SUMO-targeted ubiquitin ligase (STUbL) Slx5 regulates proteolysis of centromeric histone H3 variant Cse4 and prevents its mislocalization to euchromatin

Kentaro Ohkuni
Yoshimitsu Takahashi
Alyona Fulp
Oliver Kerscher

College of William and Mary, opkers@wm.edu

Follow this and additional works at: https://scholarworks.wm.edu/aspubs

Part of the Genetics Commons, and the Molecular Genetics Commons

Recommended Citation
Ohkuni, Kentaro; Takahashi, Yoshimitsu; Fulp, Alyona; and Kerscher, Oliver, SUMO-targeted ubiquitin ligase (STUbL) Slx5 regulates proteolysis of centromeric histone H3 variant Cse4 and prevents its mislocalization to euchromatin (2016). Molecular Biology of the Cell, 27(9), 1500-1510. https://doi.org/10.1091/mbc.E15-12-0827
SUMO-targeted ubiquitin ligase (STUbl) Slx5 regulates proteolysis of centromeric histone H3 variant Cse4 and prevents its mislocalization to euchromatin

Kentaro Ohkuni\textsuperscript{a}, Yoshimitsu Takahashi\textsuperscript{a}, Alyona Fulp\textsuperscript{b}, Josh Lawrimore\textsuperscript{b}, Wei-Chun Au\textsuperscript{a}, Nagesh Pasupala\textsuperscript{a}, Reuben Levy-Myers\textsuperscript{a,c}, Jack Warren\textsuperscript{a}, Alexander Strunnikov\textsuperscript{d}, Richard E. Baker\textsuperscript{a}, Oliver Kerscher\textsuperscript{a}, Kerry Bloom\textsuperscript{b}, and Munira A. Basrai\textsuperscript{a,*}

\textsuperscript{a}Genetics Branch, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD 20892; \textsuperscript{b}Department of Biology, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599; \textsuperscript{c}Biology Department, The College of William & Mary, Williamsburg, VA 23187; \textsuperscript{d}Guangzhou Institutes of Biomedicine and Health, Guangzhou 510530, China; \textsuperscript{e}Department of Microbiology and Physiological Systems, University of Massachusetts Medical School, Worcester, MA 01655

ABSTRACT  Centromeric histone H3, CENP-A\textsuperscript{Cse4}, is essential for faithful chromosome segregation. Stringent regulation of cellular levels of CENP-A\textsuperscript{Cse4} restricts its localization to centromeres. Mislocalization of CENP-A\textsuperscript{Cse4} is associated with aneuploidy in yeast and flies and tumorigenesis in human cells; thus defining pathways that regulate CENP-A levels is critical for understanding how mislocalization of CENP-A contributes to aneuploidy in human cancers. Previous work in budding yeast shows that ubiquitination of overexpressed Cse4 by Psh1, an E3 ligase, partially contributes to proteolysis of Cse4. Here we provide the first evidence that Cse4 is sumoylated by E3 ligases Siz1 and Siz2 in vivo and in vitro. Ubiquitination of Cse4 by the small ubiquitin-related modifier (SUMO)-targeted ubiquitin ligase (STUbl) Slx5 plays a critical role in proteolysis of Cse4 and prevents mislocalization of Cse4 to euchromatin under normal physiological conditions. Accumulation of sumoylated Cse4 species and increased stability of Cse4 in \textit{slx5}\textsuperscript{Δ} strains suggest that sumoylation precedes ubiquitin-mediated proteolysis of Cse4. Slx5-mediated Cse4 proteolysis is independent of Psh1, since \textit{slx5}\textsuperscript{Δ} \textit{psh1}\textsuperscript{Δ} strains exhibit higher levels of Cse4 stability and mislocalization than either \textit{slx5}\textsuperscript{Δ} or \textit{psh1}\textsuperscript{Δ} strains. Our results demonstrate a role for Slx5 in ubiquitin-mediated proteolysis of Cse4 to prevent its mislocalization and maintain genome stability.

