CDK-Dependent Hsp70 Phosphorylation Controls G1 Cyclin Abundance and Cell-Cycle Progression

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SUMMARY

In budding yeast, the essential functions of Hsp70 chaperones Ssa1–4 are regulated through expression level, isoform specificity, and cochaperone activity. Suggesting a novel regulatory paradigm, we find that phosphorylation of Ssa1 T36 within a cyclin-dependent kinase (CDK) consensus site conserved among Hsp70 proteins alters cochaperone and client interactions. T36 phosphorylation triggers displacement of Ydj1, allowing Ssa1 to bind the G1 cyclin Cln3 and promote its degradation. The stress CDK Pho85 phosphorylates T36 upon nitrogen starvation or pheromone stimulation, destabilizing Cln3 to delay onset of S phase. In turn, the mitotic CDK Cdk1 phosphorylates T36 to block Cln3 accumulation in G2/M. Suggesting broad conservation from yeast to human, CDK-dependent phosphorylation of Hsp70 T38 similarly regulates Cyclin D1 binding and stability. These results establish an active role for Hsp70 chaperones as signal transducers mediating growth control of G1 cyclin abundance and activity.

INTRODUCTION

The 70 kDa heat shock proteins (Hsp70s) are highly conserved and ubiquitous molecular chaperones essential for cell viability. They bind a range of client proteins, directing key events in their life cycle from folding to destruction (Craig and Marszalek, 2011; Mayer and Bukau, 2005; Meimaridou et al., 2009). Hsp70 proteins share an N-terminal ATPase domain, a substrate binding domain and a C-terminal regulatory domain that mediates cochaperone interaction (Mayer and Bukau, 2005). The budding yeast Saccharomyces cerevisiae genome encodes four functionally redundant cytosolic Hsp70s, Ssa1–4, which differ in expression pattern but are together essential for cell viability (Newcomb et al., 2003).

The yeast DnaJ-related cochaperones (J-proteins) Ydj1 and Sis1 regulate Hsp70 ATP hydrolysis and client interactions (Brehmer et al., 2001; Kampina and Craig, 2010). Interestingly, despite partially overlapping functions, only Sis1 is essential (Caplan and Douglas, 1991; Jones et al., 2004).

Among many known functions of yeast Hsp70 and J-domain proteins, a complex role in cell proliferation has been described. One Ssa client is the cyclin Cln3, the yeast homolog of Cyclin D. Cln3 accumulation activates the cyclin-dependent kinase (CDK) Cdk1 to phosphorylate Whi5. This releases SBF (Swi4-Swi6) and MBF (Swi6-Mbp1) to promote Cln1 and Cln2 cyclin expression, G1 exit, and S phase onset (de Bruin et al., 2004; Ferrezuelo et al., 2010; Sherlock and Rosamond, 1993). Diverse stress signals, including mating pheromone stimulation and nitrogen starvation can delay G1/S progression by promoting phosphorylation of PEST sequences in Cln3 leading to proteasome-mediated Cln3 degradation (Benanti, 2012). Significantly, Ssa proteins and Ydj1 are required for normal Cln3 phosphorylation and destruction (Verges et al., 2007; Yaglom et al., 1995; Yaglom et al., 1996). Unlike other Ssa clients, Cln3 encodes a J-like domain that competes with Ydj1 for binding. As a result, Ssa proteins can sequester accumulating Cln3 on the ER in early G1. Then, Ydj1 displaces Cln3 in late G1, allowing its transit to the nucleus to drive cell cycle progression (Verges et al., 2007). The mechanism of this switch remains poorly understood.

A second yeast CDK, Pho85, has a special role in responding to stress signals by targeting multiple survival, morphogenesis, and proliferation pathways (Carroll and O’Shea, 2002; Huang et al., 2007; Yang et al., 2010). Pho85 cyclins (Pcls) direct the kinase to specific targets, including substrates shared with Cdk1 (Huang et al., 1998; Mazanka and Weiss, 2010). Like Cln3, Pcl9 induces Pho85 phosphorylation of Whi5 in early G1 (Huang et al., 2009; Kung et al., 2005) to promote Cln1/2 and Pcl1 expression. Then, like Cln1/2, Pcl1 targets Pho85 to Sic1 in late G1 (Nishizawa et al., 1998; Wysocki et al., 2006) to release Cdk1-Clb activity in S phase.
Despite proteomic evidence of extensive Ssa phosphorylation and the recent finding that mutation of putative phosphorylation sites affects essential functions (Beltrao et al., 2012), a regulatory role remains to be established. However, cell-cycle-dependent phosphorylation of yeast Hsp90 alters chaperone-client interactions, suggesting functional significance (Mollapour et al., 2010). Here, we show that Ssa1 can be phosphorylated by Cdk1 or Pho85 on T36, a CDK consensus site conserved across the yeast Hsp70s and among mammalian Hsp70 isoforms (including Hsp70 and Hsc70 as shown here). (B) T36 resides adjacent to the ATP-binding pocket on Hsc70. T36 is marked in red on the Hsc70 structure (PDB: 1YUW). NBD is nucleotide-binding domain, SBD is substrate binding domain. (C) Temperature sensitivity of the Ssa1 T36 phosphomutants. Cells expressing wild-type Ssa1 (SSA1) or Ssa1 phosphosite mutants T36A or T36E as their sole Ssa protein were spotted in serial 10-fold dilutions onto YPD media and were incubated for 48 hr at 30°C, 37°C or 39°C. (D) Mutation of T36 affects nucleotide binding. The intrinsic ATPase activity of WT, T36A and T36E Ssa1 was assayed and the $k_{cat}$ values (min$^{-1}$) are shown as mean ± SD (n = 3). Nucleotide binding of WT, T36A and T36E was calculated by isothermal calorimetry. The $K_d$ (mM) for the Ssa1 proteins are shown as mean ± SD (n = 3). (E) Ssa1 T36E mutation confers a large G1 cell phenotype. Cells grown at 30°C to mid-log phase were analyzed by flow cytometry. Cells in G1 stage of cell cycle were gated based on 1N DNA content, and the size distribution based on Forward Scatter (FSC) of each strain is plotted. (F) T36E cells display delayed G1/S progression. Cells were synchronized in G1 by nitrogen starvation then released into rich media and incubated at 30°C. At 20 min intervals, cells were fixed and assessed for DNA content by flow cytometry. (G) Halo assay of response of SSA1, T36A and T36E to αF pheromone reveals an arrest defect in T36A, expressing the nonphosphorylatable Ssa1 mutant. (H) Ssa1 T36 is phosphorylated in response to αF. His$_e$-Ssa1 was purified from untreated or αF-treated SSA1 or T36A cells. Ssa1 phosphorylation was assessed with CDK phosphosite-specific anti-Phos-T-P antibody. See also Figure S1.

