Skp1 Independent Function of Cdc53/Cul1 in F-box Protein Homeostasis

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Abstract

Abundance of substrate receptor subunits of Cullin-RING ubiquitin ligases (CRLs) is tightly controlled to maintain the full repertoire of CRLs. Unbalanced levels can lead to sequestration of CRL core components by a few overabundant substrate receptors. Numerous diseases, including cancer, have been associated with misregulation of substrate receptor components, particularly for the largest class of CRLs, the SCF ligases. One relevant mechanism that controls abundance of their substrate receptors, the F-box proteins, is autocatalytic ubiquitylation by intact SCF complex followed by proteasome-mediated degradation. Here we describe an additional pathway for regulation of F-box proteins on the example of yeast Met30. This ubiquitylation and degradation pathway acts on Met30 that is dissociated from Skp1. Unexpectedly, this pathway required the cullin component Cdc53/Cul1 but was independent of the other central SCF component Skp1. We demonstrated that this non-canonical degradation pathway is critical for chromosome stability and effective defense against heavy metal stress. More importantly, our results assign important biological functions to a sub-complex of cullin-RING ligases that comprises Cdc53/Rbx1/Cdc34, but is independent of Skp1.

Author Summary

Protein ubiquitylation is the covalent attachment of the small protein ubiquitin onto other proteins and is a key regulatory pathway for most biological processes. The central components of the ubiquitylation process are the E3 ligases, which recognize substrate proteins. The best-studied E3 complexes are the SCF ligases, which are composed of 3 core components—Cdc53, Skp1, Rbx1—that assemble to the functional ligase complex by binding to one of the multiple substrate adaptors—the F-box proteins. Maintaining a balanced repertoire of diverse SCF complexes that represent the entire cellular panel of substrate adapters is challenging. Depending on the cell type, hundreds of different F-box proteins can compete for the single binding site on the common SCF core complex. Rapid degradation of F-box proteins helps in maintaining a critical level of unoccupied Cdc53/Skp1/Rbx1 core, complexes and alterations in levels of F-box proteins has been linked to diseases including...
Introduction

Ubiquitin dependent proteolysis controls many cellular processes including signal transduction and cell cycle progression. Ubiquitin is covalently linked to substrates in a multistep process that requires coordinated action of 3 classes of enzymes- E1 ubiquitin activating enzyme, E2 ubiquitin conjugating enzyme, and E3 ubiquitin ligase [1–5]. E3 ubiquitin ligases are the key players in this system as they mediate substrate specific covalent attachment of ubiquitin. Within the E3 ligase family, cullin-RING ligases (CRLs) comprise the largest class, and in this group the SCF ubiquitin ligases are one of the best-understood complexes [2,6]. They are composed of yeast Cdc53 (mammalian cullin-1), Skp1, Rbx1, and one of the multiple F-box proteins, which bind substrates and confer specificity to the complex [7,8].

Amongst the SCF components, F-box proteins are relatively unstable in nature, which contributes to the dynamic assembly of a diverse repertoire of SCF complexes within the cell [9–13]. Accordingly, over expression of a single F-box protein in yeast can change the balanced distribution and diversity of available SCF complexes by sequestering cullin and Skp1 and thus block formation of functional SCF complexes with other F-box proteins [10,11,14]. Many F-box proteins control degradation of critical oncogenes and tumor suppressors and variation in their abundance has been linked to cancer [15,16]. Thus, it is important to understand how cells maintain F-box protein homeostasis. F-box proteins are known to be regulated by autoubiquitylation where their degradation is dependent upon their incorporation into a functional SCF complex [10,11]. The autocatalytic F-box protein degradation pathway is thought to be suppressed by substrate binding resulting in coordination of substrate availability with abundance of the corresponding assembled SCF complex [17,18]. Additional degradation pathways for F-box proteins are likely as it is also important to restrict abundance of unbound F-box proteins to prevent substrate shielding effects that would compete with substrate recognition by fully assembled ligases. Indeed, mammalian Skp2 is targeted for degradation by the anaphase promoting complex or cyclosome [19,20], Fbx5 (Emi1) is degraded by SCFβTrCP/Slimb [21], and the level of the budding yeast F-box protein Dia2, which is required for genomic stability, is restricted by the HECT domain E3 ligase Tom1 [22].

In *Saccharomyces cerevisiae*, Met30 is one of three essential F-box proteins. SCFMet30 coordinates metabolic pathways of sulfur containing compounds with cell cycle progression. The transcription factor Met4 is a key target of SCFMet30 [23,24]. Low levels of the methyl donor, S-adenosylmethionine cause a block in SCFMet30 dependent ubiquitylation of Met4, activating it and resulting in cell cycle arrest and transcription of methionine response genes [25]. SCFMet30 also represses expression of enzymes responsible for glutathione synthesis and is thus a key factor in response to heavy metal stress. Cadmium exposure induces active dissociation of Met30 from Skp1, thereby inhibiting SCFMet30 and inducing glutathione production and cell cycle arrest, which together protect cellular integrity [26–28]. Therefore, the SCFMet30 system generates unbound Met30 via heavy metal stress induced dissociation from Skp1. To prevent unwanted effects of excess unbound Met30, such as substrate sequestration, it seemed important, that a degradation mechanism exists in addition to autocatalysis that plays an integral role in maintaining Met30 homeostasis.
Here we report such an additional mechanism for Met30 regulation in addition to autoubiquitylation. This degradation pathway targets Met30 that is detached from Skp1 and involves the SCF core components Cdc53 and Rbx1, as well as the cognate SCF ubiquitin conjugating enzyme Cdc34. Importantly, this ubiquitylation pathway does not require Skp1 (Skp1-independent Cul1-dependent ubiquitylation) and suggests a function of Cdc53/Cul1 that is independent from association with Skp1.