INTRODUCTION  Centromeres are specialized chromosomal loci that are essential for faithful chromosome segregation. The kinetochore (centromeric DNA and associated proteins) provides an attachment site for microtubules for segregation of sister chromatids during mitosis. Despite the wide divergence of centromere DNA sequences, kinetochore proteins such as centromeric histone H3 variant are evolutionarily conserved from yeast to humans (Cse4 in \textit{Saccharomyces cerevisiae}, Cnp1 in \textit{Schizosaccharomyces pombe}, CID in \textit{Drosophila}, and CENP-A in mammals) and are essential for chromosome segregation (Kitagawa and Hieter, 2001; Smith, 2002; Biggins, 2013). The function of CENP-A is also evolutionarily conserved, as budding yeast Cse4 can rescue a depletion of mammalian CENP-A (Wieland et al., 2004).

Stringent regulation of CENP-A expression is essential for genome stability. Overexpression of CENP-A causes ectopic mislocalization to chromosome arms and promotes aneuploidy in humans, flies, and yeast (Scott and Sullivan, 2014). Overexpression and
mislocalization of CENP-A are observed in many cancers and contribute to tumorigenesis in human cells (Tomonaga et al., 2003; Amato et al., 2009; Hu et al., 2010; Li et al., 2011; Wu et al., 2012; Lacoste et al., 2014; Athwal et al., 2015). In flies, mislocalization of CID causes formation of ectopic kinetochores and leads to mitotic delays, anaphase bridges, chromosome fragmentation, aneuploidy, and lethality (Heun et al., 2006). In fission yeast, overexpression of Cnp1 leads to indiscriminate deposition of Cnp1 at noncentromeric regions, resulting in growth defects and severe chromosome missegregation during mitosis and meiosis (Choi et al., 2012; Castillo et al., 2013; Gonzalez et al., 2014). In budding yeast, mislocalization of Cse4 to euchromatin leads to chromosome segregation defects, and the extent of Cse4 mislocalization directly correlates with the level of chromosome loss (Au et al., 2008). Furthermore, various pathways involving kinetochore protein Spt4 (Crotti and Basrai, 2004), histone chaperones Cac1 and Hir1 (Sharp et al., 2002; Lopes da Rosa et al., 2011), and chromatin remodeler Snf2 (Gikopoulos et al., 2011) act to prevent the mislocalization of Cse4.

Protein posttranslational modifications, such as ubiquitination (Kerscher et al., 2006), are important for regulating steady-state levels and preventing mislocalization. For example, proteolysis of CID prevents its mislocalization to ectopic regions in flies (Heun et al., 2006; Moreno-Moreno et al., 2011). Protein posttranslational modifications such as ubiquitination and sumoylation are important for regulating steady-state levels of cellular proteins (Kerscher et al., 2006; Everett et al., 2013). Although canonical histones are sumoylated (Nathan et al., 2006), there is no evidence for sumoylation of Cse4. Optimization of the biochemical purification of Cse4 allowed us to detect sumoylation of Cse4 in vivo. We performed a pull down of octahistidine-hemagglutinin (8His-HA)–tagged Cse4 using nickel-nitrilotriacetic acid (Ni-NTA) agarose beads and detected SUMO-modified Cse4 by Western blot analysis with an anti-Smt3 antibody (Figure 1A). Protein levels of cse4 16KR, in which all lysine (K) residues are mutated to arginine (R), were greatly increased due to its stabilization, as reported previously (Collins et al., 2004). At least three high–molecular weight bands were observed after transient overexpression of 8His-HA–Cse4 in wild-type cells (Figure 1A, long exposure, denoted by arrows). In contrast, these SUMO-modified Cse4 species, which are visible on wild-type 8His-HA–Cse4, were not detected with vector alone or 8His-HA–cse4 16KR. These results show that Cse4 is sumoylated in vivo.