**RESULTS**

**Cell Proliferation Defects in Ssa1 T36 Mutants**

Global phosphoproteomic analysis has identified 18 phosphorylation sites in Ssa proteins (Albuquerque et al., 2008) but biological significance has yet to be established. Of these phosphosites, only T36 lies within a consensus S/T-P CDK phosphorylation motif. T36 is highly conserved among Hsp70 family proteins (Figure 1A) and is situated in the N-terminal domain, proximal to the ATP binding and cochaperone binding region (Figure 1B), suggesting a potential regulatory role.
To examine functions of T36 phosphorylation, we used a yeast strain in which all four SSA genes have been deleted and functionally complemented by SSA1 expressed from a URA3-marked centromeric plasmid (Jaiswal et al., 2011). The strain was transformed with a LEU2-marked plasmid bearing either wild-type SSA1, the nonphosphorylatable mutant ssa1-T36A, or the phosphorylating mutant ssa1-T36E. The URA3 plasmid was evicted on 5-fluoro-orotic acid (5-FOA) media to yield strains expressing wild-type SSA1, SSA1-T36A (mimic for nonphosphorylated form), or SSA1-T36E (mimic for phosphorylated form) as the sole Ssa protein in the cell, hereafter referred to as SSA1, T36A, and T36E cells. The SSA1, T36A, and T36E cells were similarly viable at 30°C, but the T36E mutation conferred impaired growth at 37°C and inviability at 39°C (Figure 1C). Both T36A and T36E cells demonstrated increased sensitivity to incubation at 42°C (Figure S1 available online).

We analyzed the effect of T36 mutation on the in vitro properties of Ssa1. Whereas intrinsic ATPase activity of WT, T36A, and T36E proteins was not significantly altered, nucleotide binding was decreased in both mutants, suggesting an important regulatory role for this site in Ssa1 function (Figure 1D).

To further dissect effects on cell proliferation, we examined the growth of SSA1, T36A, and T36E cells as they progressed through the cell cycle. In asynchronous growth, T36E cells attained a larger cell size before exiting G1 compared to WT, T36A, and T36E cells as they progressed toward 2N DNA content by 80 to 100 min after release, many T36E cells remained in G1 past 120 min (Figure 1F). In turn, when SSA1, T36A, and T36E cells were exposed to the peptide mating pheromone α-Factor (αF), T36A cells failed to arrest, unlike SSA1 or T36E (Figure 1G). To examine SSA1 T36 phosphorylation in response to αF, we generated strains expressing hexahistidine-tagged WT or T36E as the sole Ssa protein in the cell. The His6-Ssa1 and -T36A cells were treated with αF, and His6-Ssa1 protein was purified. Immunoblotting with anti-phospho-Thr-Pro antibody (anti-Phos-T-P, specific to phosphorylated form) as the sole Ssa protein in the cell, hereafter referred to as SSA1, T36A, and T36E cells. The SSA1, T36A, and T36E cells were similarly viable at 30°C, but the T36E mutation conferred impaired growth at 37°C and inviability at 39°C (Figure 1C). Both T36A and T36E cells demonstrated increased sensitivity to incubation at 42°C (Figure S1 available online).

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**Proteomic Analysis of Phosphoregulation of the Ssa1 Interactome**

Toward identifying Ssa1 partners regulated by T36 phosphorylation, we treated the His6-Ssa1 and T36A cells with αF, purified the His6-Ssa1 interactomes and compared them by isotope-coded tandem mass spectrometry (LC-MS/MS, Figure 2A). Gene Ontology (GO) analysis of 317 candidate Ssa partners, identified based on high confidence peptide matches, revealed significant enrichment of multiple cellular functions (Figure 2B; Table S1; Figure S2). The GO term “protein folding” was most enriched, reflecting the wide range of chaperones and co-chaperones identified (Figure 2C). Other enriched categories include “cell death” and “morphogenesis,” “protein transport,” “metabolism,” and “ribosome biogenesis.” Proteins that displayed 18O:16O peptide ratios >> 1 were inferred to be candidates for interaction partners that dissociate from Ssa1 upon T36 phosphorylation (Figure 2C, pink). Among chaperones/co-chaperones known to directly bind Ssa1, those displaying the highest ratios were the ribosomal Hsp70 Ssb1, the Hsp110 homologs Sse1 and 2 (Hsp70 nucleotide exchange factors), the J-protein Ydj1, and Hsp26. Of these, Ydj1 has previously been ascribed a key role in G1/S cell cycle regulation (Yaglom et al., 1995; Vergès et al., 2007).

To directly test Ydj1 dissociation upon T36 phosphorylation, we isolated His6-WT and T36A proteins from cells treated with αF. Western blotting indicated that T36 phosphorylation antagonizes Ydj1 binding to Ssa1 without affecting the essential J-protein Sis1 in SSA1 cells, whereas Ydj1 and Sis1 binding are similarly insensitive to pheromone stimulation in T36A cells (Figure 2D).

**Mutation of Ssa1 T36 Affects Cln3 Accumulation and Functions**

The J-protein Ydj1 and the G1 cyclin Cln3 display reciprocal patterns of binding to Ssa proteins (Vergès et al., 2007), suggesting that Ssa1 T36 phosphorylation might affect Cln3 activity or expression. Western analysis revealed a striking decrease in Cln3 protein abundance in T36E cells, although residual Cln3 was detected in longer exposures (Figure 3A). CLN3 transcription was not affected by T36 mutation (Figure 3B), indicating a posttranslational mechanism. Consistent with regulation via ubiquitin-proteasome-mediated degradation, a Cln3 mutant lacking the carboxyl-terminal PEST domains was similarly stable in SSA1, T36A, and T36E (Figure 3C).