Results

Dissociation of the F-box protein Met30 from Skp1 targets it for degradation

Defense against heavy metal toxicity requires coordinated changes of metabolic pathway flux connected to glutathione synthesis, induction of a cell cycle checkpoint response to avoid continued cell division during stress conditions, and cell protective measures known as sulfur sparing [25]. SCF<sub>Met30</sub> is the key regulator of this concerted response [24,26]. Coordinated regulation is achieved because cadmium stress disrupts ubiquitylation of all SCF<sub>Met30</sub> substrates by the active and selective disassembly of the SCF<sub>Met30</sub> protein complex, but not other SCF ligases [24,26,27]. This is accomplished by Cdc48-mediated dissociation of the F-box component Met30 from Skp1 [24,26,27], which results in generation of a pool of unbound Met30. In addition, Met30 transcription is induced by over seven fold during cadmium stress [29], which further increases the amount of Met30 that is not associated with core SCF components (referred to as unbound or 'Skp1-free' Met30). We were interested in how cells cope with the generated excess of Met30 because the well-described autocatalytic F-box protein degradation pathway mechanism [10,11] cannot act on Met30 during these conditions. Interestingly, degradation of the F-box protein Met30 was maintained and even slightly induced in response to cadmium stress (Fig 1A). We next asked whether cadmium stress induces a degradation pathway for unbound Met30, or if dissociation of Met30 from Skp1 might be sufficient to induce its degradation. To this end we examined stability of Met30 that cannot associate with Skp1 even in the absence of cadmium due to mutations in the F-box motif, which forms the Skp1 interaction surface. A mutant form of Met30 lacking its entire F-box domain (Met30<sup>ΔF-box</sup>) was constitutively unstable even though cells did not experience cadmium stress (Fig 1B). Rapid degradation of Met30<sup>ΔF-box</sup> was observed both in cycloheximide chase and promoter shut-off experiments, indicating that components of this degradation pathway are constitutively present and that new protein synthesis is not required (S1A Fig). Disruption of the Met30-Skp1 interaction by the single amino acid change L187D [30], rather than complete deletion of the F-box domain, was sufficient to induce Met30 degradation (Figs 1C and S1B) suggesting that Met30 that is not bound to Skp1 is degraded.

To further test this idea and exclude that mutating the F-box region results in conformational changes that target Met30 to a non-physiological degradation pathway, we measured Met30 stability in another condition where Met30 is dissociated from Skp1. To this end we used a yeast strain carrying the temperature sensitive <i>skp1</i>-25 allele, which is inactivated by a temperature shift and disrupts the integrity of SCF ligases at the restrictive temperature [31]. Met30 was efficiently degraded in <i>skp1</i>-25 mutants and cadmium exposure did not further destabilize Met30 (S1C Fig).

Collectively these results demonstrate that disruption of the Met30-Skp1 interaction, by either active signal-induced dissociation (cadmium stress) or by mutations in Met30 or Skp1, induces rapid degradation of the F-box protein Met30. These results suggest a proteolytic pathway that recognizes unbound 'Skp1-free' Met30 to avoid accumulation of excess unbound
Met30, which could bind substrates and shield them from recognition by fully assembled SCF\textsuperscript{Met30} complexes.

Degradation of ‘Skp1-free’ Met30 requires Cdc53, Cdc34, and Rbx1 but not Skp1

We sought to further characterize proteolysis of ‘Skp1-free’ or unbound Met30 and asked whether it was dependent upon the ubiquitin-proteasome system. In wild-type cells Met30
may exist either bound or unbound to the SCF core. In order to specifically study the degradation pathway targeting ‘Skp1-free’ Met30, we used Met30ΔFbox as a tool to generate a homogeneous population of Met30 free from Skp1. Inhibition of proteasome activity with MG-132 led to stabilization of Met30ΔFbox, suggesting that the ubiquitin proteasome pathway is involved in degradation of ‘Skp1-free’ Met30 (Fig 2A). We next asked what E2 ubiquitin conjugating enzyme might be involved in this degradation process. Surprisingly, degradation of Met30ΔFbox was dependent on the canonical SCF E2, Cdc34 (Fig 2B). The requirement for Cdc34 compelled us to test dependence on SCF core-components even though our previous experiments

![Figure 2A](Image)

![Figure 2B](Image)

![Figure 2C](Image)

![Figure 2D](Image)

**Fig 2.** Degradation of ‘Skp1-free’ Met30 depends on the proteasome, Cdc53, Cdc34, and Rbx1, but is independent of Skp1. (A) Cells expressing either endogenous 12MycMet30 or 12mycMet30ΔFbox were grown at 30°C. Proteasomes were inhibited with 50μM MG-132 for 45 min before cycloheximide was added to block translation. Cells carried a deletion of PDR5 to increase MG-132 permeability. (B) 12MycMet30ΔFbox stability was analyzed in wild type, cdc53-3, and cdc34-1 and rbx1-13myc temperature sensitive mutants by cycloheximide chase experiments and immunoblotting with anti-myc antibodies as described for Fig 1A. Cells were grown at 25°C, shifted to 37°C for 1.5 h to inactivate temperature sensitive mutants (C) Experiment as in panel B, but 12mycMet30ΔFbox stability was analyzed in skp1-25 single and skp1-25 cdc53-1 double mutants. (D) Cells expressing HBTHMet30ΔFbox under control of the GAL1 promoter were shifted to 37°C for 1.5 h to inactivate temperature sensitive alleles. HBTHMet30ΔFbox was purified on Ni2+-sepharose under denaturing conditions and analyzed by immunoblotting using antibodies directed against ubiquitin (upper panel) or the RGS6H epitope in the HBTH tag (lower panel). Cells expressing untagged Met30ΔFbox were processed as control.