To identify the SUMO E3 ligase responsible for Cse4 sumoylation, we tested the role of two functionally redundant SUMO E3 ligases, Siz1 and Siz2, that are responsible for sumoylation of a majority of substrates (Johnson and Gupta, 2001; Johnson, 2004; Takahashi et al., 2001; Montpetit et al., 2006; Reindle et al., 2006), including the kinetochore protein Ndc10 and histones H2B and H4 in S. cerevisiae (Montpetit et al., 2006; Nathan et al., 2006). In vitro sumoylation assays using purified Cse4 (Supplemental Figure S1) revealed that Siz1 serves as an E3 for Cse4 sumoylation (Figure 1B). We tested a siz1Δ siz2Δ mutant to determine the role of Siz1 and Siz2 in sumoylation of Cse4 in vivo (Figure 1C). We failed to detect SUMO-modified Cse4 species in the siz1Δ siz2Δ strain compared with the wild-type strain (Figure 1C, pull down). The lower levels of input Cse4 in the siz1Δ siz2Δ strain may be due to their slow growth and/or a defect in transcriptional induction from the GAL promoter (Figure 1C, input); however, SUMO-modified Cse4 species were not detected in the siz1Δ siz2Δ strain even upon a longer exposure.

RESULTS

Cse4 is sumoylated in vitro and in vivo

Protein posttranslational modifications such as ubiquitination and sumoylation are important for regulating steady-state levels of cellular proteins (Kerscher et al., 2006; Everett et al., 2013). Although canonical histones are sumoylated (Nathan et al., 2006), there is no evidence for sumoylation of Cse4. Optimization of the biochemical purification of Cse4 allowed us to detect sumoylation of Cse4 in vivo. We performed a pull down of octahistidine-hemagglutinin (8His-HA)–tagged Cse4 using nickel-nitrilotriacetic acid (Ni-NTA) agarose beads and detected SUMO-modified Cse4 by Western blot analysis with an anti-Smt3 antibody (Figure 1A). Protein levels of cse4 16KR, in which all lysine (K) residues are mutated to arginine (R), were greatly increased due to its stabilization, as reported previously (Collins et al., 2004). At least three high–molecular weight bands were observed after transient overexpression of 8His-HA–Cse4 in wild-type cells (Figure 1A, long exposure, denoted by arrows). In contrast, these SUMO-modified Cse4 species, which are visible on wild-type 8His-HA–Cse4, were not detected with vector alone or 8His-HA–cse4 16KR. These results show that Cse4 is sumoylated in vivo.

To identify the SUMO E3 ligase responsible for Cse4 sumoylation, we tested the role of two functionally redundant SUMO E3 ligases, Siz1 and Siz2, that are responsible for sumoylation of a majority of substrates (Johnson and Gupta, 2001; Johnson, 2004; Takahashi et al., 2001; Montpetit et al., 2006; Reindle et al., 2006), including the kinetochore protein Ndc10 and histones H2B and H4 in S. cerevisiae (Montpetit et al., 2006; Nathan et al., 2006). In vitro sumoylation assays using purified Cse4 (Supplemental Figure S1) revealed that Siz1 serves as an E3 for Cse4 sumoylation (Figure 1B). We tested a siz1Δ siz2Δ mutant to determine the role of Siz1 and Siz2 in sumoylation of Cse4 in vivo (Figure 1C). We failed to detect SUMO-modified Cse4 species in the siz1Δ siz2Δ strain compared with the wild-type strain (Figure 1C, pull down). The lower levels of input Cse4 in the siz1Δ siz2Δ strain may be due to their slow growth and/or a defect in transcriptional induction from the GAL promoter (Figure 1C, input); however, SUMO-modified Cse4 species were not detected in the siz1Δ siz2Δ strain even upon a longer exposure.
FIGURE 1: Cse4 is sumoylated by Siz1/2 in vitro and in vivo. (A) Cse4 is sumoylated in vivo. Wild-type strain (BY4741) transformed with vector (pYES2), pGAL-8His-HA-CSE4 (pMB1345), or pGAL-8His-HA-cse4 16KR (pMB1344) was grown in raffinose/galactose (2%) for 4 h to induce expression of Cse4. Sumoylation levels of Cse4 and nonmodified Cse4 were detected using Ni-NTA pull down, followed by Western blot analysis with anti-Smt3 and anti-HA (Cse4) antibodies, respectively. At least three high molecular weights of 8His-HA–Cse4 (arrows) were detected (Long exposure). Input samples were analyzed using anti-HA (Cse4) and anti-Tub2 antibodies. Asterisk shows nonspecific sumoylated proteins that bind to the beads. The mutations of lysine to arginine in 8His-HA–cse4 16KR slightly affect its mobility compared with wild-type 8His-HA–Cse4. (B) In vitro assay for Cse4 sumoylation. E1 (GST-Uba2/GST-Aos1), E2 (Ubc9), Smt3gg, and ATP were incubated with or without Siz1 (∆440). After the reaction, SUMO and SUMO-conjugated Cse4 were detected by Western blot analysis with anti-Smt3 and anti-Cse4 antibodies, respectively. (C) SUMO E3 ligases Siz1 and Siz2 sumoylate Cse4 in vivo. Wild-type (BY4741) and siz1∆ siz2Δ (YMB7277) strains expressing pGAL-8His-HA-CSE4 (pMB1345) were assayed as described in A. High–molecular weight species of 8His-HA–Cse4 and nonspecific sumoylated proteins are marked with arrows and an asterisk, respectively.
Slx5 regulates ubiquitin-mediated proteolysis of Cse4