Vergès et al. (2007) describe a mechanism by which binding of Ydj1 to Ssa1 promotes release of Cln3. We considered whether this process might be regulated by T36 phosphorylation. Pull-down of His6-Ssa1 revealed binding of stabilized Cln3 can be induced by nitrogen starvation in SSA1, but is lost from T36A, and becomes constitutive in T36E (Figure 3D). Suggesting that T36 phosphorylation disrupts the Ydj1-Ssa1 interaction to allow Cln3 access, loss of Ydj1 (ydj1Δ) restored Cln3 binding to Ssa1 in nitrogen-starved T36A cells (Figure 3E). Interestingly, in SSA1 cells lacking Ydj1, T36E phosphorylation upon nitrogen starvation was attenuated.

As a functional test of Cln3 activity, we expressed Whi5, a Cdk1-Cln3 target and repressor of G1/S transcription (Figure 3F), in SSA1, T36A, T36E, and cln3Δ cells under control of a strong, galactose-inducible promoter. Overexpression of Whi5 in cells lacking Cln3 function results in loss of viability (Costanzo et al., 2004). Like the cln3Δ control, the T36E mutant was unable to grow on galactose media, suggesting a critical deficit of Cdk1-Cln3 activity (Figure 3G). Similarly, we examined genetic interactions of the Ssa1 T36 mutants with Bck2, a positive regulator of G1/S transcription (Di Como et al., 1995; Ferrezuelo et al., 2009; Wijnen and Futcher, 1999). Cln3 and Bck2 serve partly redundant, essential functions. As such, bck2Δ cln3Δ double mutant cells are unable to transition to S phase, arresting in late G1 (Di Como et al., 1995; Ferrezuelo et al., 2009; Wijnen and Futcher, 1999). Whereas SSA1 and T36A cells lacking...
Bck2 remained viable, T36E was synthetically lethal with the \( bck2 \Delta \) mutation (Figure 3H). Consistent with these results, \( CLN2 \) expression was decreased significantly in T36E, nearly to the level of a \( cln3 \Delta \) mutant but was restored in the \( whi5 \Delta \) background (Figure 3I).

**Figure 2. Phosphorylation Alters the Ssa1 Interactome**

- (A) Scheme for proteomic analysis of Ssa1 interactome. Cells expressing wild-type (SSA1) or T36A mutant His\(_6\)-Ssa1 were exposed to αF, Ssa1 complexes were affinity purified and digested. Peptides from Ssa1-T36A interactors were isotopically labeled with \( ^{18}\)O, mixed 1:1 with wild-type Ssa1 interactor peptides, and analyzed by quantitative LC-MS/MS.
- (B) Functional classification of the Ssa1 interactome. Ssa1 interactors were categorized by cellular function using GO Slim analysis, and plotted by relative enrichment compared to occurrence in the nonessential genome.
- (C) Chaperones and cochaperones in the Ssa1 interactome. The 18 chaperone/cochaperone proteins identified were analyzed for interactions using STRING and visualized by Cytoscape, grouped by homology and function. Pink nodes represent proteins that decreased interaction with Ssa1 upon T36 phosphorylation.
- (D) Differential effect of T36 phosphorylation on Sis1 and Ydj1 binding. His\(_6\)-Ssa1 was pulled down from WT and T36A cells and probed for Ydj1 or Sis1 coprecipitation. See also Table S1 and Figure S2.

**Ssa1 T36 Is Phosphorylated by Cyclin-Dependent Kinases Cdk1 and Pho85**

Although T36 phosphorylation appeared absent from growing yeast cells compared to cells treated with αF (Figure 1H), overexposure of western blots detected potential low-level
phosphorylation (Figure S3). To determine whether T36 phosphorylation might be cell cycle regulated, we isolated enriched G1 (unbudded) and G2/M (large budded) fractions from growing His6-SSA1 cells via cytometric cell sorting. Ssa1 appeared unphosphorylated in G1 (high Cln), whereas T36 phosphorylation in G2/M (high Clb) was comparable to that after aF stimulation or nitrogen starvation (no Cln or Clb, Figure 4A). This raised the paradox that in a normal G1, when Cdk1-Cln1/2 is active, T36 remains unphosphorylated, but during G1 arrest in aF-treated and nitrogen-starved cells where Cdk1 is inactive, T36 is phosphorylated.

Because the CDKs Cdk1 and Pho85 share both specificity and substrates, we considered that both might be able to phosphorylate Ssa1 T36. We purified HA-Cdk1 or -Pho85 from cells treated with nocodazole (large budded mitotic checkpoint arrest, high Clb), nitrogen starvation, or aF and assessed their ability to phosphorylate recombinant Ssa1 in vitro. Only Cdk1 isolated from nocodazole-arrested cells and Pho85 purified from nitrogen-starved or aF-stimulated cells were able to phosphorylate Ssa1 (Figure 4B).

To confirm Cdk1-dependent phosphorylation of Ssa1 in vivo, we utilized a yeast strain expressing an analog-sensitive mutant Cdk1, Cdk1-as1 (Bishop et al., 2000). The inhibitor 1-NM-PP1 selectively binds to Cdk1-as1 and inhibits kinase activity within minutes. Cdk1-as1 cells expressing either His6-SSA1 WT or His6-SSA1 WT or T36A, along with stabilized, PEST mutant Cln3 were treated with 15 μg/ml nocodazole for 3 hr. Ssa1 was pulled down to determine T36 phosphorylation by anti-Phos-T-P blotting and assess Ssa1-Cln3 interaction by coprecipitation of HA-Cln3ΔPEST2. (E) Dissociation of Ydj1 from Ssa1 upon T36 phosphorylation allows Cln3 to bind Ssa1. Ydj1 wild-type or deletion mutant cells expressing either His6-Ssa1 WT or T36A, along with stabilized, PEST mutant Cln3 were treated with 15 μg/ml nocodazole for 3 hr. Ssa1 was pulled down to determine T36 phosphorylation by anti-Phos-T-P blotting and assess Ssa1-Cln3 interaction by coprecipitation of HA-Cln3ΔPEST2. (F) Schematic of regulation of G1/S transcription by Cdk1-Cln3 and Bck2.