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demonstrated that Skp1 is not involved in this degradation pathway. Unexpectedly, Cdc53 was indispensable for Met30ΔFbox degradation, because inactivation of the temperature sensitive cdc53-1 allele blocked degradation (Fig 2B). Consistent with these results Met30ΔFbox degradation was greatly reduced in a strain expressing a 13Myc-tagged version of the RING finger component Rbx1, which has previously been shown to be a hypomorph allele that results in reduced SCF function at high temperature [32] (Fig 2B). These experiments not only suggest a degradation pathway for Met30 that is independent of the canonical autoubiquitylation mechanism, but more surprisingly, indicate that the cullin-1 (Cdc53) based ligase complex might have functions independent of its adaptor component Skp1. Given these unexpected results we wanted to further test this hypothesis and ensure that skp1-25 and cdc53-1 mutants probe the same degradation pathway and do not induce any secondary effects that might affect interpretation of the degradation results. We thus tested Met30ΔFbox half-life in skp1 single and skp1 cdc53 double mutants. As previously observed, unbound Met30 was rapidly degraded in skp1-25 mutants but, importantly, was stabilized upon inactivation of cdc53-1 in the double mutant (Fig 2C), confirming that degradation was dependent on Cdc53 but not Skp1. In agreement with the Met30ΔFbox degradation data, ubiquitylated Met30ΔFbox was readily detectable in skp1 mutants but absent in cdc53 mutants further supporting the hypothesis of a Skp1-independent degradation function for Cdc53 (Fig 2D).

In addition of being a SCFMet30 substrate itself, the transcription factor Met4 has been shown to function as a substrate receptor in the context of SCFMet30/Met4 to coordinate degradation of its own co-factors [33]. Analysis of Met30ΔFbox degradation in met4Δ mutants showed that it was not involved in degradation of ‘Skp1-free’ Met30 (S2A Fig).

Cullins are regulated by covalent modification with ubiquitin like protein Nedd8 (Rub1 in yeast), which induces a conformational rearrangement of cullin and stimulates ubiquitin transfer by the SCF-bound E2 [6]. Deneddylated cullins interact with Cand1 (Lag2 in yeast), which inhibits binding of Skp1- F-box protein complex and prevents SCF ligase function [12,34,35]. As rubberylation is dispensable in yeast [36], we posited that Lag2 bound to Cdc53 may serve as an adaptor for regulating F-box proteins dissociated from Skp1. Deletion of LAG2 failed to stabilize Met30ΔFbox demonstrating that degradation of ‘Skp1-free’ Met30 is independent of Lag2 (S2B Fig).

Together these results suggest existence of a novel mechanism of Met30 regulation that specifically targets Met30 that is displaced from Skp1 and is dependent on the ubiquitin proteasome system and requires the function of Cdc53, Rbx1 and Cdc34, but not Skp1.

**Met30ΔFbox degradation is independent of Skp1**

Temperature sensitive skp1 alleles have been previously shown to differentially affect SCF ligases depending on the identity of F-box protein subunits [10,37]. Although the skp1-25 allele was specifically selected to represent a complete loss of Skp1 function, including inactivation of SCFCdc4 and SCFMet30, we could not unambiguously exclude that Skp1-25 forms an intact SCF ligase that could ubiquitylate Met30ΔFbox in trans. To address this issue we employed the temperature inducible degron tag (td) strategy to deplete Skp1 protein from cells [38], rather than rely on inactivation of temperature sensitive alleles. A skp1-td strain was constructed by expressing Skp1 fused to the temperature inducible degron under control of the inducible CUP1 promoter. Attenuation of Skp1 induced the expected biological response such as cell cycle arrest with elongated multibudded cell morphology indicative of SCFCdc4 inactivation, and block of SCFMet30 function as assayed by loss of ubiquitylated forms of Met4 (Fig 3A and 3B). Combined CUP1 promoter repression and temperature induced Skp1-td thus efficiently ablated Skp1 function and protein level (Fig 3). Consistent with results using temperature
sensitive alleles of \textit{skp1}, Met30\textsuperscript{ΔFbox} degradation was unaffected when Skp1 function was blocked using the \textit{skp1-td} strategy (Fig 3C). These results strongly support our hypothesis of Skp1-independent degradation of Met30.

**Cdc53 mutant unable to bind Skp1 can degrade Met30**

The experiments with \textit{skp1} single and \textit{skp1 cdc53} double mutants strongly suggested that the ‘Skp1-free’ degradation pathway for Met30 was dependent on Cdc53 and independent of Skp1. We reasoned that in such a scenario, a Cdc53 mutant defective in interacting with Skp1 should be capable to degrade Met30\textsuperscript{ΔFbox}. To examine this, a \textit{GAL1} inducible Cdc53\textsuperscript{Y133R} mutant was constructed. Mutation of tyrosine in position 133 to arginine has previously been suggested to disrupt the Cdc53-Skp1 interaction [39]. Immunopurification experiments confirmed that Cdc53\textsuperscript{Y133R} does not interact with Skp1 \textit{in vivo} (Fig 4A). Accordingly, expression of Cdc53\textsuperscript{Y133R} was unable to rescue the \textit{cdc53-1} growth arrest phenotype at restrictive temperature (Fig 4B). Importantly, congruous with our hypothesis, Cdc53\textsuperscript{Y133R} supported degradation...
of Met30ΔFbox to the same extent as wild type Cdc53 (Fig 4C). These results support the hypothesis of a cullin-1 (Cdc53) function in protein degradation independent of its adaptor component Skp1.

**Hydrophobic residues proximal to the F-box domain are required for degradation of ‘Skp1-free’ Met30**

Instability of Met30 in skp1 mutants led us to hypothesize that the ubiquitin ligase responsible for degrading ‘Skp1-free’ Met30 may recognize a domain close to the F-box domain, which is
directly or indirectly obstructed by Skp1 binding. In accordance with this idea, a so-called R-motif has been described in the yeast F-box protein Cdc4, which is adjacent to its F-box domain. In addition, F-box—Skp1 interaction acts to suppress R-motif mediated Cdc4 degradation [14]. Thus, to identify the degradation sequences (degron) in Met30 recognized by the ‘Skp1-free’ degradation pathway, we generated deletions in Met30ΔFbox near the F-box domain and compared their stability to that of Met30ΔFbox.