Previous studies showed that STUbLs link SUMO and ubiquitin modification pathways to facilitate proteolysis of cellular substrates (Garza and Pilus, 2013; Srimanachandran and Dohmen, 2014). Slx5, one of four STUbL proteins (Slx5, Slx8, Uls1, Rad18) in S. cerevisiae, forms a complex with Siz1 (Westerbeck et al., 2014), and slx5Δ strains exhibit chromosome segregation defects (van de Pasch et al., 2013). Hence we investigated the role of Slx5 in Cse4 proteolysis. To investigate whether Slx5 interacts with Cse4 in vivo, we performed a glutathione S-transferase (GST) pull-down assay using a strain expressing HA-tagged Cse4 (Figure 2E). Ubiquitinated Cse4 was detected as a lagging pattern in wild-type cells expressing HA-Cse4 but was absent in strains with vector alone. Faster-migrating Cse4 species (Figure 2B, asterisk) similar in size to those in the input lane were observed from both wild-type and slx5Δ strains. These species were also observed in experiments with wild-type Cse4 and cse4 16KR mutant, in which all lysines are mutated to arginines (Au et al., 2013; Hewawasam et al., 2014). Because cse4 16KR cannot be ubiquitinated, this faster-migrating species represents unmodified Cse4, which likely interacts with ubiquitinated proteins such as canonical histones. The lagging pattern of higher-molecular weight forms of Cse4 was greatly reduced in an slx5Δ strain (Figure 2B). Quantification of ubiquitinated Cse4 showed a fivefold reduction in high-molecular weight forms of Cse4 when normalized to input Cse4 in the slx5Δ strain (Figure 2C). We next investigated whether defects in Cse4 ubiquitination result in increased protein stability in vivo. Overexpressed HA-tagged Cse4 was transiently induced from a GAL promoter by the addition of galactose, and cells were shifted to glucose medium containing cycloheximide (CHX) to inhibit translation. Western blot analysis with protein extracts from different time points was used to measure levels of Cse4 after CHX treatment (Figure 2D). HA-Cse4 was rapidly degraded in the wild-type strain (t1/2 = 39.0 min) yet was stabilized in the slx5Δ strain (t1/2 = 73.2 min). Consistent with this observation, we detected a similar stabilization of Cse4 in the siz1Δ siz2Δ strain (t1/2 = 74.8 vs. 35.8 min in wild type; Supplemental Figure S2). Thus we conclude that Slx5 is required for ubiquitination and proteolysis of Cse4 in vivo.

Because slx5Δ strains show defects in Cse4 ubiquitination and increased stability of Cse4, we examined whether sumoylated Cse4 accumulates in these strains. We first constructed a strain expressing His-Flag-tagged Smt3 (HF-Smt3) and Myc-tagged Cse4. HF-Smt3 was purified from cell extracts using Ni-NTA agarose beads, and the level of sumoylated proteins and sumoylated Cse4 was determined using anti-Flag (Smt3) and anti-Myc (Cse4) antibodies, respectively. When Myc-Cse4 was transiently overexpressed, SUMO-modified Cse4 species were barely detectable in the wild-type strain (Figure 2E, α-Myc). In contrast, the slx5Δ strain showed substantial levels of sumoylated Cse4, especially high-molecular weight, SUMO-modified Cse4 (Figure 2E, α-Myc). Therefore reduced STUbL activity in slx5Δ strain contributes to the accumulation of sumoylated Cse4 species, suggesting that Slx5-mediated proteolysis is a downstream consequence of Cse4 sumoylation.