(G) Overexpression of Whi5 is lethal in T36E cells. SSA1, T36A or T36E cells transformed with either GAL1-WHI5-FLAG or empty vector pRS316 were spotted in serial 10-fold dilutions on either glucose or galactose medium and incubated for 48 hr at 30°C.

(H) Bck2 is essential for cell viability in T36E cells. Both ssa1-4Δ and ssa1-4Δ, bck2Δ cells were transformed with LEU2-marked plasmids carrying SSA1, ssa1-T36E or ssa1-T36E or empty vector control (V) and then spotted in serial 10-fold dilutions on either YPD or 5-FOA media to evict aURA3-marked wild-type SSA1 plasmid, then incubated for 48 hr at 30°C.

I T36E cells are defective in CLN2 expression. SSA1, T36A and T36E cells, bearing deletions of CLN3 or WHI5 as indicated, were transformed with a CLN2-lacZ plasmid and CLN2 expression measured by β-galactosidase assay. Each value represents the mean ± SD (n = 3). See also Figure S3.
with nucodazole and assessed for ability to phosphorylate recombinant His$_6$-Cln3 in vitro. Suggesting that phosphorylation of Cln3 by Cdk1-Cib does not require Ssa1-Cln3 interaction, Cln3 phosphorylation was similar independent of whether any coprecipitated Ssa1 was WT, T36A, or T36E (Figure 4D).

To confirm the role of Pho85 in vivo, we examined Ssa1 phosphorylation and Cln3 accumulation in nitrogen-starved or zF-treated pho85Δ cells (Figure 4E; Figure S4A). Much like T36A cells under either condition, T36 phosphorylation was lost and Cln3 was stabilized in SSA1 cells lacking Pho85. However, expression of T36E in pho85Δ triggered degradation of Cln3, placing Pho85 upstream of Ssa1 with regard to Cln3 regulation (Figure 4F). As expected, lack of Pho85 also abolished the binding of stabilized Cln3 to Ssa1 in nitrogen-starved or zF-treated SSA1 cells (Figure 4G; Figure S4B).

Removal of the PEST domain stabilizes Cln3 even under conditions such as nitrogen starvation, where Cdk1 activity is low (Gallego et al., 1997), implying that a second kinase may phosphorylate Cln3 to promote degradation. Consistent with a dual role for Pho85 as an Ssa1 and Cln3 kinase, HA-tagged Pho85 purified from nitrogen-starved cells could directly phosphorylate recombinant His$_6$-Cln3 (Figure 4H). Taken together, the results suggest that, (1) both Cdk1 and Pho85 can target Cln3 for destruction via direct phosphorylation of both Ssa1 and Cln3 and, (2) Pho85 activity prevents Cln3 accumulation during nitrogen starvation and zF stimulation.

Roles of Ssa Proteins and Pcl Cyclins in Pho85-Dependent Regulation of Cln3

T36 is conserved among the yeast Ssa proteins (Figure 1A). Thus, we tested whether, like Ssa1, Ssa2, 3, or 4 might serve as alternative Pho85 substrates and similarly associate with Cln3 upon nitrogen starvation. Indeed, isolation of His$_6$-Ssa1, 2, 3, or 4 from cells also expressing stabilized Cln3 demonstrated increased Cln3 binding to each Ssa protein after nitrogen starvation (Figure 5A).

Like Cdk1 regulation by Clns and Clbs, Pho85 substrate specificity is determined through Pcl cyclin protein binding (Huang et al., 2007; Measday et al., 1997; Moffat et al., 2000). To detect which Pcl(s) might activate Pho85 to phosphorylate the Ssa proteins, we assessed physical interaction between Pcl proteins and Ssa1, 2, 3, and 4 by yeast two-hybrid analysis. Ssa1 associated most strongly with Clg1 and Pcl2 but displayed distinct patterns of binding to other Pcl cyclins. Ssa2 bound to Pcl6 and 8,
whereas Ssa3 and 4 only bound to Pcl8, suggesting specificity with respect to interaction with Pho85-cyclin complexes. Suggesting that Clg1 and/or Pcl2 may target Pho85 to Ssa proteins as a substrate, His6-Ssa1 isolated from cells expressing HA-Clg1 or HA-Pcl2 displayed enhanced binding of Ssa1 to Clg1 and Pcl2 upon low nitrogen stimulation (Figure 5C). In turn, binding of Pho85 to Ssa1 induced by nitrogen starvation was lost in cells lacking both the Clg1 and Pcl2 cyclins (Figure 5D).

Many kinases lose affinity for substrates after their phosphorylation. Further, consistent with a role in T36 phosphorylation, Clg1 and Pcl2 interaction in the two-hybrid assay was strengthened against T36A but decreased by T36E (Figure S5). Suggesting roles unrelated to Ssa1 phosphorylation, two-hybrid interactions of Pcl6 and 7 were independent of T36 mutation (Figure S5). These data suggest that Clg1 and/or Pcl2 may serve as the Pcl proteins that activate Pho85 to bind and phosphorylate Ssa proteins and target Cln3 for degradation.

**Phosphorylation of Hsc70 Alters Cyclin D1 Binding, Stability, and Cyclin D1-CDK-Mediated Signaling**

Overall, Hsp70 family members are highly conserved. Among them, Ssa1 in yeast and Hsc70 in mammalian cells are considered to be functional homologs (Jaiswal et al., 2011). The Ssa1 T36 consensus CDK site is conserved in Hsc70 as T38 (Figure 1A) and Cyclin D1, the mammalian homolog of Cln3, has been shown to bind to Hsc70 (Diehl et al., 2003), raising the question of whether chaperone-mediated cyclin destruction may be conserved from yeast to human. Purification of HaloTag-Hsc70 WT, T38A, and T38E proteins overexpressed in HEK293T cells and probed with the anti-Phos-T-P CDK phosphosite antibody revealed Hsc70 phosphorylation at T38 (Figure 6A). Consistent with CDK-mediated phosphorylation, incubation with the CDK inhibitor SU9516 moderately decreased T38 phosphorylation (Figure S6).

