Specific SKN-1/Nrf Stress Responses to Perturbations in Translation Elongation and Proteasome Activity

Citation

Published Version
doi:10.1371/journal.pgen.1002119

Permanent link
http://nrs.harvard.edu/urn-3:HUL.InstRepos:5978684

Terms of Use
This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA

Share Your Story
The Harvard community has made this article openly available. Please share how this access benefits you. Submit a story.

Accessibility
Specific SKN-1/Nrf Stress Responses to Perturbations in Translation Elongation and Proteasome Activity

Xuan Li1,2,3, Olli Matilainen4, Congyu Jin4, Kira M. Glover-Cutter1,2, Carina I. Holmberg4*, T. Keith Blackwell1,2*

1 Joslin Diabetes Center, Harvard Stem Cell Institute, Harvard Medical School, Boston, Massachusetts, United States of America, 2 Department of Genetics, Harvard Medical School, Boston, Massachusetts, United States of America, 3 College of Life Science and Technology, Huazhong University of Science and Technology, Wuhan, China, 4 Research Programs Unit, Molecular Cancer Biology, and Institute of Biomedicine, Biomedicum Helsinki, University of Helsinki, Helsinki, Finland

Abstract

SKN-1, the Caenorhabditis elegans Nrf1/2/3 ortholog, promotes both oxidative stress resistance and longevity. SKN-1 responds to oxidative stress by upregulating genes that detoxify and defend against free radicals and other reactive molecules, a SKN-1/Nrf function that is both well-known and conserved. Here we show that SKN-1 has a broader and more complex role in maintaining cellular stress defenses. SKN-1 sustains expression and activity of the ubiquitin-proteasome system (UPS) and coordinates specific protective responses to perturbations in protein synthesis or degradation through the UPS. If translation initiation or elongation is impaired, SKN-1 upregulates overlapping sets of cytoprotective genes and increases stress resistance. When proteasome gene expression and activity are blocked, SKN-1 activates multiple classes of proteasome subunit genes in a compensatory response. SKN-1 thereby maintains UPS activity in the intestine in vivo under normal conditions and promotes survival when the proteasome is inhibited. In contrast, when translation elongation is impaired, SKN-1 does not upregulate proteasome genes, and UPS activity is then reduced. This indicates that UPS activity depends upon presence of an intact translation elongation apparatus; and it supports a model, suggested by genetic and biochemical studies in yeast, that protein synthesis and degradation may be coupled processes. SKN-1 therefore has a critical tissue-specific function in increasing proteasome gene expression and UPS activity under normal conditions, as well as when the UPS system is stressed, but mounts distinct responses when protein synthesis is perturbed. The specificity of these SKN-1-mediated stress responses, along with the apparent coordination between UPS and translation elongation activity, may promote protein homeostasis under stress or disease conditions. The data suggest that SKN-1 may increase longevity, not only through its well-documented role in boosting stress resistance, but also through contributing to protein homeostasis.

Introduction

Maintenance of protein homeostasis is critical for organismal health, and protection against environmental challenges. Protein homeostasis depends upon the balance among the processes of protein synthesis, folding, and degradation. Disruptions in this balance result in accumulation of abnormal proteins, which over time leads to deterioration of cellular functions, and ultimately to cell death [1,2]. Imbalances in proteostasis are central to progression of numerous disorders, including some cancers, neurodegenerative and alcoholic liver disease, and type 2 diabetes [3,4].

Most intracellular proteolysis is mediated by the 26S proteasome, a multicatalytic protease that degrades polyubiquitinated proteins [5]. The ubiquitin-proteasome system (UPS) regulates the stability of proteins involved in a wide range of cellular processes [6]. The 26S proteasome is composed of two subcomplexes: a barrel-shaped 20S catalytic core structure, and a 19S regulatory particle that caps it at either or both ends. The 19S regulatory particle facilitates the entry of polyubiquitinated proteins, and is composed of base and lid subcomplexes [6,7]. It is a major challenge to understand how the levels and activity of the proteasome are regulated to maintain the balance of protein synthesis and degradation.

Several lines of evidence indicate that the proteasome associates with the mRNA translation machinery, and that the processes of protein synthesis and degradation may be linked. Proteins are synthesized through the steps of translation initiation, elongation, and termination. The elongation cycle adds amino acids to a growing polypeptide chain, and requires a set of translation elongation factors (TEFs) (Figure S1; Table S1). The elongation process is regulated through phosphorylation of TEFs in response to growth and nutrient availability signals [8]. In addition, some TEFs are involved in functions besides translation. The elongation factor eEF1A binds to proteasome subunits and ubiquitinated proteins, and thereby seems to promote degradation of damaged nascent proteins [7,9–11]. Given that up to 30% of nascent polypeptides may be degraded cotranslationally [12,13], this
The mechanisms through which organisms defend against environmental stresses are critical during diverse disease processes and are likely to be important for longevity. The nematode *C. elegans* is advantageous for genetic analysis of how stress defenses function and contribute to survival. The evolutionarily conserved *C. elegans* protein SKN-1 promotes stress resistance and longevity, and it defends against toxic small molecules. We now report that in certain tissues SKN-1 also maintains production of the proteasome, a structure that degrades proteins in a regulated fashion. SKN-1 mounts distinct stress responses to perturbations in protein synthesis and degradation, in which it boosts proteasome levels only in response to proteasome impairment. Remarkably, proteasome activity also depends upon the proper functioning of the proteasome synthesis apparatus. The specificity of SKN-1 stress responses may be important for protein homeostasis, allowing SKN-1 to maintain levels and activity of the proteasomal degradation apparatus, but not increase degradation when protein synthesis is impaired. This role of SKN-1 in regulating protein turnover may be important for many of its stress defense functions and for protection against disease and aging.