Congruous with our hypothesis, deletion of 100 amino acids proximal and distal to the F-box domain (amino acids 137–277) not only increased steady-state Met30ΔFbox levels (time point 0) but also completely prevented its degradation (Fig 5A). To further narrow down the degron sequence, shorter deletions encompassing either the C terminal or the N terminal 50 amino acids were constructed. Deletion of the N terminal amino acids adjacent to the F-box domain (amino acids 137–277) (Fig 5A).

Fig 5. Mutation of methionine 178 and isoleucine 179 in Met30 abolishes ‘Skp1-free’ Met30 degradation. (A) Identification of a degron region for the ‘Skp1-free’ Met30 degradation pathway. Cells expressing either endogenous 12mycMet30ΔFbox or different Met30ΔFbox deletion mutants were grown at 30°C. Protein translation was inhibited by addition of cycloheximide and cells were collected at the time intervals indicated. Met30ΔFbox stability was analyzed by immunoblotting with anti-myc antibodies. (B & C) Experiment as in panel A, with cells expressing endogenous 12mycMet30ΔFbox, full-length 12mycMet30, or the respective degron point mutants. Results are presented as mean ± standard error for three independent experiments (right panels).

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box motif (amino acids 137–187) was sufficient for Met30\textsuperscript{ΔFbox} stabilization (Fig 5A). Interestingly, this region overlapped with a 45 amino acid stretch immediately N-terminal to the F-box domain, which mediates dimerization of WD-40 repeats containing F-box proteins and is conserved from yeast to humans [40]. Overlap of the degron region and the dimerization domain raised the possibility that the ligase for ‘Skp1-free’ Met30 degradation recognized the dimerization motif in Met30. However, mutation of isoleucine 159 and leucine 160, two amino acids crucial for Met30 dimerization [40], in Met30\textsuperscript{ΔFbox} failed to stabilize the protein (S3A Fig), suggesting that different residues within this stretch were being recognized by the ligase.

Smaller deletions within the N terminal 50 amino acids contiguous to the F-box domain suggested that amino acids 170–187 in Met30, corresponding to a region rich in hydrophobic residues, were important for ligase binding because various Met30\textsuperscript{ΔFbox} mutants containing this region were efficiently degraded and mutants lacking this region were stabilized (Figs 5A and S3B). To identify key residues in the degron, we mutated methionine 178 and isoleucine 179, a hydrophobic patch close to the F-box domain and conserved amongst WD-40 repeat containing F-box proteins. Mutation of both residues to glutamate (M178E and I179E) blocked ‘Skp1-free’ Met30\textsuperscript{ΔFbox} degradation (Fig 5B). Introduction of the same mutations into full length Met30 dramatically stabilized Met30 (Fig 5C), suggesting that under normal growth conditions the majority of Met30 in the cell was being targeted for proteolysis via the ‘Skp1-free’ degradation pathway.

Cdc53/Rbx1 can bind Met30 in absence of Skp1

To determine the composition of the ligase and identify unknown adaptor components we performed mass spectrometry with purified Met30\textsuperscript{ΔFbox} to analyze its binding partners. In addition, we used the same strategy to profile Cdc53 interacting proteins, with the hope to identify adaptors that function as Skp1 alternatives by searching for commonalities between these two mass spectrometry datasets. We failed to identify any proteins that fit these criteria. Although negative result cannot be conclusive, this result suggested that perhaps Cdc53/Rbx1 might directly bind Met30 without an adaptor protein. To examine binding in absence of Skp1, we used a yeast strain harboring a \textit{GAL1-SKP1} allele such that Skp1 depletion could be achieved by growing the strain in media containing dextrose, which efficiently suppresses the \textit{GAL1} promoter (Fig 6A, left panel). This yeast strain served as a source of protein extract lacking Skp1. Maltose-binding protein (MBP) fused to the N-terminal region of Met30 was expressed in bacteria and used as substrate. The \textit{in vitro} binding assay was performed with immobilized (MBP)-Met30\textsuperscript{1–186} and Skp1 depleted yeast lysates. In the absence of Skp1, Cdc53 bound effectively to (MBP)-Met30\textsuperscript{1–186} and binding was significantly reduced when (MBP)-Met30\textsuperscript{1–186}M178E/I179E was used as the bait (Fig 6A, right panel). Therefore, the same mutations, M178E and I179E that prevent degradation of Met30 by the ‘Skp1-free’ pathway \textit{in vivo} also reduce Skp1-independent binding of Cdc53 to Met30 \textit{in vitro}. Because this binding assay contained total yeast lysates, albeit lacking Skp1, it was possible that an unknown yeast protein mediated the interaction between (MBP)-Met30\textsuperscript{1–186} and Cdc53. To test whether any other factor apart from Cdc53/Rbx1 were necessary for this interaction, we utilized 6XHisCdc53/GST Rbx1 expressed in bacteria [41] for \textit{in vitro} binding experiment. Immobilized (MBP)-Met30\textsuperscript{1–186} was incubated with Cdc53/Rbx1 expressed in bacteria and binding was analyzed by immunoblotting with anti-Cdc53 antibodies. Similar to the result with yeast lysate, Cdc53/Rbx1 could specifically interact with (MBP)-Met30\textsuperscript{1–186} and binding was significantly decreased in the degron mutations that stabilized Met30 \textit{in vivo} (Fig 6B). Cdc53 expressed in \textit{E. coli} is spontaneously cleaved at the N-terminal region resulting in a truncated version (residues 267–851)[41]. Importantly, the removed residues 1–266 harbor the Skp1-binding region.
Therefore, Met30 can interact with Cdc53/Rbx1 in vitro at a site distinct from the Skp1 binding domain of Cdc53.