We next examined whether higher levels of sumoylated Cse4 species accumulate in the slx5Δ strain under normal physiological conditions. Even though sumoylated Cse4 species were detected in wild-type cells when Cse4 is overexpressed (Figure 1A), we failed to detect sumoylated Cse4 species in the wild-type strain when Cse4 is expressed from its own promoter (Figure 2F). The failure to detect sumoylated Cse4 species may be due to low Cse4 expression and/or ongoing proteolysis of sumoylated Cse4. In contrast, higher levels of sumoylated Cse4 species were clearly observed in the slx5Δ mutant (Figure 2F, arrows). A defect in STUbL activity may in part contribute to accumulation of polysumoylated (high-molecular weight) Cse4 species in the slx5Δ strain. Sumoylated Cse4 does not accumulate in strains deleted for PSF1, an E3-ubiquitin ligase targeting Cse4, or in siz1Δ/siz2Δ-deleted strains. These results indicate that lack of STUbL activity in slx5Δ strains contributes to the accumulation of sumoylated Cse4 species under normal physiological conditions.

Slx5 regulates ubiquitin-mediated proteolysis of Cse4 in a Psh1-independent manner

Previous studies showed that Psh1 interacts with Cse4 and CSE4 overexpression causes growth inhibition in a psh1Δ strain (Hewawasam et al., 2010; Ranjtkar et al., 2010). Similar to the growth defect observed for psh1Δ strains, slx5Δ and siz1Δ siz2Δ strains also showed growth inhibition with GAL-CSE4 on galactose medium (Supplemental Figure S3). Given that Slx5 and Psh1 are E3 ligases that ubiquitinate Cse4 and that deletion of SLX5 results in accumulation of sumoylated Cse4 species, we examined whether Slx5-mediated proteolysis of Cse4 is dependent on Psh1. We constructed psh1Δ slx5Δ strains using standard yeast mating and sporulation. The psh1Δ slx5Δ strains do not exhibit growth defects at 30°C but exhibit a slow-growth phenotype at low (22, 25°C) and high (37°C) temperatures compared with each single mutant (Supplemental Figure S4A). The psh1Δ slx5Δ strains also exhibit sensitivity to growth on benomyl (microtubule-depolymerizing agent)–containing plates. Furthermore, psh1Δ slx5Δ strains exhibit defects in segregation of a reporter chromosome in a colony color assay to measure chromosome transmission fidelity (Supplemental Figure S4B).

We next analyzed the stability of Cse4 after transient overexpression of HA-Cse4 in wild-type, psh1Δ, slx5Δ, and psh1Δ slx5Δ strains (Figure 3A). As expected, deletion of PSF1 or SLX5 moderately stabilized HA-Cse4 protein levels. In contrast, the double-deletion mutant psh1Δ slx5Δ showed a dramatic increase in HA-Cse4 protein stability. The half-life of HA-Cse4 in psh1Δ slx5Δ (t1/2 = 138.6 min) is twice that of psh1Δ (t1/2 = 77.0 min) or slx5Δ (t1/2 = 69.3 min) strains (Figure 3B). We next analyzed Cse4 stability in strains expressing HA-Cse4 from its own promoter. Protein stability assays showed that Cse4 is rapidly degraded in wild-type cells (t1/2 = 34.7 min), modestly stable in psh1Δ (t1/2 = 46.2 min) and slx5Δ (t1/2 = 53.3 min) single mutants, and highly stable in psh1Δ slx5Δ strain (t1/2 = 77.0 min; Figure 3, C and D). We conclude that Slx5 regulates ubiquitin-mediated proteolysis of Cse4 independently of Psh1.