**Results**

Induction of distinct SKN-1–mediated stress responses by inhibition of translation initiation or elongation

To investigate whether SKN-1 activity is generally influenced by translation elongation, we performed RNAi against 5 of the 7 predicted *C. elegans* TEFs (Table S1). We first monitored expression of a transgene in which the promoter for the SKN-1 target gene gcs-1 (γ-glutamyl cysteine synthetase) is fused to green fluorescent protein (GFP) (Figure S2A) [24]. RNAi against each TEF upregulated gcs-1::GFP in the anterior intestine (Figure 1A) and increased expression of endogenous gcs-1 mRNA (Figure 1B). Mutation of an important SKN-1 binding site (Figure S2A) [24] diminished gcs-1 promoter induction (Figure S2B), and upregulation of endogenous gcs-1 mRNA was eliminated in a *skn-1* mutant (Figure 1C), indicating that SKN-1 was required for gcs-1 induction in response to TEF RNAi.

We next investigated how TEF knockdown influences expression of other SKN-1 target genes. The SKN-1-dependent genes atf-5 and haf-7 [20,23] were upregulated in a manner that was either partially or completely dependent upon *skn-1* (Figure 1B and Figure S2C). In contrast, the SKN-1 targets gst-4, gst-10 and *F20D6.11* were generally not induced in response to TEF RNAi (Figure 1D and Figure S2D). This was surprising, because *gst-4* is upregulated by SKN-1 under normal conditions, in response to various stresses, and after inhibition of insulin-like signaling (IIS) or translation initiation [20,23,25–27]. Similarly, *gst-10* and *F20D6.11* are induced by SKN-1 in response to reduced IIS and TIF RNAi, respectively [23,25]. We further compared effects of translation initiation and elongation by analyzing animals subjected to RNAi against the TIFs *tfg-1* (eIF4G), *eif-1* (eIF-1) and *eif-1.4* (eIF-1A). In contrast to the effects of TEF RNAi, RNAi against these TIFs consistently upregulated endogenous *gst-4* and *gst-10*, along with *gcs-1* and *atf-5* (Figure 1E and Figure S2D). Taken together, our data indicate that SKN-1 upregulates overlapping but distinct sets of target genes in response to inhibition of translation initiation or elongation.

Cycloheximide (CHX) blocks translation elongation by competing with the binding of ATP to the 60S ribosomal subunit, and inhibiting eEF2-mediated translocation (Figure S1) [28]. Treatment with CHX generally mimicked the effects of TEF RNAi on SKN-1 target gene expression, except that *F20D6.11* was also upregulated (Figure 1B and 1D). This suggests that a SKN-1-dependent stress...
response is induced by inhibition of the translation elongation process per se, not simply by a lack of TEFs.

We next investigated how TEF knockdown influences the levels of SKN-1 in intestinal nuclei. A transgenic protein that includes two SKN-1 isoforms fused to GFP (SKN-1 B/C::GFP) readily accumulates in intestinal nuclei in response to various stresses, or reductions in IIS [24–26]. TEF knockdown also dramatically increased SKN-1 accumulation in intestinal nuclei, without upregulating endogenous skn-1 transcripts, indicating that elongation inhibition increases SKN-1 nuclear accumulation post-transcriptionally (Figure 1F, Figure S2E and S2F). In striking contrast, TIF RNAi does not detectably increase the overall levels of nuclear SKN-1 [23]. TIF inhibition therefore appears to upregulate SKN-1 target genes through a different mechanism, and may act on processes that cooperate with SKN-1 but do not influence its nuclear accumulation.

The evolutionarily conserved p38 mitogen-activated protein kinase (MAPK) signaling pathway is required for oxidative stress to induce SKN-1 nuclear accumulation and target gene activation [29]. The activity of this pathway can be assessed in C. elegans by Western blotting for the dually phosphorylated, active form of p38 kinase [29,30]. We observed that both TEF RNAi and CHX
treatment dramatically elevated the levels of phospho-p38 (Figure 1G). This signal and gsr-1 promoter induction were markedly reduced in the MAPKK and MAPKKK null mutants sek-1(lem4) and nyr-1(ok393) respectively, indicating that the canonical p38 pathway was required (Figure S2G and S2B, respectively). With the exception of eif-1, RNAi against TIFs did not robustly activate sek-1-dependent p38 MAPK activity, further supporting the idea that TIFs and TEFs influence SKN-1 activity largely through distinct mechanisms (Figure S2H).

Impaired translation elongation does not induce stress defenses non-specifically

It is an important question whether the SKN-1-mediated response to reduced translation elongation might derive simply from a non-specific activation of multiple stress defenses. To test this idea, we investigated how other stress responses involved in protein homeostasis are influenced by TEF RNAi. An accumulation of misfolded proteins in the endoplasmic reticulum (ER) or mitochondria triggers the ER unfolded protein response (UPRer), or mitochondrial UPR (UPRmt), respectively. To investigate whether the UPRer or UPRmt is activated in response to inhibition of TEF RNAi, we examined transcriptional levels of hsp-4, hsp-60, and hsp-70, an indicator of the UPRer [31], along with the UPRmt indicators hsp-16.2, hsp-20, and hsp-60 [32]. In general, TEF RNAi did not robustly increase the levels of hsp-4, hsp-60, or hsp-60 mRNAs (Figure 2A and 2B). Heat shock proteins (HSPs) act as chaperones that cope with misfolded cytoplasmic proteins during multiple stresses. As an indicator of effects on this network, we assayed for induction of genes representing four major classes of heat shock proteins: small HSPs (hsp-16.2), DnaJ/HSP40s (grp-19, grp-12), Hsc/HSP70s (hsc-70), and HSP90s (T05E11.3, daf-21) [33]. These HSP genes were also not upregulated in response to inhibition of most TEFs (Figure 2C, Figure S3A and S3B). Taken together, the data indicate that RNAi against TEFs does not broadly activate stress responses involved in proteostasis.