As binding studies strongly suggested that Cdc53/Rbx1 could directly interact with Met30 without an adaptor protein, we tested whether Cdc53/Rbx1 could ubiquitylate 'Skp1-free' Met30
and was sufficient to function as a ligase. (MBP)-Met30$^{(1–186)}$ was immobilized to amylose resin and incubated with bacterial lysate expressing Cdc53/Rbx1. The substrate-ligase complex was eluted and the ubiquitylation reaction was initiated by addition of the reaction mix containing E1 enzyme, E2 conjugating enzyme, ubiquitin and ATP. (MBP)-Met30$^{(1–186)}$ was ubiquitylated in vitro and the reaction was dependent on Cdc53/Rbx1 complex (S4A Fig). However, the reaction is very inefficient and only a small fraction of Met30$^{(1–186)}$ was ubiquitylated even after 16 h incubation of the reaction. To test whether this weak activity was specific for the ‘Skp1-free’ degradation pathway of Met30, we compared ubiquitylation in (MBP)-Met30$^{(1–186)}$ and (MBP)-Met30$^{(1–186)M178E/I179E}$ mutant. Ubiquitylation of (MBP)-Met30$^{(1–186)M178E/I179E}$ was visibly reduced (S4B Fig). Although these experiments demonstrate ubiquitylation of Met30 by a minimal cullin-1 (Cdc53) complex lacking Skp1 the observed activity is not very robust and requires a long reaction time (~ 16 hours) and yet only a relatively small fraction of the substrate is ubiquitylated. This suggests possible involvement of another factor or a post-translational modification, which is likely not required for binding Cdc53/Rbx1 to Met30 but is required for effective ubiquitylation of the substrate. Alternatively, Cdc53 expressed in E. coli may not efficiently fold into its active structure and thus be only partially active.

Skp1-independent degradation of F-box proteins Ctf13 and Cdc4

Our results strongly supported the hypothesis of Skp1-independent degradation of ‘free’ Met30. We next asked whether this Skp1-independent degradation pathway was unique for Met30 or may be a more general mechanism to limit F-box protein abundance. Such a mechanism for F-box protein homeostasis could be important not only to limit the overall abundance, but also to limit competition for substrates between assembled SCF ligases and the ‘free’ F-box protein subunits, which could lead to substrate shielding and thus prevent substrate ubiquitylation. Although degradation of the F-box protein Cdc4 has been demonstrated to follow the autoubiquitylation pathway [10,11] evidence has also been reported that Cdc4 continues to be degraded in skp1-3 temperature sensitive mutants, and Cdc4 was also shown to be stabilized when Skp1 is overexpressed [14]. In addition, the kinetochore component and F-box protein Ctf13 was reported to be rapidly degraded in a Cdc34 dependent mechanism when Skp1 was inactivated [42]. These examples are consistent with ‘Skp1-free’ Cdc4 and Ctf13 degradation pathways as we suggest here for Met30. To further test this idea, we measured degradation of the F-box proteins Ctf13 and Cdc4 in skp1-td mutants (Fig 7A and 7B). Consistent with a previous report [42] Ctf13 degradation was accelerated in skp1-td mutants (Fig 7A). Cdc4 is mainly regulated via autoubiquitylation. In skp1-td mutants, Cdc4 was slightly more stable compared to wild type cells, but still degraded rapidly even though Skp1 was depleted as evident by deubiquitylated Met4 (Fig 7B) and elongated, multibudded cells. Rapid degradation of Cdc4 even in the absence of Skp1 is inconsistent with previous reports showing that deletion of the F-box region in Cdc4 significantly stabilizes the protein [11]. However, in the Cdc4$^{ΔFbox}$ mutant used in this study the F-box deletion extended into the region corresponding to the degron region in Met30 [43] providing a possible explanation for these conflicting results.

If the autocatalytic pathway was the major mode of degradation responsible for maintaining F-box protein homeostasis then reduction in Skp1 levels should induce complete stabilization of these proteins. Thus, these results provide evidence for existence of an additional, Skp1-independent, degradation pathway for several F-box proteins, which appears to target F-box proteins that are not bound to the SCF core complex. We refer to this degradation pathway as ‘Skp1-Free’ F-box protein degradation pathway to demarcate it from the autoubiquitylation mode of F-box protein regulation.
Skp1-free F-box degradation is important for cellular function

To explore the significance of the ‘Skp1-free’ F-box protein degradation pathway in normal cellular dynamics, we generated yeast strains bearing either wild type Met30 or the Met30M178E/I179E mutant, each controlled by the native MET30 promoter. As expected, Met30 displayed increased abundance in cells expressing the degron point mutant in comparison to those expressing the wild type allele (Fig 8A). Interestingly, despite the increased protein abundance of Met30M178E/I179E steady-state ubiquitylation of the major SCF<sup>Met30</sup> substrate, the transcription factor Met4, [25], was slightly reduced (Fig 8A). The M178E/I179E double mutant specifically blocks Skp1-independent degradation of Met30 and it is thus conceivable that Met30 not bound to Skp1, which is normally rapidly degraded, is particularly increased in the Met30M178E/I179E strain. Consequently, a fraction of Met4 could be protected from ubiquitylation if it interacts with excess Met30<sup>M178E/I179E</sup> that cannot find a Skp1 binding partner.

