscopy

Mammalian cells were grown on glass coverslips, and fixed at 4°C in 4% paraformaldehyde for 10 minutes before cell membranes were permeabilized in -20°C cold methanol for 10 minutes. Phosphate buffered saline (PBS) containing 0.1% sodium-azide and 5% horse serum was used for blocking and antibody dilution. Cy3- or Cy2-conjugated secondary donkey antibodies (Jackson Immunoresearch) were used for detection of primary antibodies. Cells were mounted onto glass slides using a solution of 14% polyvinol-alcohol (P8136, Sigma) and 30% glycerol in PBS. SGs were counted on an upright epi-fluorescence microscope (BX60, Olympus). Images were acquired at the Nikon Imaging Center, Heidelberg, on an upright epi-
fluorescence microscope (90i, Nikon) using an EM-CCD camera (Hamamatsu) and at the Imaging Facility of the ZMBH using the Olympus Xcellence Pointfrap microscope and a Hamamatsu Orca-R2 camera.
Yeast cells were grown at 30°C, centrifuged at room temperature, resuspended in ice-cold SCD and incubated in ice water for indicated time periods. Cells were fixed with 4% paraformaldehyde/PBS pH 6.5 for 15 minutes on ice. Before microscopy, cells were washed 3x with PBS pH 6.5. To visualize the entire cell volume, optical sections at a distance of 0.2 µm were acquired on a spinning disc confocal microscope (Ultraview ERS, Perkin Elmer, on a TE2000 inverted microscope, Nikon) equipped with an EM-CCD camera (Hamamatsu) at the Nikon Imaging Center, Heidelberg. The entire stack was used for deconvolution using Huygens Software (Scientific Volume Imaging, Netherlands). A maximum intensity projection of three optical sections was generated for image representation, and contrast was enhanced using imageJ software. For quantitative analysis, single plane images were acquired and normalized to the exposure time.

Automated image analysis
An algorithm to calculate cell number, cell area, signal intensity within the cell, number of aggregates, area of aggregates and signal intensity within aggregates from micrographs of *S. cerevisiae* was written in Matlab software. Images were first normalized according to exposure times before cell and nuclear boundaries were determined. For the detection of aggregates in the cytoplasm, the local baseline fluorescence for each pixel within cells was calculated using opening by reconstruction, and aggregates were defined as pixels at which the fluorescence increase is greater than 0.75 times the local baseline. The algorithm is available upon request.

Fluorescence *in situ* hybridization (FISH)
Yeast spheroplasts were prepared as described previously (Finger et al., 1993), spotted onto poly(L-lysine)-coated glass slides and stored in 70% ethanol at -20°C. Acetylation was performed according to (Schwab et al., 1998). Briefly, the cells were washed once with 0.1 M triethanolamin pH 8.0, incubated in 0.1 M triethanolamine/0.25% acetic anhydride for 10 minutes and washed with PBS and 2xSSC. Hybridization with Alexa488-conjugated oligo(dT)50 (Invitrogen) was performed over night at 37°C in hybridization buffer containing 20% formamide, 2xSSC, 0.1% Triton X-100, 2% blocking reagent (Roche) and 10% dextran sulphate. After sequential washes with 2xSSC, 0.2xSSC and PBS, samples were incubated for 1 hour at room temperature in blocking buffer containing 1% blocking solution and 0.1% Triton X-100 in PBS. Cells were incubated with α-myc antibody (9E10, Roche, 1:500) over night at 4°C in blocking buffer, and further stained with 2 µg/ml Hoechst 33422 dye and Cy3-labeled secondary antibody diluted 1:500 in blocking buffer for 1 hour at room temperature. Finally, cells were mounted in PBS containing 12.5% polyvinyl alcohol (Sigma), 25% glycerol and 0.25% sodium azide.
Mammalian cells were fixed as described for IF, washed in 2x SSC and incubated in a 1:5,000 dilution of Alexa555-coupled oligo(dT)50 probe (100 pmol/µl, Invitrogen) in hybridization buffer (1 mg/ml yeast RNA, 20% formamide, 2 mg/ml BSA, 0.1 g/ml dextrane sulphate, 1x SSC) for 1 hour at room temperature. Cells were then washed 3x in 2x SSC at room temperature before mounting.
Mitotracker staining
Cells were subjected to cold shock at 10°C for 10 hours or kept under control conditions. 1 hour before the end of the treatment, 0.1 µM Mitotracker Orange CM-H$_2$TMRos (Molecular Probes) was added to the cell culture. Cells were then collected by trypsinization and centrifugation, resuspended in PBS containing 2% fetal bovine serum and analyzed on a FACSCanto II (Becton Dickinson) flow cytometer using Flowjo software. For microscopy, cells were grown on glass coverslips, stained with mitotracker as above, and fixed with 4% paraformaldehyde and -20°C methanol. Images were taken with a Leica DM5000B epi-fluorescence microscope and a CCD-camera (Andor).