In *C. elegans*, interference with translation initiation or elongation decreases brood size (Figure S3C) [34–36], raising the concern of whether the activation of SKN-1 that results from TEF RNAi might derive in part from reduction in germline proliferation. Interference with germ cell proliferation stimulates translocation of the transcription factor DAF-16/FOXO into intestinal nuclei, resulting in increased DAF-16 target gene expression and a daf-16-dependent increase in longevity [37,38]. In contrast, TEF RNAI only minimally affected either DAF-16 nuclear levels, or expression of the DAF-16 target sod-3 (Figure S3D and S3E). Interference with germ cell proliferation also dramatically upregulated expression of the SKN-1 target gfp-4 (Blackwell lab, unpublished), which is not induced by TEF RNAI (Figure 1D and Figure S2D). Together, these results suggest that the effects of translation elongation inhibition on SKN-1 activity do not derive from either a non-specific stress response, or indirect effects mediated by the germline.

**SKN-1 increases stress resistance in response to reduced translation elongation**

RNAi against TIF or ribosomal protein genes increases resistance to various environmental stresses [23,34–36]. We therefore examined whether TEF knockdown affects resistance to two different sources of oxidative stress, the organic hydroperoxide tert-butyl hydrogen peroxide (TBHP), and the metalloid sodium arsenite [As] [20]. TBHP resistance was dramatically increased after knockdown of multiple TEFs in wild type animals (Figure 3A; Table S2). In contrast, RNAi against eef-2 or eef-1G did not robustly increase oxidative stress resistance in *skn-1*(wa135) mutants, indicating that *skn-1* is essential for the TBHP resistance that derives from TEF knockdown (Figure 3B; Table S3). TEF inhibition also increased resistance to As (Figure 3C; Table S4). We conclude that the SKN-1-mediated transcriptional response to impaired translation elongation increases oxidative stress resistance.

**C. elegans** lifespan is increased by mutation or adulthood knockdown of several TIFs, ribosomal proteins, or other translation regulators [23,34,35]. TIF and TEF mRNAs are expressed at lower levels in the long-lived IIS mutant daf-2, also consistent with an opposing correlation between protein synthesis and longevity [39]. However, when we performed TEF RNAi by feeding during adulthood, lifespan was increased slightly by knockdown of *efg-1A*, *efg-1B* and *efg-2*, but not by *efg-1A* or *efg-1G* (Figure 3D; Table S5A; Figure S3F; Table S5B). This failure of TEF RNAi to increase lifespan robustly could arise from TEF RNAi having more pleiotropic effects on the animal than TIF knockdown, or could be related to the differences in gene expression responses that result from interference with translation elongation and initiation.

**SKN-1 mediates a proteasome bounce-back response and maintains UPS activity tissue-specifically in vivo**

For multiple reasons, we examined the involvement of SKN-1 in proteasome gene regulation and activity. Firstly, our microarray-based expression profiling suggested that SKN-1 contributes to transcription of 14 proteasome subunit genes (44% of the apparent total), under both normal and oxidative stress conditions [20]. Secondly, a transgenic SKN-1::GFP fusion protein was detected with high confidence at the promoter regions of 25 proteasome genes (78% of the apparent total) during the L1 larval stage [22]. These included all of the proteasome genes that expression profiling suggested are regulated by SKN-1, with only a single exception (*ppt-5*). In addition, some SKN-1 target genes are induced by RNAi knockdown of proteasome genes [23,26,27]. Finally, as suppression of translation elongation might increase the fraction of incompletely translated proteins, it seemed possible that SKN-1 might increase proteasome gene expression and activity in response to interference with translation elongation.

We first investigated the extent to which *skn-1* is required for proteasome gene expression under normal conditions. The 26S proteasome consists of at least 32 subunits in *C. elegans*, including 19S ATPases involved in substrate unfolding (*ppt-1*–*6*), other 19S subunits (*rpm-1*–*12*), 20S α-rings (*pas-1*–*7*) and 20S β-rings (*pbs-1*–*7*) [11]. We examined how *skn-1* RNAi affected the expression of the endogenous proteasome subunit genes *rpm-3*, *rpm-12*, *pas-4* and *pbs-6*, which represent the four subunit classes above. Each of these genes is a predicted SKN-1 target at which at least four canonical SKN-1 binding sites lie within 1 kb upstream of the translation initiation codon, and SKN-1::GFP was detected by ChIP [20,22] (data not shown). In whole animals *skn-1* RNAi slightly decreased the expression of each gene, except for *rpm-3* (Figure 4A). We also examined expression of transcriptional reporters in which proteasome promoters are fused to GFP. RNAi against *skn-1* slightly decreased expression of reporters for *rpm-5*, *rpm-11* and *pas-5*, particularly in the intestine, but did not detectably affect *rpm-2* or *pbs-4* (Figure 4B and 4C, Figure S4A and S4B, Table S6). The data suggest that under normal conditions SKN-1 contributes to but is apparently not essential for the expression of many proteasome subunit genes.

In mammalian cells, Nrf1 and Nrf2 have been implicated in the “bounce-back” response whereby inhibition of the proteasome results in a compensatory upregulation of proteasome subunit gene expression [17–19]. To test this model in *C. elegans* tissues in vivo,
we blocked proteasome activity by performing RNAi against an essential proteasome subunit gene, then examined expression of other proteasome genes. Knockdown of pas-5 or rpn-2 resulted in dramatic upregulation of the pbs-4, rpt-5 and rpn-11 transcriptional reporters, as well as an RPN-11::GFP translational fusion protein (Figure 4C, Figure S4A and S4B, Table S6). These increases in proteasome gene expression were largely dependent upon skn-1 in the intestine, where SKN-1 is prominently expressed [24], as well as in some muscles. Additionally, pas-5 or rpn-2 knockdown increased endogenous proteasome subunit mRNA levels in a

**Figure 2. TEF inhibition does not globally induce stress responses.** In (A–C), Relative levels of the indicated endogenous mRNAs were assayed by qRT-PCR after RNAi against the indicated TEF, or CHX treatment. N = not significant. In (A), all other *P*<0.025; in (B), all other *P*<0.05; in (C), all other *P*<0.02.
doi:10.1371/journal.pgen.1002119.g002
SKN-1-dependent manner (Figure 4D). In certain tissues, therefore, SKN-1 is required in vivo for the compensatory induction of proteasome gene upregulation that occurs in response to proteasome inhibition.