We reasoned that the Skp1-independent degradation pathway should be particularly important for the recovery from heavy metal stress. Cadmium exposure leads to dissociation of Met30 from Skp1 [24,26,27] thereby generating a burst of ‘Skp1-free’ Met30, which needs to be controlled by the ‘Skp1-free’ F-box protein degradation pathway. We therefore tested cadmium sensitivity of wild type and <sup>MET30M178E/I179E</sup> strains. Cells expressing Met30M178E/I179E were significantly more sensitive and exhibited a growth arrest in response to cadmium stress (Fig 8B). We hypothesized that excess dissociated Met30 may bind Met4 and shield it from ubiquitylation by fully assembled SCF<sup>Met30</sup> ligase during the recovery phase. The cell cycle checkpoint arrest, initiated by deubiquitylated Met4 to cope with cadmium stress, may therefore be erroneously maintained in <sup>MET30M178E/I179E</sup> mutants resulting in apparent cadmium sensitivity. The observed growth defect in the presence of cadmium may not indicate a failure to detoxify cadmium but a defect in reversing cell cycle arrest. We tested this hypothesis by deleting <sup>MET32</sup> in <sup>MET30M178E/I179E</sup> mutants (Fig 8C). Met32 is essential for execution of the Met4-induced cell cycle arrest, but its transcriptional role, which is important for cadmium detoxification, is redundant with Met31 [24,26]. In accordance with our hypothesis, deletion of <sup>MET32</sup> suppressed the growth defect of cells expressing Met30<sup>M178E/I179E</sup> under cadmium stress.
stress (Fig 8C), indicating that excess dissociated Met30M178E/I179E interferes with timely inactivation of Met4. Consistent with this idea, two tested Met4 target genes, MET3 and GSH1, were derepressed in Met30M178E/I179E mutants confirming untimely Met4 activation (Fig 8D).

Together, these results indicate that the ‘Skp1-free’ F-box protein degradation pathway plays an important role in cellular function to prevent substrate shielding effects by excess unbound F-box proteins.
In addition to enhanced cadmium sensitivity, Met30^{M178E/I179E} mutants displayed increased chromosome loss (Fig 8E). The mechanism for this defect is not known. Protection of an unknown substrate in analogy to Met4 shielding during recovery from cadmium stress is a possible mechanism. However, it is also conceivable that stabilized Met30^{M178E/I179E} interferes locally with Skp1 functions in kinetochore assembly [42,44].

Discussion

We describe a novel pathway for regulation of F-box protein abundance in addition to autoubiquitylation that specifically targets F-box proteins that are dissociated from Skp1. The architectural theme of SCF ubiquitin ligases employs multiple F-box proteins that bind a common Skp1/Cdc53/Rbx1 core. This arrangement is effective in providing an array of diverse ubiquitin ligases. However, the modular design presents cells with the challenge of balancing the diversity and abundance of different SCF complexes when many F-box proteins, in the case of plants several hundred [45], compete for the shared SCF core components. Cycles of cullin neddylation and CAND1 association maintain a critical level of unoccupied SCF core complexes [9,12,46] while Skp1-F-box protein heterodimers are displaced to bind substrates and recruit them to the Cdc53/Rbx1 complex [47]. This CAND1/Nedd8 cycle maintains dynamic exchange of substrate adapters, but abundance of individual SCF ligases and overall SCF diversity is dictated by the distribution of F-box protein concentrations. It is thus critical to regulate F-box protein levels. In this study we characterize a ‘Skp1-free’ F-box protein degradation pathway that plays an important role in maintaining F-box protein homeostasis. F-box proteins that associate with Skp1 form functional ligases while those that do not, are recognized by the ‘Skp1-free’ F-box protein degradation pathway and degraded by the Cdc53/Rbx1 ligase thereby preventing competition between F-box proteins, limiting substrate shielding effects and ensuring representation even of low abundance F-box proteins in the cellular SCF repertoire. Degradation of F-box proteins that are not bound to Skp1 may also provide an important quality control mechanism to remove damaged F-box proteins. Such a mechanism may be critical for cells because F-box proteins incapable of forming active SCF ligases could maintain an intact substrate binding domain and thus shield their substrates from degradation.

We describe the ‘Skp1-free’ F-box protein degradation pathway in detail for Met30, the substrate adaptor for SCF{Met30} ubiquitin ligase, which negatively regulates transcription factor Met4 by proteolysis-independent ubiquitylation [23,48,49]. The ‘Skp1-free’ F-box protein degradation pathway is of particular importance for Met30. First, because Met4 ubiquitylation does not induce its degradation under normal growth conditions, Met4 remains associated with Met30 and therefore prevents the canonical F-box-protein degradation pathway through autoubiquitylation. Accordingly, we observed that the ‘Skp1-free’ degradation pathway is the predominant pathway that ensures turn over of excess Met30 (Fig 5C). Second, heavy metal stress induces active dissociation of Met30 from Skp1 resulting in a burst of ‘Skp1-free’ Met30, which interferes with recovery from cadmium stress when the ‘Skp1-free’ degradation pathway is blocked (Fig 8B and 8C).

Indications for a degradation pathway that targets F-box proteins that are not bound to Skp1 have been reported previously [14,42]. In addition, we show that apart from Met30, the two other essential yeast F-box proteins—Cdc4 and Ctf13 are also degraded in the absence of Skp1 (Fig 7A and 7B), suggesting that this pathway is a common mechanism to restrict F-box protein abundance outside the SCF complex. However, not all F-box proteins are subject to this degradation mechanism, because consistent with other reports [10] we found that deletion of the F-box region in Grr1 or inactivation of Skp1 stabilized Grr1 (S5 Fig). The F-box protein degradation pathway we describe here is thus not universal and is probably
functional for only those F-box proteins, which harbor the hydrophobic region adjacent to the F-box domain, which is paramount for Cdc53/Rbx1 ligase binding.

In addition to advancing understanding of SCF ligase regulation, our results also demonstrate a function for Cdc53 (cullin-1) independent from its adaptor Skp1. Not only was Met30 degradation active in the absence of Skp1 in vivo (Fig 3C), but in addition a Cdc53 mutant incapable of binding to Skp1 could fully complement the Met30 degradation defect of cdc53 mutants (Fig 4). In addition, Cdc53/Rbx1 can directly bind Met30 in the absence of Skp1 in vitro and binding depends on the degron region adjacent to the F-box motif (Fig 6). However, Met30 ubiquitylation in this minimal in vitro system with Cdc53/Rbx1, Cdc34, and E1 was very inefficient and required a long reaction time suggesting possible involvement of additional factors, inefficient protein folding in E. coli, or a post-translational modification lacking in this expression system. Further studies need to be conducted to explore these options in detail.