Western blot analysis
Cells were lysed in SDS sample buffer with 100 mM DTT. Proteins were resolved on 5-20% polyacrylamide gradient Tris-glycine gels and transferred onto 0.2 µm pore size nitrocellulose membrane (Piqlab) for Western blotting. Membranes were then blocked in 5% horse serum in PBS containing 0.1% sodium azide, incubated with antibodies diluted in the same solution, and washed in 150 mM NaCl, 50 mM Tris pH 7.5, 1% Tween-20. Horseradish peroxidase-coupled secondary antibodies (Jackson Immunoresearch) in combination with Western Lightning enhanced chemiluminescence substrate (Perkin Elmer) were used for detection.

Antibodies
The following antibodies were used for Western blot and IF: Mouse monoclonal antibodies against G3BP1 (TT-Y, sc-81940, Santa Cruz) and eIF2α (ab5369, Abcam); polyclonal rabbit antibodies against phospho(S51)-eIF2α (KAP-CP131, Stressgen), eIF4G1 (#2498, Cell Signaling), monoclonal rabbit phospho(T172)-AMPK (40H9, #2535, Cell Signaling), phospho(S792)-raptor (#2083, Cell Signaling); monoclonal rabbit antibodies against AMPKα (23A3, #2603, Cell Signaling), 4EBP1 (53H11, #9644, Cell Signaling), phospho(T37/46)-4EBP1 (#2855, Cell Signaling), and raptor (#2280, Cell Signaling); polyclonal goat antibody against eIF3B (sc-16377, Santa Cruz); and rat monoclonal antibody against α-tubulin (ab6160, Abcam).

Polysome analysis
Mammalian cells were treated with Na-arsenite (500 µM, 1 hour), rapamycin (0.2 µM, 1 hour) or DTT (2 mM, 1 hour), or were exposed to cold shock either in the absence of presence of compound C (20 µM) for the times indicated. Prior to lysis, 100 µg/ml cycloheximide (Sigma) was added to cells for 5 minutes, and cells were washed with cold PBS containing 100 µg/ml cycloheximide. Cells were harvested by scraping and lysed in 0.2 ml lysis buffer containing 15 mM Tris pH 7.4, 15 mM MgCl$_2$, 300 mM NaCl, 1% Triton X-100, 100 µg/ml cycloheximide, 500 µg/ml heparin, 0.2 U/ml RNasin (Promega), 0.1% 2-mercaptoethanol, and EDTA-free protease inhibitor (Roche). Lysates were cleared by centrifugation at 10,000 rpm for 10 min at 4°C. Supernatants were loaded onto linear gradients of 17.5% - 50% sucrose in 15 mM Tris, pH 7.4, 15 mM MgCl$_2$, 300 mM NaCl; and centrifuged in a SW60 rotor at 35,000 rpm for 2.5 hours at 4°C. Fractions were eluted from the top of the gradient using a Teledyne ISCO gradient elution system; polysome profiles were obtained by measuring absorbance at 254 nm.
Yeast cultures were treated with 100 µg/ml cycloheximide on ice for 5 min, collected by centrifugation, washed once with ice-cold dH$_2$O and resuspended in ice-cold yeast
polysome lysis buffer (20 mM HEPES pH 7.5, 50 mM KCl, 10 mM MgCl₂, 300 mM NaCl, 1% TritonX-100, protease inhibitor cocktail (Roche), 1 mM PMSF, 1 mM DTT, 100 μg/ml cycloheximide and 50 U/ml Superasein (Ambion)). Cell suspensions were then frozen in drops in liquid nitrogen and pulverized by mixer milling (Retsch MM400). Lysates were clarified by centrifugation at 14,000 g for 10 minutes, and the amount corresponding to 1 mg of total RNA was loaded on 7% - 47% sucrose gradients. Gradients were centrifuged in a SW40 rotor at 35,000 rpm for 2.5 hrs and processed as described for mammalian cells. For quantification, empty gradients were recorded with the same settings. Normalization was carried out by subtracting “empty gradient” values from “sample gradient” values, and the areas under the curve corresponding to the amount of polysomal and total ribosomes were determined by integration. Polysomal ribosomes were divided by total ribosomes as a measure for the translation rate.