Slx5 prevents mislocalization of Cse4 in a Psh1-independent manner

We investigated the physiological consequence of defects in STUbL activity by analyzing Cse4 localization in strains expressing Cse4 from its endogenous promoter. Subcellular fractionation and chromosome spreads were used to examine whether Cse4 was
FIGURE 2: The STUbL Slx5 interacts with Cse4 and regulates ubiquitin-mediated proteolysis of Cse4. (A) Slx5 associates with Cse4. Expression of pGAL-3HA-CSE4 (pMB1515) and/or pGAL-GST-SLX5 (BOK629) in ubc4∆ ubc6∆ (YOK2501) was induced by the addition of galactose (2%) for 6 h. Glutathione–Sepharose beads were used for GST-Slx5 pull down, and the eluate was analyzed by Western blot analysis with anti-HA (Cse4) and anti-GST (Slx5) antibodies. (B) Slx5 regulates Cse4 ubiquitination. Wild-type (BY4741) and slx5∆ (YMB9035) strains expressing pGAL-3HA-CSE4 (pMB1597) were grown in raffinose/galactose (2%) for 2 h. Agarose-TUBE1 was used for pull down with tandem ubiquitin-binding entities. Ubiquitination levels of Cse4 were detected by Western blot analysis with anti-HA antibody, and input samples were analyzed using anti-HA (Cse4) and anti-Tub2 antibodies. Wild-type (BY4741) strain transformed with vector (pMB1433) was used as a negative control. Asterisk shows nonmodified Cse4. (C) Relative ubiquitination of Cse4 with average deviation of two biological repeats. Cse4 was normalized using input Cse4 levels. (D) Increased stability of Cse4 in slx5∆ strain. Cse4 expression from pGAL-6His-3HA-CSE4 (pMB1458) in wild-type (BY4741) and slx5∆ (YMB9035) strains was induced by the addition of galactose (2%) for 2 h. Glucose (2%) containing CHX (10 μg/ml) was added, and cells were collected at the indicated time points. Blots were probed with anti-HA (Cse4) or anti-Tub2 (loading control) antibody. Cse4 protein half-life ($t_{1/2}$) represents the mean of two biological repeats with average deviation. (E) Deletion of SLX5 shows an accumulation of sumoylated Cse4 species. Wild-type (YMB7278) and slx5∆ (YMB7875) strains expressing pGAL-13Myc-CSE4 (pSB816) were grown in raffinose/galactose (2%) for 4 h. His-Flag–tagged Smt3 (HF-Smt3) was pulled down by Ni-NTA agarose beads. Cellular levels of sumoylated proteins and sumoylated Cse4 were detected by
mislocalized in the slx5Δ strain. These approaches were previously used to show that defects in ubiquitin-mediated proteolysis of Cse4 in a psh1Δ strain led to the enrichment of Cse4 in chromatin and mislocalization to euchromatin when Cse4 was overexpressed (Hewawasam et al., 2010; Ranjitkar et al., 2010; Deyter and Biggins, 2014). Subcellular fractionation of whole-cell lysates was performed with psh1Δ, slx5Δ, and psh1Δ slx5Δ strains. Cse4 was barely detectable in the chromatin fraction in a wild-type strain, as its localization is restricted to centromeres (Figure 4A). In contrast, Cse4 was enriched in chromatin in psh1Δ slx5Δ strains, and this enrichment was further enhanced in psh1Δ slx5Δ strains. Similar results were observed for chromatin enrichment of Cse4 transiently overexpressed from a GAL promoter in psh1Δ and slx5Δ strains, with maximum enrichment in the psh1Δ slx5Δ strain (Supplemental Figure S5).