To examine whether T38 phosphorylation may regulate the Hsc70-Cyclin D1 interaction, we utilized a stabilized Cyclin D1 mutant, T286A (Newman et al., 2004). Cells cotransfected with HA-tagged Cyclin D1T286A and HaloTag-Hsc70 WT, T38A, or T38E were assessed for Hsc70-Cyclin D1 association via
**DISCUSSION**

**Regulation of Hsp70 through Phosphorylation**

The prevailing view of Hsp70 is that regulation is achieved via a combination of altered expression of Hsp70, subtle differences among Hsp70 isoforms and the diversity of cochaperones that recruit specific clients. Here, we describe a mode of Hsp70 chaperone regulation mediated by direct phosphorylation, resulting in a dramatic switch in Hsp70-client interactions. Via proteomic analysis of the Ssa1 interactome, we observed a distinct pattern in the association of cochaperones and clients upon Ssa1 T36 phosphorylation. Among cochaperones, phosphorylation of T36 similarly decreased association of the J-protein Ydj1 and the Hsp70 nucleotide exchange factors Sse1 and 2. This is notable, given the complementary roles of J-proteins and Hsp70 NEFs in accelerating Hsp70 ATPase activity (Kampinga and Craig, 2010).

We do not infer that phosphorylation of T36 simply inactivates Hsp70, insofar as the effect is to decrease binding of the J-protein cochaperone Ydj1 while leaving interaction with a second J-protein, Sis1, relatively intact. In turn, our data suggest that the reciprocal binding of Ydj1 and the G1 cyclin Cln3 to Ssa1 described by Vergès et al. (2007) is mediated by T36 phosphorylation. Exchange of Ydj1 for Cln3 on Ssa proteins has been suggested as the key step that allows Cln3 to leave the ER, transit to the nucleus, and promote G1/S progression, but the switch-like kinetics of the START event do not favor a simple competition model. Our data offer a candidate mechanism underlying the observed Cln3/Ydj1 exchange, but suggest added complexity (Figure 7). Preventing the displacement of Ydj1 from Ssa proteins via the T36A mutation allows Cln3 protein to accumulate, much like the phenotype of mutation of the inhibitory J domain of Cln3 as reported by Vergès et al. (2007). In turn, the T36E mutant phenotype indicates that the Cln3 association with phosphorylated Ssa proteins mediates Cln3 destruction.

Our new data may help resolve the apparently conflicting views of Ydj1 function in prior literature. Although loss of Ydj1 results in decreased Cdk1-mediated phosphorylation of the Cln3 PEST domain and stabilization of Cln3 (Yaglom et al., 1996), ydj1Δ cells are shifted toward G1, a defect suppressed through overexpression of Cln3 (Vergès et al., 2007). The decreased Cln3 phosphorylation and lower Ssa1 T36 phosphorylation in cells lacking Ydj1 may each be explained by a decrease in Cdk1 (and perhaps Pho85) abundance in ydj1Δ cells (Mandal et al., 2008). Nonetheless, in cells lacking Ydj1, the Ssa1-Cln3 interaction becomes constitutive, perhaps limiting Cln3 access to the nucleus, and thereby partially uncoupling PEST domain phosphorylation, Cln3 stability, and Cdk1-Cln3 activity.

Our data suggest that the phosphorylation of the Cln3 PEST domain required for its degradation may be independent of Ssa1 binding. Bacterially expressed Cln3 can still be phosphorylated in vitro by Cdk1 purified from T38A cells. Additionally, Cln3 remains stabilized in cells where Cln3-Ssa1 interaction is
made constitutive but phosphorylation of Cln3 cannot occur, such as T36E cells expressing Cln3 lacking PEST domains. Irrespective of dependency, we find that phosphorylation of Cln3 and the Cln3-Ssa1 interaction are each necessary but neither individually sufficient for degradation of Cln3.

A significant constraint on models is that the low abundance of Cln3 relative to Ssa1 or Ydj1 argues against a simple competition mechanism. We imagine a large pool of Ssa proteins, which may shift dynamically between dephosphorylated and phosphorylated states, depending on cell signals and/or cell cycle progression.

In turn, whereas the T36E mutation phenocopied a deletion of CLN3 in several respects, it is striking that the T36A mutation displayed such a subtle phenotype under normal growth conditions. Were CDK-dependent Ssa phosphorylation the sole determinant of Cln3 abundance, we might anticipate that the T36A mutant would phenocopy CLN3-1, a hyperstabilized truncation mutant (Tyers et al., 1992). Unlike CLN3-1, Cln3 protein does not accumulate significantly in T36A under normal growth conditions, but fails to be destabilized under conditions that normally trigger Cln3 degradation. We infer that the nearly normal Cln3 levels in T36A may reflect alternative pathways for Cln3 degradation and/or the action of other mechanisms regulating Cln3 expression and abundance.

**Direct Control of the Cell Cycle by CDKs through Chaperone Phosphorylation**

The CDKs Pho85 and Cdk1 are known to have overlapping substrate specificities and can phosphorylate the same residues in their targets (Huang et al., 2007; Kung et al., 2005; Mazanka and Weiss, 2010). In the case of Ssa chaperones, we have uncovered a mechanism where a single CDK consensus site on Ssa1, T36, can be phosphorylated by each CDK in response to specific cellular conditions. Thereby, both Cdk1 and Pho85 can promote Cln3 degradation, though under distinct circumstances.

Cdk1 has long been thought to control Cln3 degradation by direct phosphorylation at multiple sites within the carboxyl-terminal PEST domain (Tyers et al., 1992). Our data offer a second, indirect role for CDKs in Cln3 stability, mediated by Ssa protein phosphorylation. Significantly, we are able to detect Cdk1-mediated Ssa1 phosphorylation in vivo only in G2/M and in vitro only with Cdk1 complexes isolated from nocodazole-arrested cells. One implication is that Cln3 stability and activity may be maintained despite accumulation of Cdk1-Cln1/2 complexes by their inability to phosphorylate Ssa proteins. As such, that T36 is a substrate of Cdk1-Clb cyclin complexes, leading to Cln3 degradation, offers a novel mechanism for differentiating gene expression between G1 and G2/M in the yeast cell cycle. In turn, Ssa phosphorylation initiated by Cdk1-Clb complexes may persist through anaphase, so that daughter cells are born in G1 with destabilized Cln3.