**Polysome fractionation**

Huh7 cells were kept under control conditions at 37°C or exposed to cold shock at 10°C for 10 hours. Prior to lysis, cells were treated with 100 μg/ml cycloheximide for 5 minutes, washed with cold PBS containing 100 μg/ml cycloheximide, harvested by scraping and lysed in 0.2 ml lysis buffer containing 10 mM HEPES, 2.5 mM MgCl₂, 62.5 mM KCl, 1% NP-40, 100 μg/ml cycloheximide, 500 μg/ml heparin, 0.2 U/ml RNAsin, 1 mM DTT, and EDTA-free protease inhibitor (Roche). Lysates were cleared by centrifugation at 10,000 rpm for 10 minutes at 4°C and subjected to sucrose density gradient centrifugation as described above. After fractionation, proteins were precipitated using acetone and resuspended in SDS sample buffer.

**35S-Methionine/Cysteine labelling**

COS7 cells were seeded 8–12 hours prior to incubation in methionine- and cysteine-free DME medium supplemented with 5% fetal bovine serum (PAA Laboratories), 2 mM L-glutamine, 100 U/ml penicillin and 0.1 mg/ml streptomycin (all PAN Biotech) for 1 hour. Then, 200 μCi of 35S-labelled methionine and cysteine (EasyTag, Perkin Elmer) was added to each dish and cells were simultaneously exposed to cold shock at 10°C or kept at 37°C for different periods of time. As a control, one dish was treated with 500 μM arsenite for 1 hour. Cells were then washed with PBS, collected, and solubilized in 150 μl lysis buffer containing 15 mM Tris pH 7.4, 15 mM MgCl₂, 300 mM NaCl and 1% Triton X-100. After centrifugation at 9,000 rpm for 3 minutes, proteins were precipitated out of the supernatants by spotting 20 μl of each lysate onto Whatman paper and soaking in 5% trichloroacetic acid followed by acetone. 35S incorporation was measured in 4 ml Econofluor-2 (Perkin Elmer) using a scintillation counter (Beckman, LS 6000IC). For normalization, the total protein concentration of each sample was determined using the BCA protein assay reagent kit (Sigma). For each sample, 100 ng total protein was resolved on a 5–20% polyacrylamide gradient Tris-glycine gel and stained using colloidal coomassie. The gel was dried at 80°C for 2 hours under vacuum and 35S incorporation into newly synthesized proteins was detected by autoradiography using a Phosphoimager (FLA-7000, Fujifilm).

**Cap pulldown assay**

Huh7 cells were seeded in 15 cm-dishes and allowed to adhere for 8–12 hours. To account for the reduced cell mass after cold shock, two dishes were subjected to 10°C cold shock for 10 hours, one was treated with 0.2 μM rapamycin for 1 hour, and one dish was kept under control conditions. Cells were lysed in 0.6 ml of cap binding
buffer containing 50 mM Tris-HCl (pH 7.0), 100 mM NaCl, 1 mM EDTA, 0.5% NP-40 and complete protease inhibitors (Roche). Lysates were cleared via centrifugation at 25,000 x g for 15 minutes at 4°C. 50 µl of 7-methyl-GTP-conjugated sepharose beads (GE Healthcare) were added to each sample. After rotation at 4°C for 2 hours, beads were washed four times in a buffer containing 15 mM Tris-HCl (pH 7.2), 100 mM NaCl, 1 mM EDTA and 0.1% NP-40. Proteins were eluted in 2x SDS sample buffer and separated on a 5-20% polyacrylamide gradient gel.

**Measurement of ATP levels**

After cold shock, cells were collected by trypsinization, and cell pellets were weighed on a fine balance before lysis in 20 mM Tris (pH 7.4), 0.1 mM EDTA, 2.67 mM MgSO4, 33.3 mM DTT. Lysates were incubated on ice for 5-10 minutes and centrifuged at 13,000 rpm for 1 minute. For ATP measurements, 20 µl of serially diluted lysates were added to 80 µl of lysis buffer containing 1 nM of firefly luciferase recombinantly expressed in *E. coli* and 500 µM luciferin. Light emission was measured with a luminometer (Lumat LB 9507, Berthold Technologies). Results were normalized to the weight of the cell pellets and calculated as percentage of control.