As our data suggested that skn-1 contributes to proteasome gene expression, particularly when proteasome activity is impaired, we used a novel in vivo assay to investigate whether SKN-1 is important for UPS activity under normal conditions [40]. We generated a strain (Pvha-6::UbG76V-Dendra2) in which the intestine-specific promoter vha-6 drives expression of a photoswitchable green-to-red fluorescent protein (Dendra2) that is fused to a non-hydrolyzable ubiquitin moiety (UbG76V) [40,41]. By monitoring this fusion protein after photoconversion, we could assess ubiquitin-dependent protein degradation activity in living animals [40]. In control RNAi animals, at 9 hours after photoconversion the levels of red-fluorescing intestinal UbG76V-Dendra2 had been reduced to 40% of that present just after photoconversion, but a control Dendra2 that lacked UbG76V was still stable (Figure 5A, upper left panels). UbG76V-Dendra2 degradation was dramatically inhibited by RNAi against the proteasome genes pbs-5, rpn-2, or rpt-4, indicating that this degradation required the proteasome (Figure 5B and S4C). Together, the data show that this intestinal UbG76V-Dendra2 protein is degraded by the UPS. Degradation of intestinally-expressed UbG76V-Dendra2 was also markedly reduced by skn-1 RNAi, indicating that UPS activity in the intestine depends upon SKN-1 (Figure 5A, upper panels). In contrast, skn-1 RNAi did not impair degradation of UbG76V-Dendra2 that was expressed specifically in the body-wall muscle, and slightly increased its degradation in dopaminergic neurons (Figure S4D and S4E, respectively). skn-1 RNAi also decreased the total proteasome activity in the animal under normal conditions, as detected in vitro by a proteasome in-gel activity assay (Figure S5A). Treatment with the proteasome inhibitor MG132 was more toxic for animals in which skn-1 had been knocked by RNAi than for control animals (Figure S5B), further supporting the idea that SKN-1 is important for proteasome gene expression and activity. We conclude that SKN-1 functions tissue-specifically to maintain UPS activity in the intestine under normal conditions, and that a significant proportion of total C. elegans UPS activity is skn-1-dependent.

Dependence of the UPS on translation elongation factors

Having determined that SKN-1 is important for proteasome gene expression and UPS activity in the intestine, and that RNAi against TEFs induces SKN-1 to upregulate particular target genes, we wanted to investigate whether interference with translation elongation might direct SKN-1 to increase proteasome expression and degradation activity. This seemed like a plausible model, because it might be advantageous for proteasome activity to be increased upon interference with elongation, in order to ensure that any incompletely translated proteins are degraded. Surprisingly, however, the levels of endogenous mRNAs encoding four proteasome subunits decreased slightly in response to RNAi against each TEF that we examined, with the exception of eef-1B.1 (Figure S6A). Intestinal fluorescence from the pas-5p::GFP reporter was not increased by either eef-1A.1 or eef-2 RNAi, but was slightly decreased by eef-2 knockdown (Figure S6B; Table S6). Furthermore, in whole animals the levels of proteasome 20S α subunits
were decreased slightly in response to RNAi against each TEF (Figure S6C). Expression of proteasome subunits was similarly reduced slightly by RNAi against TIFs (Figure S6A and S6D). We conclude that whereas SKN-1 directly upregulates proteasome gene transcription under normal conditions, and particularly after depletion of individual proteasome subunits, it does not do so after translation elongation or initiation. In yeast, eEF1A interacts with proteasome subunits and may escort incompletely translated proteins to the proteasome, thereby facilitating their degradation [7,9,10]. This raised an alternative possibility, that the translation elongation apparatus might be important for proteasome activity. Consistent with this notion, in C. elegans EEF-1A.1 interacts with proteasome subunits RPN-2 and RPT-4 [11] and inhibition of three TEFs resulted in the premature aggregation of transgenic proteins, suggesting a possible downregulation of proteasome activity [42]. When we monitored UbG76V-Dendra2 degradation in the intestine, we observed that its degradation was significantly impaired by knockdown of multiple different TEFs, but not TIFs (Figure 5; Table S7). Having observed that proteasome gene expression is affected similarly by TEF and TIF RNAi (Figure S6A–S6D), this suggests that UPS activity may be mechanistically dependent upon the translation elongation machinery.

These findings raised an unexpected model for why SKN-1 target genes are induced by RNAi against TEFs: that the resulting reduction in proteasome activity might stimulate a SKN-1-dependent stress response. However, several observations argue against this interpretation. In contrast to the effects of TEF RNAi, knockdown of proteasome subunit genes induced ska-1-dependent expression of other proteasome genes, and did not increase p38 MAPK signaling or SKN-1 nuclear occupancy (Figure 4C, 4D and S6E–S6G; Table S6). Also different from TEF RNAi effects, proteasome gene RNAi activated the ska-1-regulated gst-4::GFP reporter [26,27], and knockdown of pas-5, tpa-2 or tpt-4 induced ska-1-dependent endogenous gst-4 and gst-10 expression (Figure S6G and S6H). Finally, proteasome subunit but not TEF RNAi activated heat shock promoters hsp-70 and hsp-16.2 (Figure S3A and S3B). Induction of a SKN-1-mediated stress response by TEF RNAi therefore does not derive from an indirect effect on the proteasome, and may result directly from signals associated with slowed translation elongation.

Discussion

We have determined that interference with either mRNA translation or proteasome integrity results in induction of SKN-1-mediated stress responses. These responses are remarkably specific, in that SKN-1 upregulates distinct suites of target genes in response to impairment of translation initiation, translation elongation, or proteasome activity (Figure 6). When protein synthesis is inhibited, SKN-1 increases oxidative stress resistance. If proteasome subunit expression is blocked, SKN-1 attempts to compensate by upregulating proteasome genes in multiple tissues. In contrast, proteasome gene expression is not increased when translation is impaired, and proteasome activity is actually decreased in response to reduced translation elongation, suggesting that the specificity of these SKN-1-mediated functions may be important for maintaining protein homeostasis.