In searching for a CDK that phosphorylates Ssa proteins in G1, we uncovered a role for the stress-activated kinase Pho85 in inhibiting G1/S cell cycle progression. We found that Pho85 can phosphorylate Ssa1 in response to nitrogen starvation or pheromone stimulation, leading to Cln3 degradation and a delay in S phase onset (Figure 7). We also uncovered an unanticipated role for Pho85 in the direct phosphorylation of Cln3. This may explain how PEST-mediated destruction of Cln3 can still occur in conditions where Cdk1 activity is low, such as nitrogen starvation. This is particularly interesting in light of previously established roles for Pho85 in promoting G1/S progression through direct phosphorylation of Whi5 (Huang et al., 2009) and inhibition of Sic1 (Wysocki et al., 2006). Opposing roles for Pho85 kinase have previously been ascribed to association with distinct Pcl cyclin partners. Clg1 and Pcl2 interact with Ssa proteins and appear to be candidates for the Pcls that direct Pho85 to target Ssa proteins as substrates and delay G1/S progression. Notably, Pcl2 expression is uniquely induced by pheromone stimulation (Measday et al., 1997). By contrast, neither Pcl9, a cyclin that binds Pho85 to promote Whi5 phosphorylation (Tennyson et al., 1998), nor Pbo8, a candidate for the cyclin mediating Sic1 phosphorylation (Wysocki et al., 2006), appeared to interact with Ssa proteins, consistent with Pcl expression determining whether Pho85 serves as a positive or negative regulator of cell cycle progression. The Ssa1-Pcl6/7 interaction observed is also interesting, particularly as our proteomic analysis revealed a dependence of the interaction of Glc7, a regulator of glycogen accumulation with Ssa1 on T36 phosphorylation. Notably, Pcl6/7 activate Pho85 to regulate glycogen metabolism, via Glc7 (Huang et al., 1998; Tan et al., 2003; Timblin et al., 1996), suggesting further connections between Ssa protein phosphorylation, metabolism, and cell-cycle progression.

The Ssa1 phosphorylation site T36 is present in each Ssa isoform, suggesting that Ssa1 through 4 may be similarly regulated by CDK phosphorylation. In our studies, although some Pcl cyclins appeared to bind all four isoforms, isoform-specific interactions were also observed between Ssa proteins and Pcls, suggesting both overlapping and distinct functions for isoforms in cell-cycle control. A pattern of functional redundancy and
specificity among Ssa proteins has previously been observed for both yeast prion propagation and protein folding activities (Sharma et al., 2009; Sharma and Masison, 2011).

**Phosphorylation of Hsp70 Family Members as a Conserved Determinant of G1 Cyclin Function**

The mammalian homolog of Cln3, Cyclin D1, is an important regulator of the G1/S progression in normal cells and commonly deregulated in cancer (Alao, 2007; Enserink and Kolodner, 2010). Hsc70 associates with Cyclin D1 and is present as an element of the active CDK4-Cyclin D1 complex, although a specific functional role in the complex remains to be described (Diehl et al., 2003; Trotter et al., 2001). We found that CDK-dependent phosphorylation of Hsc70 promotes Cyclin D1 binding and destruction, thereby lowering Rb phosphorylation and Cyclin A expression. Promoting Hsc70 T38 phosphorylation may provide a novel target for cancer therapeutics, via destabilizing Cyclin D to slow tumor cell proliferation.

Overall, this study reveals an unanticipated layer of Hsp70 chaperone regulation mediated by phosphorylation. Much like recent work with Hsp90 (Mollapour et al., 2010), we find that client binding can be regulated through posttranslational modification, although here with critical consequences to cell-cycle progression. We show that Hsp70 chaperones serve as more than simple housekeeping proteins but are dynamically activated in response to cell-cycle progression and environmental conditions and serve a critical role as effectors that transduce cell signaling to cell cycle control.

**EXPERIMENTAL PROCEDURES**

**Yeast Culture, Strains, and Plasmids**

A list of yeast strains and plasmids used in this study is available in Tables S2 and S3. Standard methods were used for yeast, bacteria, and mammalian cell culture, as described in Extended Experimental Procedures. For ± stimulation or nitrogen starvation experiments, cells were treated as described (Gallego et al., 1997).

**Analysis of the Ssa1 Interactome by Mass Spectrometry**

Yeast cells expressing either His10-Ssa1 WT or T36A as the sole Ssa1 protein were grown to mid-log phase, treated with 20 μM nF for 2.5 hr and lysed. His10-Ssa1 WT or T36A interactomes were purified on His-Tag Isolation Dynabeads (Invitrogen), separated by SDS-PAGE and subjected to proteomic analysis. Briefly, gel slices were subjected to in-gel proteolysis; tryptic peptides were purified, differentially labeled by carboxyl-terminal 15N exchange, and analyzed via LC-MS/MS as described in Extended Experimental Procedures.

**Flow Cytometry**

Analysis of DNA content, cell size measurement, and cell sorting were performed as described (Jorgensen et al., 2002).

**Protein Analysis, Pull-Down, and Immunoblotting**

Extracts of total protein were prepared as described (Kamada et al., 1995). Affinity-based enrichment by pull-down and detection by western blotting are detailed in Extended Experimental Procedures.

**β-Galactosidase Assays**

Cells transformed with the appropriate promoter-LacZ fusions were grown to mid-log phase and total protein was extracted. 100 μg of cell lysate were used in the assay as described (Kamada et al., 1995).

**SUPPLEMENTAL INFORMATION**

Supplemental Information includes Extended Experimental Procedures, six figures, and three tables and can be found with this article online at http://dx.doi.org/10.1016/j.cell.2012.10.051.