**Cell viability assay**

Cells were subjected to cold shock for different time periods and treated with 20 µM compound C (Calbiochem) or 20 µM Src inhibitor-1 (S2075, Sigma) where indicated. Cells were collected from the media and combined with those recovered from the dish by trypsinization, resuspended in 10 mM HEPES, pH 7.4, 150 mM NaCl, 1 mM MgCl2, 1.8 mM CaCl2 and stained for 10 minutes on ice with 50 µg/ml propidium iodide (Applichem). Propidium iodide uptake was measured by flow cytometry using a FACSCanto II (Becton Dickinson).

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FIGURE 1: Cold shock induces SGs and represses translation in mammalian cells. (A) COS7 cells were grown at 37°C or incubated at 30°C, 20°C or 10°C for 10 hours or 4°C for 8 hours. Subcellular localization of eIF3B was determined by IF staining followed by wide-field fluorescence microscopy. (B) As positive control for SG formation, cells were treated with 500 µM Na-arsenite for one hour. (C) COS7 cells exposed to cold shock were stained by FISH for poly(A) mRNA and counterstained for eIF3B by IF. (D–F) COS7 cells exposed to cold shock at 10°C for 10 hours were stained for the SG markers eIF4G (D), eIF2α (E) and G3BP (F) in combination with eIF3B. (G) COS7 cells were transiently transfected with a vector encoding GFP-PABP, exposed to cold shock and fixed. Localization of GFP-PABP was analyzed in relation to endogenous eIF3B. (H) To quantify SG formation over time, the relative number of cells containing SGs was determined. Average values ± SE from four experiments are shown. (I) COS7 cells were exposed to cold shock at 10°C or kept at 37°C for different time periods, as indicated. Newly synthesized proteins were labelled with 35S-methionine/cysteine. Cell lysates were separated on 5–20% polyacrylamide gels and stained with colloidal coomassie (lower panel) or visualized...
by autoradiography (upper panel). (J) COS7 cells were labelled as in (I), and translation rates were quantified by measuring incorporation of $^{35}$S-methionine/cysteine into precipitated protein using a scintillation counter. Counts per minute (cpm) normalized to the total amount of proteins are depicted in the graph. (K) Polysome profiles were recorded from COS7 cells either grown under control conditions at 37°C or subjected to cold shock at 10°C for up to 10 hours. To determine the percentage of polysomal ribosomes, the area below the polysomal part of the curve was divided by the area below the sub-polysomal and polysomal parts of the curve, and represented as average ± SD in the bar graph.
FIGURE 2: Cold shock induces SGs in *S. cerevisiae*. (A) A genomically tagged yeast strain expressing Pub1-GFP was grown under control conditions at 30°C or incubated at 15°C or 10°C for four hours. Subcellular localization of Pub1-GFP was analyzed by confocal microscopy. (B) Yeast was either grown under control conditions at 30°C or exposed to cold shock at 0°C for 4 and 24 hours. Localization of genomically tagged Pub1-GFP (green) and Pab1-mCherry (red) was analyzed by confocal microscopy. (C) Spheroplasts were prepared from a genomically tagged yeast strain expressing Pab1-myc after it was either grown under control conditions or exposed to cold shock at 0°C for 4 hours. Poly(A) RNA (green) was localized by FISH, and Pab1-myc (red) was visualized by IF staining. (D) The formation of SGs
over time was quantified using automated image analysis. Two parameters were measured: the number of SGs per cell and optical section (yellow bars) and the percentage of Pub1-GFP signal in SGs (brown bars). Average values ± SE from three experiments are shown.
FIGURE 3: Rapid disassembly of SGs upon recovery from cold shock in *S. cerevisiae*. (A) Cells expressing Pub1 genomically tagged with GFP were exposed to cold shock at 0°C for 4 hours and then returned to 30°C. Cells were fixed at 30 second intervals and Pub1-GFP was visualized by confocal microscopy. Four optical sections were used for deconvolution and the resulting maximum projection is depicted in the images. (B) The disassembly of yeast SGs over time was quantified using automated image analysis. Two parameters were measured: the number of SGs per cell and optical section (yellow bars) and the percentage of Pub1-GFP signal in SGs (brown bars). Average values ± SE from three experiments are shown. (C) Polysome profiles were recorded from yeast during recovery from cold shock. (D) The percentage of polysomal ribosomes was quantified as in Figure 1K, average ± SD.