It is intriguing that different mechanisms seem be involved when SKN-1 is directed to activate target genes in response to inhibition of translation initiation or elongation. It is unlikely that the differences between these SKN-1-dependent responses derive simply from different degrees of translation activity or stress, because these responses are qualitatively distinct. Whereas TIF but not TEF RNAi upregulates transcription of the SKN-1 target genes gst-4 and gst-10 (Figure 1B, 1D and 1E), TEF but not TIF RNAi leads to accumulation of SKN-1 in intestinal nuclei (Figure 1F) [23]. In addition, TEF RNAi increases p38 pathway signaling more robustly (Figure 1G and Figure S2G). One possible model is that interference with translation initiation might upregulate SKN-1-dependent gene expression by acting on transcription factors that cooperate with SKN-1. Consistent with this idea, several mRNAs are translated preferentially when translation initiation is inhibited, including some that encode stress response factors [43]. It may be important to increase oxidative and xenobiotic stress resistance when either translation initiation or elongation is impaired, because broad reductions in protein synthesis could disrupt cellular metabolism or redox buffering, particularly in a key metabolic and synthetic tissue like the C. elegans intestine [23]. In addition, oxidizing conditions facilitate IIS, suggesting that under conditions of growth and high translation rates it could be advantageous to suppress SKN-1-regulated oxidative stress defenses [44].

In addition to its well-documented role in small molecule detoxification, we have found that SKN-1 is also important for regulating proteasome gene expression and sustaining UPS activity, particularly in the intestine. The SKN-1 orthologs Nrf1 or Nrf2 have been reported to induce compensatory proteasome gene expression when proteasome activity is impaired in cultured mammalian cells [17–19]. We have shown that this SKN-1/Nrf function is both important in vivo and evolutionarily conserved, and involves each class of proteasome genes. We also obtained the novel finding that SKN-1 orchestrates this response in multiple post-mitotic tissues, including the intestine. It will be important to investigate the extent to which the proteasome bounce-back response might rely on different Nrf1/2/3 isoforms or other mechanisms in various mammalian cell types, particularly the gut, liver, and adipose tissues, which are counterparts to the C. elegans intestine.

Under non-stressed conditions, lack of SKN-1 or Nrf decreased proteasome gene expression only modestly in C. elegans and mammalian cells, respectively (Figure 4A and 4B) [18,20]. However, this seemingly small effect of SKN-1 evidently has substantial consequences, because we determined that under...
normal conditions SKN-1 has a major effect on UPS activity in vivo in the intestine (Figure 5A, upper panels), and contributes to the total proteasome activity in the animal (Figure S5A). Taken together with recent ChIP data indicating that SKN-1 occupies the promoters of most proteasome genes under non-stressed conditions [22], our findings suggest that SKN-1/Nrf proteins are critical regulators of proteasome genes even under normal circumstances. Perhaps the “bounce-back” function of SKN-1 is needed for fine-tuning the levels of proteasomal subunits in the intestine, so that proteasome assembly can proceed efficiently.

Our observation that animals fed skn-1 RNAi bacteria are sensitized to treatment with a proteasome inhibitor (Figure S5B) suggests that SKN-1 is critical for sustaining proteasomal defenses against proteotoxicity in vivo. The involvement of SKN-1/Nrf proteins in regulating proteasome gene expression might be important not only under acute stress conditions, but also in situations of chronic proteotoxic stress such as alcoholic liver and neurodegenerative diseases. Interestingly, in mice liver-specific inactivation of Nrf1 results in non-alcoholic steatohepatitis and hepatic cancer [45]. This syndrome is associated with oxidative damage in hepatocytes, but our results suggest that impaired proteasome activity might also be involved. SKN-1/Nrf proteins have been shown to increase longevity in both C. elegans and Drosophila [13,25]. Our new results predict that this effect may derive not only from their function in protecting against reactive small molecules, but also may involve their role in sustaining proteasome expression and activity, and thereby helping to maintain protein homeostasis. Consistent with this idea, a recent study showed that skn-1 is required for C. elegans lifespan to be extended by an amyloid-binding compound that suppresses toxicity deriving from misfolded proteins [46].

We also observed that UPS activity is dependent upon the translation elongation machinery. A conclusive assessment of how TEF RNAi affected total proteasome activity in the animal, as measured in vivo, was problematic because translation inhibition reduced the total amount of protein present (data not shown). However, our in vivo assay [40] demonstrated clearly that intestinal UPS activity was reduced by TEF but not TIF RNAi (Figure 5). Previous work in yeast had noted that TEFs interact with the proteasome, and that eEF1A may facilitate degradation of defective newly synthesized proteins by escorting them to the proteasome (see Introduction). Working in a metazoan, we have now obtained support for the idea that UPS-mediated protein degradation and translation elongation are mechanistically coupled processes.

We determined that inhibition of translation elongation but not initiation reduced UPS activity in the intestine in vivo, an effect that seems unlikely to be mediated by the modest decline in proteasome gene expression seen after RNAi of either TEFs or TIFs (Figure 5 and Figure S6A–S6D). It also seems unlikely that this effect derived simply from the UPS being swamped by incompletely translated proteins arising from inhibition of elongation, because we did not see simultaneous upregulation of proteasome genes. Interestingly, our assay measured degradation of fluorescent and presumably folded UbG76V-Dendra2, suggesting that the translation elongation apparatus may promote UPS-mediated degradation of complete polypeptides that are no longer associated with the translation apparatus. The physical interactions that have been described between the proteasome and elongation factors [6,14] therefore may be generally important for UPS activity.