The findings reported here illustrate a Skp1 independent function for the cullin Cdc53 in substrate ubiquitylation. Consistent with these results, a Skp1 independent cullin-1 based ubiquitylation event has been suggested previously in human cells where Rictor, a component of mTORC2 complex associates with Cullin-1 instead of Skp1, to form a functional E3 ubiquitin ligase that promotes ubiquitylation of SGK1 [50].

Together, our findings shed light on the regulation and complexity of E3 ligases and suggest additional diversity in the cullin-RING family of ubiquitin ligases.

Materials and Methods

Yeast strains and growth conditions

Yeast strains used in this study are isogenic to 15DaubΔ, a bar1Δ ura3Δns; a derivative of BF264-15D [51] and are listed in S1 Table. Standard culture media and yeast genetic techniques were employed [52]. Determination of protein degradation rates was done using cycloheximide chase experiments and galactose shut-off experiments. For cycloheximide chase experiments, strains carrying plasmids expressing tagged genes of interest placed under their endogenous promoter were cultured to logarithmic phase and cycloheximide (final concentration 100 μg/ml) was added and cells were collected at time points as indicated. For galactose shut-off experiments, strains expressing genes of interest under the control of GAL1 promoter were cultured in media containing 2% sucrose to logarithmic phase and cultures were transferred to rich media containing 2% galactose (YEPG) for 2 hours or as otherwise indicated. To terminate expression from the GAL1 promoter cells were transferred to YEPD and collected at the indicated time intervals. Quantitation of protein levels was performed using a Fuji LAS-4000 imaging system followed by analyses with the Multi Gauge v3 software.

Protein analysis

For immunoblot analysis, yeast whole cell lysates were prepared under denaturing conditions in urea buffer and for immunoprecipitation cells were lysed in Triton X-100 Buffer, as previously described [53]. For purification of HBTH-tagged Met30ΔFbox, cells were lysed and purified under denaturing conditions in binding buffer (8M urea, 300mM NaCl, 0.5% NP-40, 50mM PO4, pH 8, 50mM Tris-HCl pH 8, 20mM imidazole). 1 mg of total protein lysates was used for binding to Nitr2⁺-sepharose (GE Healthcare). Beads were then washed 3 times in binding buffer (without imidazole and pH adjusted to 6.3) and eluted in 150μl elution buffer (8M urea, 200mM NaCl, 50mM PO4, 2% SDS, 10mM EDTA, 100mM Tris-HCl, pH 4.3).

For immunoblot analyses proteins were separated by SDS-PAGE and transferred to a polyvinylidene difluoride membrane. Proteins were detected with the following primary antibodies: anti-Met4 (1:10000; a gift from M. Tyers), anti-Skp1 (1:5000; a gift from R. Deshaies), anti-myc...
and anti-HA (1:2000; Covance, Princeton, NJ), anti-RGS6H (1:2000; QIAGEN, Germantown, MD), anti-ubiquitin (1:2000; P4G7, #sc-53509, Santa Cruz), anti-Cdc53 (1:1000; yN-18, #sc-6716, Santa Cruz) and anti-MBP (1:2000; N-17, #sc-809, Santa Cruz).

Purification of recombinant proteins
Plasmids expressing MBP- Met30(1–186) and MBP- Met30(1–186)M178E/I179E were cloned by standard techniques into the pET28 vector and transformed into Rosetta cells. Cells were grown at 37°C and induced with 0.5 mM IPTG for 3 hours. Cells were collected, washed once with cold water, pelleted and frozen. Pellets were later suspended in recombinant protein buffer (0.05% Triton-X100, 0.05% NP-40, 150 mM NaCl, 1 mM PMSF, 1 μg/ml each aprotenin, leupeptin and pepstatin), sonicated and cleared by centrifugation at 13,000 rpm at 4°C for 10 minutes. Lysates were then bound to prewashed amylose beads (New England Biolabs) for 3 hours at 4°C. Beads were then washed twice with lysis buffer and thrice with buffer U (50 mM Tris pH 8, 50 mM NaCl, 5 mM ATP, 10 mM MgCl2, 0.2 mM DTT). MBP-tagged proteins were eluted in buffer U supplemented with 10 mM maltose. Purified protein was concentrated using Amicon Ultra 50 kDa centrifugal filter and flash frozen.

In vitro binding assay
For in vitro binding assay with yeast lysates, yeast cells containing a GAL1-controlled SKP1 allele and expressing endogenous TAP-tagged Cdc53 were grown in YEP galactose overnight, washed and then transferred to YEP dextrose media for 12 hours to deplete Skp1 protein levels. At this point cells were arrested and showed the characteristic elongated buds. MBP, (MBP)-Met30(1–186) and (MBP)-Met30(1–186)M178E/I179E were lysed and bound to amylose resin as described above. Yeast cell pellets were also lysed in recombinant protein buffer and 3 mg of lysate was incubated with MBP tagged proteins bound to amylose resin, for 2 hours at 4°C. Beads were washed thrice with recombinant protein buffer and bound proteins were eluted by boiling beads in 2x SDS loading buffer.

For the in vitro binding experiment performed with Cdc53/ GST-Rbx1 expressed from bacteria, bacterial cell pellets were lysed in recombinant protein buffer, sonicated and 3 mg of lysate was incubated with MBP tagged proteins conjugated to amylose resin, for 2 hours at 4°C. Beads were washed thrice with recombinant protein buffer and bound proteins were eluted by boiling beads in 2x SDS loading buffer.

Real time PCR
RNA samples were isolated, and analyzed by real-time Reverse Transcriptase (RT)-PCR as described [53]. Three biological replicates were analyzed for each experiment.