FIGURE 4: Rapid disassembly of mammalian SGs upon recovery from cold shock. (A) SG disassembly was monitored in COS7 cells that were subjected to cold shock at 10°C for 10 hours and then returned to 37°C for 5, 10, 15 and 20 minutes. SGs were visualized by fluorescence wide-field microscopy after IF staining for eIF3B. (B) To quantify SG disassembly over time, the relative number of COS7 cells containing SGs was determined. Average values ± SE from four experiments are shown. (C) Polysome profiles were recorded from COS7 cells that were grown under control conditions at 37°C, or subjected to cold shock at 10°C for 10 hours and then allowed to recover at 37°C for the indicated time points. In the bar graph, the percentage of polysomal ribosomes was quantified as in Figure 1K, average ± SD.
FIGURE 5: Cold shock induces PERK-dependent eIF2α phosphorylation. (A) COS7 cells were subjected to cold shock at 10°C for up to 12 hours (lanes 1–7), and total protein lysates were analyzed by Western blotting for phospho(S51)-eIF2α and total eIF2α. α-tubulin serves as loading control. As a positive control, COS7 cells were treated for one hour with 500 µM Na-arsenite (lane 8). (B) Wild-type (eIF2α-SS) MEFs were subjected to cold shock at 10°C (lanes 1–8) and analyzed by Western blotting as in panel A. For control, eIF2α-SS and -AA MEFs were treated for one hour with 500 µM Na-arsenite (lanes 9 and 10). (C) COS7 cells were subjected to cold shock at 10°C for 10 hours and returned to 37°C. During the recovery phase, phospho(S51)-eIF2α levels were monitored as in panel A. (D) Wt and PERK ko MEFs were subjected to cold shock (CS) at 10°C for 10 hours (lanes 5 and 6) and analyzed by Western blotting as in panel A. As controls, cells were treated for one hour with 500 µM Na-arsenite (lanes 3 and 4) or 2 mM DTT (lanes 7 and 8). (E) Polysome profiles were recorded from wt and PERK ko MEFs. Cells were grown under control conditions, subjected to cold shock at 10°C for 10 hours or treated with 2 mM DTT for one hour. Polysome profiles were recorded as in Figure 1K; the bar graph shows quantification of two independent experiments.
**FIGURE 6:** Cold shock-induced translation arrest and SG formation in the absence of phospho-eIF2α in mammalian cells. (A) Polysome profiles were recorded from eIF2α-SS and -AA MEFs. Cells were grown under control conditions, treated with 500 µM Na-arsenite for one hour, or subjected to cold shock at 10°C for 10 hours. Polysomal ribosomes were quantified as in Figure 1K; average values ± SE from three independent experiments are shown in the bar graph. (B) SG formation was monitored in eIF2α-SS and -AA MEFs grown at 37°C (control), subjected to cold shock for 10 hours at 10°C or treated for one hour with 500 µM Na-arsenite. SGs were visualized by IF microscopy after staining for eIF3B. (C) The percentage of cells containing SGs was quantified; average values ± SE are based on three experiments.
FIGURE 7: Gcn2-independent translation arrest and SG formation upon cold shock in yeast. (A) Polysome profiles were recorded from wt S. cerevisae and a gcn2Δ strain. Cells were grown under control conditions or subjected to cold shock at 0°C for one and 4 hours. (B) Translation was quantified as in Figure 1K. (C) Subcellular localization of Pab1-GFP was analyzed by confocal microscopy in the gcn2Δ strain. (D) SGs were quantified in wt and gcn2Δ S. cerevisae using automated image analysis, as in Figure 2D. Average values ± SE from three experiments are shown.