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**REFERENCES**

Alao, J.P. (2007). The regulation of cyclin D1 degradation: roles in cancer development and the potential for therapeutic invention. Mol. Cancer 6, 24.

Albuquerque, C.P., Smolka, M.B., Payne, S.H., Bafna, V., Eng, J., and Zhou, H. (2008). A multidimensional chromatography technology for in-depth phosphoproteome analysis. Mol. Cell. Proteomics 7, 1389–1396.

Beltrao, P., Albanèse, V., Kenner, L.R., Swaney, D.L., Burlingame, A., Vilîn, J., Lim, W.A., Fraser, J.S., Frydman, J., and Krogan, N.J. (2012). Systematic functional prioritization of protein posttranslational modifications. Cell 150, 413–425.

Benanti, J.A. (2012). Coordination of cell growth and division by the ubiquitin-proteasome system. Semin. Cell Dev. Biol. 23, 492–498.

Bishop, A.C., Ubersax, J.A., Petch, D.T., Matheos, D.P., Gray, N.S., Biethower, J., Shimizu, E., Tsien, J.Z., Schultz, P.G., Rose, M.D., et al. (2000). A chemical switch for inhibitor-sensitive alleles of any protein kinase. Nature 407, 395–401.

Brehmer, D., Rüdiger, S., Gäsßer, C.S., Klostermeier, D., Packschies, L., Reinistein, J., Mayer, M.P., and Bukau, B. (2001). Tuning of chaperone activity of Hsp70 proteins by modulation of nucleotide exchange. Nat. Struct. Biol. 8, 427–432.

Caplan, A.J., and Douglas, M.G. (1991). Characterization of YDJ1: a yeast homologue of the bacterial dnaJ protein. J. Cell Biol. 114, 609–621.

Carroll, A.S., and O’Shea, E.K. (2002). Pho85 and signaling environmental conditions. Trends Biochem. Sci. 27, 87–93.

Costanzo, M., Nishikawa, J.L., Tang, X., Millman, J.S., Schub, O., Breitkreuz, K., Dewar, D., Rupes, I., Andrews, B., and Tyers, M. (2004). CDK activity antagonizes Whi5, an inhibitor of G1/S transcription in yeast. Cell 117, 899–913.

Craig, E.A., and Marszalek, J. (2011). Hsp70 Chaperones. eLS. Published online March 15, 2011. http://dx.doi.org/10.1002/9780470015902.a0023188.de Bruins, R.A., McDonald, W.H., Kalashnikova, T.I., Yates, J., 3rd, and Wittenberg, C. (2004). Cln3 activates G1-specific transcription via phosphorylation of the SBF bound repressor Whi5. Cell 117, 887–898.

Di Como, C.J., Chang, H., and Arndt, K.T. (1995). Activation of CLN1 and CLN2 G1 cyclin gene expression by BCK2. Mol. Cell. Biol. 15, 1835–1846.

Diehl, J.A., Yang, W., Rimerman, R.A., Xiao, H., and Emili, A. (2003). Hsc70 regulates accumulation of cyclin D1 and cyclin D1-dependent protein kinase. Mol. Cell. Biol. 23, 1764–1774.

Enserink, J.M., and Kolodner, R.D. (2010). An overview of CdK1-controlled targets and processes. Cell Div. 5, 11.
Ferrezuelo, F., Aldea, M., and Futcher, B. (2009). Bck2 is a phase-independent activator of cell cycle-regulated genes in yeast. Cell 8, 239–252.

Ferrezuelo, F., Colomina, N., Futcher, B., and Aldea, M. (2010). The transcriptional network activated by Cln3 cyclin at the G1-to-S transition of the yeast cell cycle. Genome Biol. 11, R67.

Gallego, C., Gari, E., Colomina, N., Herrero, E., and Aldea, M. (1997). The Cln3 cyclin is down-regulated by translational repression and degradation during the G1 arrest caused by nitrogen deprivation in budding yeast. EMBO J. 16, 7196–7206.

Huang, D., Moffat, J., Wilson, W.A., Moore, L., Cheng, C., Roach, P.J., and Andrews, B. (1998). Cyclin partners determine Pho85 protein kinase substrate specificity in vitro and in vivo: control of glycosgen biosynthesis by Pci8 and Pci10. Mol. Cell. Biol. 18, 3289–3299.

Huang, D., Friesen, B., and Andrews, B. (2007). Pho85, a multifunctional cyclin-dependent protein kinase in budding yeast. Mol. Microbiol. 66, 303–314.

Huang, D., Kaluarachchi, S., van Dyk, D., Friesen, H., Sopko, R., Ye, W., Bashtain, N., Moffat, J., Sassi, H., Costanzo, M., and Andrews, B.J. (2009). Dual regulation by pairs of cyclin-dependent protein kinases and histone deacetylases controls G1 transition in budding yeast. Mol. Biol. Cell 7, e1000188.

Jaiswal, H., Conz, C., Otto, H., Wölfle, T., Fitzke, E., Mayer, M.P., and Rospert, S. (2011). The chaperone network connected to human ribosome-associated complex. Mol. Cell. Biol. 31, 1160–1173.

Jones, G., Song, Y., Chung, S., and Masison, D.C. (2004). Propagation of Saccharomyces cerevisiae [PSI+] prion is impaired by factors that regulate Hsp70 substrate binding. Mol. Cell. Biol. 24, 3928–3937.

Jorgensen, P., Nishikawa, J.L., Breitkreutz, B.J., and Tyers, M. (2002). Systematic identification of pathways that couple cell growth and division in yeast. Science 297, 395–400.

Kamada, Y., Jung, U.S., Piotrowski, J., and Levin, D.E. (1995). The protein kinase C-activated MAP kinase pathway of Saccharomyces cerevisiae mediates a novel aspect of the heat shock response. Genes Dev. 9, 1559–1571.

Kampinga, H.H., and Craig, E.A. (2010). The Hsp70 chaperone machinery: J proteins as drivers of functional specificity. Nat. Rev. Mol. Cell Biol. 11, 579–592.