It is an intriguing question why SKN-1 does not increase proteasome gene expression and activity when translation elongation is inhibited, particularly when it appears to be present at most proteasome gene promoters constitutively [22]. Perhaps it would be deleterious for SKN-1 to do so, because if translation elongation were to slow in response to limited nutrients or other conditions, an inappropriate increase in proteasome activity might prematurely degrade nascent polypeptides, and thereby could globally impair protein synthesis. This could provide a rationale not only for the failure of TEF RNAi to induce proteasome gene upregulation, but also for the apparent dependence of UPS activity on translation elongation but not initiation factors. Taken together, our findings indicate that SKN-1 plays an important role in sensing and maintaining protein homeostasis, by mobilizing distinct responses to perturbations in polypeptide chain elongation and proteasomal degradation (Figure 6). They also indicate that the stress defenses that are regulated by SKN-1/Nrf proteins are not controlled in unison through a simple on/off switch, but are remarkably customized for specific conditions. This raises important questions concerning how these stresses are sensed at the molecular level, and how different stress signals are integrated by SKN-1/Nrf proteins to achieve specificity in their responses.

Materials and Methods

RNAi

RNAi was performed by feeding essentially as described [23], except that L3 and (or) early L4-stage worms were fed RNAi bacteria for 3 days at 20°C unless otherwise indicated. Bacteria carrying the vector plasmid L4440 were used as the control. RNAi constructs were taken from the Vidal ORFeome-Based RNAi library [47] and confirmed by sequencing. In all double RNAi
experiments, RNAi and/or control bacteria were mixed at a 1:1 volume ratio. The wild-type strain is N2.

**RNA isolation and quantitative RT-PCR**

Animals subjected to RNAi were collected and washed 3 times in M9, then total RNA was extracted from approximately 60 animals for each treatment. RNA was extracted using the TRI Reagent (Sigma) and cDNA synthesized using the SuperScript First-Strand Synthesis Kit (Invitrogen). SYBR Green Real Time Quantitative PCR was carried out using the ABI 7900 and analyzed using the Standard Curve method [48]. For all RNAi experiments, qRT-PCR data were derived from 3–4 independent biological replicates. In CHX experiments, the values presented were derived from 2–3 independent PCR analyses of one biological experiment. Results were graphed so that the level of each mRNA that was seen in N2 animals fed with control (L4440) RNAi bacteria was set as 1. Unless otherwise indicated, act-1 (β-actin) was used for normalization and P values were derived from an unpaired t test (two-tailed). Primer sequences are listed in Table S9.

**Western blotting**

L2/L3 stage larvae were fed RNAi bacteria for two days, then collected and washed in M9 buffer, and snap frozen in liquid nitrogen. Worms were lysed in RIPA buffer (50 mM Tris [pH = 8.0], 150 mM NaCl, 1% Nonidet P-40, 0.5% sodium deoxycholate and 0.1% SDS) supplemented with 0.2 mM sodium vanadate, 50 mM sodium fluoride, 0.1 mM PMSF and protease inhibitor cocktail (Roche). Supernatant was quantitated by the BCA method.

**Quantification and imaging of GFP reporters**

For proteasome reporters, L2/L3 larvae were fed RNAi bacteria for 3 days, then normal-appearing worms that developed into gravid adults were analyzed. Animals were mounted on 5% agarose pads, immobilized in 1 mM levamisole and imaged with a Zeiss Axioscope 2 microscope. Confocal microscopy was used to generate z-stack projections for a representative subset of animals (LSM 510 Meta, 40× plan-neofluar objective, Zeiss, Germany; z-stacks with 0.5 μm interval). At least two stable transgenic lines for each proteasome reporter strain were examined. Fluorescent images were analyzed by the MCID system (Imaging Research) to measure the average fluorescence level of the entire worm, or particular regions. The average value of controls for each experiment was set as 100%, with values obtained in parallel from RNAi-treated worms converted to the relative fluorescence level. Data obtained from several experiments were pooled for statistical analysis.

For other reporters, an AxioVision (Zeiss) microscope was used to acquire imaging and fluorescence was scored by eye as Low, Medium, or High as described for each experiment.

**Additional Materials and Methods** are provided in Text S1.

**Supporting Information**

**Figure S1** Schematic of the translation elongation cycle. eEF1A is involved in delivering aminoacyl-tRNA to the empty A-site of the ribosome in the presence of GTP. eEF1A is a multi-subunit nucleotide exchange factor that partners with eEF1A, and enhances the recycling of eIF1A-GDP to eIF1A-GTP. eEF2 is a monomeric protein that translocates peptidyl tRNA to the P-site. After translocation, the peptidyl-tRNA is positioned in the ribosome P-site, and the next codon on the mRNA is made available for the next elongation cycle [49].

**Figure S2** SKN-1 target gene induction in response to inhibition of translation elongation. (A) Diagram of the gcs-1 promoter transgenes used in this study [24]. 1, 2, and 3 refer to SKN-1 binding sites. Mutation of site 3 abolishes most skn-1-dependent expression. (B) Expression of gcs-1::GFP is dependent upon SKN-1 binding site 3, and p38 signaling through the MAPKK SEK-1. gcs-1::GFP expression was scored as in Figure 1A, after RNAi against the indicated TEF. P values were derived from a chi² test, and were all above 0.009. (C) SKN-1-dependence of endogenous target gene induction. In all qRT-PCR figures, ***P<0.001, **P<0.01, *P<0.05, N= not significant, and error bars indicate SEM. Endogenous aff-5 or haf-7 mRNAs was detected by qRT-PCR in wild-type (N2) or skn-1(zu135) animals that had been fed with TEF RNAi bacteria, or treated with CHX for 18 hs at 15°C. A paired t test (two-tailed) was employed to compare wild-type (N2) and skn-1(zu135) animals. An unpaired t test (two-tailed) was used to compare TEF RNAi or CHX treatment vs the corresponding control in N2 animals. Compared to N2 control, all P<0.05. (D) Intestinal gst-4p::GFP expression is not robustly induced by TEF RNAi. Worms were scored for GFP expression after RNAi knockdown of the indicated TEFs or the TIF egl-1, with examples of high and low scoring provided. “High” indicates that gst-4p::GFP was present at unambiguously high levels throughout most of the intestine, while “low” refers to animals in which readily detectable GFP signal was present only in the most anterior part of the intestine.
intestine, and “medium” indicates an intermediate level of GFP signal. P values were derived from a chi squared test. **P < 0.0001, ***P < 0.0005, NS = Not Significant. (E) Examples of SKN-1::GFP accumulation in intestinal nuclei that scored as low, medium, and high in Figure 1F. “Low” refers to animals in which GFP was barely detectable in nuclei throughout the intestine, “medium” indicates that GFP was present in the anterior and/or posterior intestinal nuclei, and “High” indicates that a strong GFP signal was present in most intestinal nuclei. Arrows indicate intestinal nuclei. (F) Relative sod-3 mRNA levels after TEF RNAi or CHX treatment, measured by qRT-PCR. (G) The p38 MAPK SEK-1 and MAPKKK NSV-1 are required for p38 MAPK activation in response to TEF RNAi. In C. elegans, canonical p38 signaling is blocked by mutation of either sek-1 or nsy-1 [29]. Representative experiments are shown in which lysates from control or RNAi worms were analyzed by Western blotting for p38 kinase phosphorylation (activation) as in Figure 1G. In all panels α-tubulin was the loading control. (H) p38 activation in response to knockdown of TIFs, assayed as in (G). In this and multiple other experiments only ifg-1 RNAi increased levels of p38 phosphorylation comparably to TEF RNAi. This p38 activation required the p38 MAPKK sek-1 and MAPKKK NSV-1. (TIF)