FIGURE 8: Cold shock causes mTOR inhibition. (A) Huh7 cells were grown under control conditions at 37°C, subjected to 10°C cold shock for 10 hours or treated with 0.2 µM rapamycin for one hour. Cells were lysed, and the cytoplasmic fraction (input, lanes 1–3) was incubated with 7-methyl-GTP (cap) sepharose. Proteins retained by cap-sepharose (lanes 4–6) were visualized by Western blotting using antibodies against eIF4E, 4EBP1, eIF4AI, eIF3B and PABP. (B) 4EBP1+2 double ko MEFs as well as wt counterparts were grown under control conditions or subjected to 10 hours of cold shock at 10°C. Polysome profiles were recorded as in Figure 1K; the bar graph shows quantification of two independent experiments. (C) Huh 7 cells were exposed to cold shock at 10°C for 10 hours or kept under control conditions at 37°C. Cell lysates were loaded onto 17.5–50% sucrose gradients and separated by ultracentrifugation. After fractionation, protein extracts were resolved on 5–20% polyacrylamide gels. eIF4G, eIF4E, eIF4A, eIF3B, PABP and rpL7 were detected by Western blotting.
FIGURE 9: Cold shock causes energy depletion and AMPK activation. (A) COS7 cells were grown under control conditions at 37°C, subjected to cold shock at 10°C for up to 8 hours, or treated with FCCP (5 µM) for one hour. ATP levels in the cellular lysates were measured using recombinant firefly luciferase and represented as percent of control. Shown are average values ± SE from n = 7 (cold shock) or n = 4 (FCCP) independent experiments. (B) COS7 cells were grown under control conditions at 37°C or subjected to cold shock at 10°C for 10 hours. Cells were labelled with Mitotracker Orange CM-H2TMRos one hour before fixation, and analyzed by fluorescence microscopy. (C) COS7 cells were grown under control conditions at 37°C or subjected to cold shock (CS) at 10°C for 9 hours, and then labelled for one hour with Mitotracker Orange CM-H2TMRos at 10°C. The intensity of mitotracker staining was measured by flow cytometry. (D) COS7 cells were grown under control conditions at 37°C or subjected to cold shock at 10°C for up to 24 hours. Total protein lysates were analyzed by Western blotting for phospho(T172)-AMPK, total AMPK, and eIF3A as loading control. (E) COS7 cells were subjected to cold shock at 10°C for 10 hours and returned to 37°C. During the recovery phase, phospho(T172)-AMPK levels were monitored as in panel D.
FIGURE 10: AMPK and Scr kinase inhibitors attenuate SG formation, translation inhibition and cell survival during cold shock. (A) COS7 cells were subjected to cold shock at 10°C for 4 or 8 hours, and simultaneously treated with 20 µM compound C. Cells were fixed and stained for eIF3B by IF. (B and C) Polysome profiles were recorded from COS7 cells subjected to cold shock at 10°C for (B) 4 hours and (C) 8 hours, either in the absence or presence of 20 µM compound C. (D) Translation was quantified in cold shocked cells, either in the absence or presence of 20 µM compound C, by measuring the percentage of polysomal ribosomes as in Figure 1K. Average values ± SE from three experiments are shown. (E) COS7 cells were subjected to cold shock at 10°C for 8 hours, and simultaneously treated with 20 µM Src inhibitor-1. Cells were fixed and stained for eIF3B by IF. (F) Cell death was
measured by the uptake of propidium iodide in unpermeabilized cells using flow cytometry. Prior to propidium iodide staining, COS7 cells were grown under control conditions at 37°C, treated for 10 hours with 20 µM compound C or 20µM Src inhibitor-1, or subjected to cold shock at 10°C for up to 10 hours, in the absence or presence of 20 µM compound C or 20µM Src inhibitor-1. The percentage of damaged or dead, i.e. propidium iodide-positive cells is presented as average value ± SE, n = 5. 

(G) In addition to compound C (20 µM), cells were exposed to the translation inhibitor cycloheximide (CHX, 10 µg/ml) or puromycin (puro, 1 µg/ml) during the entire 10 hour cold shock. Cell death was measured as above, shown are average values ± SE, n = 6.
FIGURE 11: Mechanisms suppressing translation in mammalian cells exposed to cold shock. The model depicts parallel pathways that contribute to cold shock-induced translation suppression. Passive mechanisms include generally reduced enzymatic activities at lower temperatures and reduced mitochondrial function with consecutive drop in ATP levels. Active mechanisms include activation of AMPK, inhibition of TORC1, PERK-dependent phosphorylation of eIF2α, and may involve additional pathways. Translation suppression promotes cell survival under conditions of cold shock.