Kung, C., Kensi, D.M., Dickerson, S.H., Howson, R.W., Kuyper, L.F., Madhani, H.D., and Shokat, K.M. (2005). Chemical genomic profiling to identify intracellular targets of a multiplex kinase inhibitor. Proc. Natl. Acad. Sci. USA 102, 3587–3592.

Mandal, A.K., Nillegoda, N.B., Chen, J.A., and Caplan, A.J. (2008). Ydj1 protects nascent protein kinases from degradation and controls the rate of their maturation. Mol. Cell. Biol. 28, 4434–4444.

Mayer, M.P., and Bukau, B. (2005). Hsp70 chaperones: cellular functions and molecular mechanism. Cell. Mol. Life Sci. 62, 670–684.

Mazanka, E., and Weiss, E.L. (2010). Sequential counteracting kinases restrict an asymmetric gene expression program to early G1. Mol. Biol. Cell 21, 2809–2820.

Meaadav, V., Moore, L., Retnakaran, R., Lee, J., Donoviel, M., Neiman, A.M., and Andrews, B. (1997). A family of cyclin-like proteins that interact with the Pho85 cyclin-dependent kinase. Mol. Cell. Biol. 17, 1212–1223.

Meimarioud, E., Gooljar, S.B., and Chapelle, J.P. (2009). From hatching to their maturation. Mol. Cell. Biol. 25, 4189–4195.

Moffat, J., Huang, D., and Andrews, B. (2000). Functions of Pho85 cyclin-dependent kinases in budding yeast. Prog. Cell Cycle Res. 4, 97–106.

Mollapour, M., Tsutsumi, S., and Neckers, L. (2010). Hsp90 phosphorylation, Wee1 and the cell cycle. Cell Cycle 9, 2310–2316.

Newcomb, L.L., Diederich, J.A., Slattery, M.G., and Heideman, W. (2003). Glucose regulation of Saccharomyces cerevisiae cell cycle genes. Eukaryot. Cell 2, 143–149.

Newman, R.M., Mobascher, A., Mangold, U., Koike, C., Diah, S., Schmidt, M., Finley, D., and Zetter, B.R. (2004). Antizyme targets cyclin D1 for degradation. A novel mechanism for cell growth repression. J. Biol. Chem. 279, 41504–41511.

Nishizawa, M., Kawasumi, M., Fujino, M., and Toh-e, A. (1998). Phosphorylation of sic1, a cyclin-dependent kinase (Cdk) inhibitor, by Cdk including Pho85 kinase is required for its prompt degradation. Mol. Biol. Cell 9, 2393–2405.

Sharma, D., and Masison, D.C. (2011). Single methyl group determines prion propagation and protein degradation activities of yeast heat shock protein (Hsp)-70 chaperones Ssa1p and Ssa2p. Proc. Natl. Acad. Sci. USA 108, 13865–13870.

Sharma, D., Martineau, C.N., Le Dall, M.T., Reidy, M., Masison, D.C., and Kaban, M. (2009). Function of SSA subfamily of Hsp70 within and across species varies widely in complementing Saccharomyces cerevisiae cell growth and prion propagation. PLoS ONE 4, e6644.

Sherlock, G., and Rosamond, J. (1993). Starting to cycle: G1 controls regulating cell division in budding yeast. J. Gen. Microbiol. 139, 2531–2541.

Tan, Y.S., Marcos, P.A., and Cannon, J.F. (2003). Pho85 phosphorylates the Gtc7 protein phosphatase regulator Glc8 in vivo. J. Biol. Chem. 278, 147–153.

Tennyson, C.N., Lee, J., and Andrews, B.J. (1998). A role for the Pcl9-Pho85 cyclin-cdk complex at the M/G1 boundary in Saccharomyces cerevisiae. Mol. Microbiol. 28, 69–79.

Timblin, B.K., Tatchell, K., and Bergman, L.W. (1996). Deletion of the gene encoding the cyclin-dependent protein kinase Pho85 alters glycolgen metabolism in Saccharomyces cerevisiae. Genetics 143, 57–66.

Trotter, E.W., Berenfeld, L., Krause, S.A., Petsko, G.A., and Gray, J.V. (2001). Protein misfolding and temperature up-shift cause G1 arrest via a common mechanism dependent on heat shock factor in Saccharomyces cerevisiae. Proc. Natl. Acad. Sci. USA 98, 7313–7318.

Tyers, M., Tokiwa, G., Nash, R., and Futcher, B. (1992). The Cln3-Cdc28 kinase complex of S. cerevisiae is regulated by proteolysis and phosphorylation. EMBO J. 11, 1773–1784.

Vergès, E., Colomina, N., Gari, E., Gallego, C., and Aldea, M. (2007). Cyclin Cln3 is retained at the ER and released by the J chaperone Ydj1 in late G1 to trigger cell cycle entry. Mol. Cell. Biol. 26, 649–662.

Wijnen, H., and Futcher, B. (1999). Genetic analysis of the shared role of CLN3 and BCK2 at the G1/S transition in Saccharomyces cerevisiae. Genetics 153, 1131–1143.

Wysocki, R., Javaheri, A., Kristjansdottir, K., Shaf, F., and Kron, S.J. (2006). CDK Pho85 targets CDK inhibitor Sic1 to relieve yeast G1 checkpoint arrest after DNA damage. Nat. Struct. Mol. Biol. 13, 906–914.

Yalgom, J., Linskens, M.H., Sadis, S., Rubin, D.M., Futcher, B., and Finley, D. (1995). p34Cdc28-mediated control of Cln3 cyclin degradation. Mol. Cell. Biol. 15, 731–741.

Yalgom, J.A., Goldberg, A.L., Finley, D., and Sherman, M.Y. (1996). The molecular chaperone Ydj1 is required for the p34Cdc28-dependent phosphorylation of the cyclin Cln3 that signals its degradation. Mol. Cell. Biol. 16, 3679–3684.

Yang, Z., Geng, J., Yen, W.L., Wang, K., and Klionsky, D.J. (2010). Positive or negative roles of different cyclin-dependent kinase Pho85-cyclin complexes orchestrate induction of autophagy in Saccharomyces cerevisiae. Mol. Cell 38, 250–264.