Figure S3 Effects of TEF RNAi do not derive from a global induction of stress responses. (A, B) Heat shock genes are activated by proteasomal gene knockdown but not TEF RNAi. In (A), a transgenic reporter driven by the promoter for the heat-shock gene hsp-70 (hsp-70p::GFP) [50] was robustly upregulated in the anterior and posterior intestine after proteasomal subunit gene RNAi (rpm-2, rpm-4), but not TEF RNAi. In (B), the GFP-fused promoter for the small heat shock protein gene hsp-16.2 [51] was induced by proteasomal subunit RNAi but not TEF knockdown. “Low” indicates that GFP was undetectable throughout the animal, “medium” indicates that GFP was present in the middle intestinal nuclei, and “High” indicates that GFP signal was present in most intestinal nuclei. (C) RNAi against TEFs decreased fecundity. P values were derived from an unpaired t test (two-tailed). For each RNAi treatment P < 0.0001 compared with corresponding control. (D) DAF-16::GFP does not accumulate in intestinal nuclei in response to TEF knockdown, in contrast to the effect of decreased germ cell proliferation. P values were derived from a chi squared test. **P < 0.0001, ***P < 0.0005, here and in (E). Expression of the DAF-16 target gene reporter sod-3::GFP after TEF RNAi. sod-3::GFP is robustly induced by knockdown of the insulin receptor DAF-2, or by inhibition of germ cell proliferation [39], but is only modestly affected by TEF RNAi. For control and TEF RNAi, “high” corresponds to a bright GFP signal being present throughout the hypodermis (in both the cytoplasm and nucleus) and posterior intestine, “medium” refers to modest GFP expression in the anterior and posterior intestine, and “low” indicates modest GFP expression in the posterior intestine only. Fordaf-2 RNAi, a strong GFP signal was present throughout both the intestine and hypodermis. (F) Lifespan analysis of TEF RNAi worms, performed in parallel to Figure 3D. For control, ef-1A1 and ef-1G RNAi treatments, composites of two biological replicates are shown. For ifg-1 RNAi, a single experiment is shown. Statistics are provided in Table S3B. (TIF)

Figure S4 Effects of proteasomal subunit and skn-1 RNAi on proteasome gene expression and UPS activity in vivo. (A, B) Requirement for skn-1 for the “bounce-back” response to proteasome gene RNAi. Confocal z-stack projection images are shown of representative 2-day-old adult worms that carry proteasome gene reporter transgenes, and were subjected to the indicated RNAi treatments. RPN-11::GFP is a translational fusion reporter, but pbs-4::GFP includes only the pbs-4 promoter region. For all worms in double RNAi experiments, z-stack projections through the intestine or body-wall muscle are shown. Dashed lines indicate boundaries of the intestine. Abbreviations: M, body-wall muscle; SM, stomatointestinal muscle. Quantification and statistics are listed in Table S6. In all double RNAi experiments, RNAi and/or control bacteria were mixed at a 1:1 volume ratio, with single RNAi treatments mixed with control. (C) Knockdown of proteasome subunits impairs intestinal UPS activity. Representative images of animals fed control (L4440), pbs-3 (20S β-ring), rpm-2 (19S non-ATPase) and pfs-4 (19S ATPase) RNAi respectively. Bar: 20 μm. Note the difference in % UbG76V-Dendra2 fluorescence remaining after 9 hours. (D) SKN-1 does not contribute to UPS-mediated protein degradation in body-wall muscle cells. UbG76V-Dendra2 and control Dendra2 that were expressed specifically in body-wall muscle cells (from Punc-54) were imaged in control and skn-1 RNAi animals at 24 hours after photoconversion. Bar: 20 μm. Depicted in the graph: percentages of green and red fluorescence related to the initial value (t = 0) or point of photoconversion (t = C) respectively (± SEM). P = 0.1787 (Student’s t-test). (E) SKN-1 is not required for UPS-mediated UbG76V-Dendra2 degradation in dopaminergic neurons, assayed at 9 hours after photoconversion. Representative experiment is shown. UbG76V-Dendra2 and control Dendra2 that were expressed specifically in dopaminergic neurons (from Plat-1) were imaged in control and skn-1 RNAi animals at 9 hours after photoconversion. Experiments were performed in the RNAi-sensitive strain rrf-3 (pk1426) to allow penetrance in neurons. Note that degradation slightly increased by skn-1 RNAi. Bar: 5 μm. Numbers of animals and statistics for all experiments are listed in Table S7. (TIF)