Plasmid stability assay
Strains harboring a centromeric plasmid with a URA3 selection marker were grown at 30°C in minimal medium lacking uracil to force cells to maintain the centromeric plasmid. 200 cells were plated on YPD and minimal media (SC-URA) plates. The remaining cells were cultured without selection for 22 hours (~ 7 generations). Cells were counted and 200 cells were plated again on YPD and minimal media plates to measure the number of cells that have lost the centromeric plasmid. Plates were incubated for 2 days at 30°C and chromosome/plasmid loss was determined by difference in number of colonies on SC-URA plates and YPD plates. Experiments were performed in triplicates.
Supporting Information

S1 Fig. Conditions that disrupt Met30-Skp1 binding destabilize Met30. (A) Cells expressing RGS6H-Met30ΔFbox under control of GAL1 promoter were grown in sucrose medium at permissive temperature at 30°C. Expression of Met30 was induced by addition of 2% galactose for 2.5 h following which 2% dextrose was added to repress GAL1-MET30 expression. Samples were collected at the time intervals indicated and analyzed by immunoblotting with anti-RGS6H antibodies. (B) Cells expressing 12MycMet30 and 12MycMet30L187D were grown at 30°C. 12MycMet30 was immunopurified and co-purified proteins were analyzed by immunoblotting. A yeast strain expressing untagged Met30 was used as a control. WCE: Whole cell extract (C) Cells expressing RGS6H-Met30 under control of GAL1 promoter were grown in sucrose medium at permissive temperature (25°C). Expression of Met30 was induced by addition of 2% galactose for 1 h, cells were shifted to 37°C for 1.5 h to inactivate the temperature sensitive allele, and 2% dextrose was added to repress GAL1-MET30 expression. Cadmium was added to a final concentration of 200μM. Samples were collected at the time intervals indicated and analyzed by immunoblotting with anti-RGS6H antibodies.

(TIF)

S2 Fig. (A and B) Degradation of ‘Skp1-Free’ Met30 is not dependent on Met4 and Lag2. Cycloheximide chase experiment as described for Fig 1B, was performed in wild type, MET4 deleted and LAG2 deleted cells and 12myc-Met30ΔFbox stability was assayed.

(TIF)

S3 Fig. (A) Mutations in residues important for dimerization domain of Met30 are not essential for the ‘Skp1-free’ Met30 degradation pathway. Cells expressing either endogenous 12myc-Met30ΔFbox or different Met30ΔFbox deletion mutants were grown at 30°C. Protein translation was inhibited by addition of cycloheximide and cells were collected at the time intervals indicated. Met30ΔFbox stability was analyzed by immunoblotting with anti-myc antibodies. (B) Smaller deletions within Met30ΔFbox suggesting that the degron for the ‘Skp1-free’ Met30 degradation pathway lies within 170–187 amino acids of Met30. Experiment same as for panel S3A.

(TIF)

S4 Fig. Cdc53/Rbx1 can ubiquitylate Met30 in vitro. (A) (MBP)-Met30\(^{11-186}\) was immobilized to amylose resin and incubated with Cdc53\(^{267-851}\)/Rbx1 expressed in bacteria. Substrate-ligase complex was eluted with 10mM maltose and incubated with ubiquitylation reaction mix for 16 h at 30°C. Ubiquitylation was analyzed by immunoblotting with anti-MBP antibody. (B) Cdc53\(^{267-851}\)/Rbx1 was purified on glutathione sepharose beads. Efficiency of purification was determined by immunoblotting the eluate with anti-Cdc53 antibody and anti-GST antibody (top panel). In vitro ubiquitylation reaction was performed with purified (MBP)-Met30\(^{11-186}\) and (MBP)-Met30\(^{11-186}\)M178E/I179E and purified Cdc53\(^{267-851}\)/Rbx1. ‘0’ and 16 h time points were collected. Ubiquitylation profile was assayed by immunoblotting with anti-MBP antibody (bottom panel).

(TIF)

S5 Fig. Grr1 is not regulated via ‘Skp1-free’ F-box protein degradation pathway. (A) GAL1 promoter shut off experiment as described in Fig 1C, but experiment was performed with cells expressing either endogenous 3MycGrr1 or 3mycGrr1ΔFbox (residues 320–360 deleted). (B) Experiment as in panel A, but 3mycGrr1ΔFbox stability was analyzed in wild type and skp1-25 temperature sensitive mutants.

(TIF)
S1 Table. Yeast strains used in this study.

(DOCX)

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Author Contributions

Conceived and designed the experiments: RM PK JLY. Performed the experiments: RM PK JLY. Analyzed the data: RM PK JLY. Wrote the paper: RM PK.

References


dimer accommodates multiple geometries for substrate ubiquitination. Cell 129: 1165–1176. PMID:
17574027
42. Kaplan KB, Hyman AA, Sorger PK (1997) Regulating the yeast kinetochore by ubiquitin-dependent
degradation and Skp1p-mediated phosphorylation. Cell 91: 491–500. PMID: 9390558
iversity of Washington, Seattle, Washington.
44. Connelly C, Hieter P (1996) Budding yeast SKP1 encodes an evolutionarily conserved kinetochore pro-
within the plant kingdom reveals divergent evolutionary histories indicative of genomic drift. PLoS One
6: e16219. doi: 10.1371/journal.pone.0016219 PMID: 21297981
2013.02.024 PMID: 23453757
10.1038/cr.2013.55 PMID: 23609796
641. PMID: 15208638
PMID: 12150908
PMID: 20832730
51. Reed SI, Hadwiger JA, Lorincz AT (1985) Protein kinase activity associated with the product of the
yeast cell division cycle gene CDC28. Proceedings of the National Academy of Sciences of the United
States of America 82: 4055–4059. PMID: 3889921
Press, Inc.
nated Met4 from degradation by the 26S proteasome. Nat Cell Biol 8: 509–515. PMID: 16604062