Figure S5 Importance of SKN-1 for proteasome function. (A) SKN-1 is required for total C. elegans proteasome activity, as measured by a proteasome in-gel activity assay. The left panels show fluorescent (top) and Goomassie-stained (bottom) images of a representative experiment in which the chymotrypsin-like activity of the proteasome was assayed. CP refers to the 20S proteasome core particle, and RP to the 19S regulatory particle. The 20S complexes designated as RP-CP and RP2-CP include RP’s at one or both ends of the CP, respectively. The right panel shows the relative fold-change in normalized substrate fluorescence compared to control (set as 1). Results of four individual experiments are graphed, with error bars that correspond to SEM. (B) Knockdown of skn-1 by RNAi feeding increases sensitivity to proteasome inhibition. A representative experiment (of three total) is shown in which one day-old adults were fed L4440 control (in blue) or skn-1 RNAi (in red) bacteria for three days, exposed to the indicated concentration of the proteasome inhibitor MG132 in 1% DMSO for 24 hours, then scored for viability. N = approx. 50 in each of two wells, and error bars indicate SEM. (TIF)

Figure S6 Distinct effects of TEF, TIF, and proteasome subunit RNAi on proteasome subunit and SKN-1 target gene expression. (A) Relative levels of endogenous proteasome subunit mRNAs after TEF or TIF RNAi. In contrast to results seen after proteasome subunit gene knockdown, in most cases RNAi against these translation factors modestly reduced proteasome gene expression. N = not significant, all other P < 0.05. (B) Representative confocal images of the proteasome reporter pas-3p::GFP fed either control or elf-2 RNAi. Note that GFP levels were reduced in the intestine in response to knockdown of elf-2. (C, D) Reduced
levels of proteasome 20S α subunits after RNAi against TEFs or TIFs. Lysates from control or RNAi worms were Western blotted with an antibody against 20S proteasome α1, 2, 3, 5, 6 & 7 subunits [52]. For TEF RNAi (C), the nitrocellulose transfer membrane used was same as that used in Figure S2G. For TIF RNAi (D), the membrane was same as that used in Figure S2H. Representative experiments are shown. (E) p38 MAPK is not activated by RNAi against proteasome subunits, in contrast to effects of TEF RNAi. Western blot assay was performed as in Figure 1G, Figure S2G and S2H. (F) RNAi against proteasome subunits does not dramatically increase SKN-1 B/C::GFP accumulation in intestinal nuclei. Worms were scored as in Figure 1F. (G) Relative levels of endogenous proteasome (ptp-3, ptp-12, pax-4 and pha-6) and SKN-1 target (gst-4, gct-4 and gct-10) mRNAs after proteasome subunit (pmt-2 or pta-4) RNAi, assayed by qRT-PCR. These genes are not generally induced by TEF RNAi, except for gcs-1, pta-1 (α-tubulin) was used for normalization, here and in (H). N = not significant, all other P<0.02. (H) SKN-1-dependent upregulation of gst-4 and gct-10 by proteasome subunit RNAi. Statistical analysis was performed as in Figure S2C. All P<0.05 compared to control, except where not significant is indicated by N.

**Table S1** Mammalian and *C. elegans* TEFs. Identity (%) is from NCBI/basic BLAST/protein blast program. *Isoform chosen to run BLAST.

**Table S2** Effects of TEF RNAi on resistance of wild type worms to 9.125 mM TBHP. The third individual experiment described above is graphed in Figure 3A. JMP software was used for data analysis. Percentage change of mean survival time = (mean survival time of animals fed treatment RNAi - mean survival time of animals fed control RNAi)/mean survival time of animals fed control RNAi indicated as N. For each proteasome subunit reporter, two to three transgenic lines of worms were examined in each experiment. Data correspond to results shown in Figure 4B, 4C; Figure S4A, S4B and S6B.

**Table S3** *skn-1*-dependence of TBHP oxidative stress resistance. Three individual experiments are listed that were performed in parallel as in Figure 3B. The third individual experiment labeled with * is shown in Figure 3B. Data were analyzed as in Table S2.

**Table S4** Effects of TEF RNAi on resistance of wild type worms to 10 mM Arsenite. Individual experiments are listed that were performed as in Figure 3C. The first individual experiment is shown in Figure 3C. Data were analyzed as in Table S2.

**Table S5** Lifespan analysis of inhibition of translation. Corresponds to the data in Figure 3D and S3F, respectively. Data of each table was a composite of multiple individual experiments. Percentage increase in mean lifespan = (mean RNAi treatment adult lifespan - mean control adult lifespan)/mean control adult lifespan. 75th and 25th percentiles refer to the day at which 75% or 25% the population was dead. Wild type N2 animals were used for the experiments. N represents number of RNAi worms, number of observed deaths/total number of worms subjected to RNAi treatment. P values were calculated by log-rank.

**Table S6** Quantification and statistical analysis of proteasome subunit reporter expression. Fluorescence densities in whole worms or selected regions (intestine, head) were obtained from the measurement of fluorescent microscopic images by a computer-based MCID image analysis system. For each experiment, the average values of control worms (fed with L4440 RNAi bacteria) were set as 1, with values obtained from RNAi-treated worms in parallel converted to relative fluorescence levels. Data obtained from several experiments were pooled for t tests (two-tailed). The number of independent experiments was indicated as N. For each proteasome subunit reporter, two to three transgenic lines of worms were examined in each experiment. Data correspond to results shown in Figure 4B, 4C; Figure S4A, S4B and S6B.

**Table S7** Statistical analysis of in vivo UPS activity experiments. Number of individual experiments is shown in parentheses. Data correspond to results shown in Figure 5 and S4C–S4E.

**Table S8** Primer sequences. This table includes all primers used in qRT-PCR experiments.

**Text S1** Supplementary Materials and Methods.

**Acknowledgments**

We thank Naoki Hisamoto for generously providing strains and Blackwell lab members for advice and critically reading the manuscript. We thank the Biomedical Imaging Unit for help with confocal microscopy and imaging.

**Author Contributions**

Conceived and designed the experiments: TKB CIH XL OM CJ KMG-C. Wrote the paper: XL TKB.
degradation of certain N-acetyl-acylated proteins and may be substituted for by the bacterial elongation factor EF-Tu. Proc Natl Acad Sci U S A 91: 7648–7652.