Western blot analysis with anti-Flag (Smt3) and anti-Myc (Cse4) antibodies, respectively. Two different exposures are shown. (F) Deletion of SLX5, but not PSH1, shows an accumulation of sumoylated Cse4 expressed from its own promoter. Protein extracts were prepared from cells grown to logarithmic phase in YPD. Sumoylation levels of Cse4 and nonmodified Cse4 were detected using Ni-NTA pull down, followed by Western blot analysis with anti-Smt3 and anti-HA (Cse4) antibodies, respectively. Input samples were analyzed using anti-HA (Cse4) and anti-Tub2 antibodies. At least three high molecular weights of 6His-3HA–Cse4 (arrows) were detected in the slx5Δ strain. Asterisk shows nonspecific sumoylated proteins that bind to the beads. Isogenic yeast strains used are wild type (YMB7290), psh1Δ (YMB7393), slx5Δ (YMB7588), and psh1Δ slx5Δ (YMB7607). (D) Kinetics of turnover from C. Cse4 protein half-life (t1/2) is indicated, and error bars in wild-type and psh1Δ slx5Δ strains represent average deviation of two replicates.
We next used chromosome spreads, a technique that removes soluble material to visualize localization of chromatin-bound Cse4 in wild-type, \( psh1\Delta \), \( slx5\Delta \), and \( psh1\Delta \ \text{slx5}\Delta \) strains expressing Cse4 from own promoter (Figure 4B). In wild-type cells, Cse4 foci were restricted to one or two dots, which correspond to kinetochore clusters. In contrast, diffused or multiple foci of Cse4 that overlapped with the 4',6-diamidino-2-phenylindole (DAPI)-stained nucleus were observed in \( psh1\Delta \) and \( slx5\Delta \) strains, and this was further exacerbated in \( psh1\Delta \ \text{slx5}\Delta \) cells (Figure 4, B and C). On the basis of these results, we conclude that Slx5 and Psh1 prevent mislocalization of Cse4 under normal physiological conditions and that Slx5 regulates localization of Cse4 in a Psh1-independent manner.

**DISCUSSION**

In this study, we showed that sumoylation and ubiquitination of Cse4 regulate its proteolysis and prevent its mislocalization. We provide the first evidence for sumoylation of Cse4, by SUMO E3 ligases Siz1 and Siz2 in vivo and in vitro, and define a role for Slx5 in ubiquitin-mediated proteolysis of Cse4. Slx5-mediated proteolysis of Cse4 is independent of Psh1, and Cse4 is mislocalized to euchromatin in both \( psh1\Delta \) and \( slx5\Delta \) strains under normal physiological conditions. Consistent with these results, Cse4 is highly enriched in the chromatin fraction and stably incorporated into euchromatin in \( psh1\Delta \) and \( slx5\Delta \) strains. Taken together, our results support a role for Slx5 in ubiquitination of sumoylated Cse4 to regulate its proteolysis and localization.

Several lines of evidence support the role of Slx5 in proteolysis of Cse4. Overexpression of \( CSE4 \) results in growth inhibition in \( slx5\Delta \) and \( siz1\Delta \ \text{siz2}\Delta \) strains, similar to \( psh1\Delta \) strain (Hewawasam et al., 2010; Ranjitkar et al., 2010; Au et al., 2013). Second, defects in Cse4 ubiquitination observed in \( slx5\Delta \) strains correlate with an increased half-life of Cse4 in these strains. Higher stability of Cse4 is also observed in an \( slx5\Delta \) strain (unpublished data), suggesting that the heterodimeric Slx5/8 STUbL complex is important for Cse4 proteolysis. Third, deletion of \( SLX5 \) leads to accumulation of higher-molecular
Our studies on the role of STUbLs in ubiquitin-mediated proteolysis of CENP-A observed in many cancers contribute to tumorigenesis. As we do not fully understand how overexpression and mislocalization affects in proteolysis, were observed when SLX5 and/or SLX8 are deleted (Wang and Prelich, 2009). Accumulation of sumoylated Cse4 species and increased stability of Cse4 in the slx5Δ strain suggest that sumoylation precedes ubiquitin-mediated proteolysis of Cse4. These phenotypes are not limited to cases in which Cse4 is overexpressed (e.g., using the GAL promoter); higher levels of sumoylated Cse4 and increased stability of Cse4 are also observed under physiological conditions when Cse4 is expressed from its own promoter. The increased stability of Cse4 in the psh1Δ slx5Δ double mutant compared with either the slx5Δ or psh1Δ single mutant shows that Slx5-mediated proteolysis of Cse4 is independent of Psh1 under normal physiological conditions. The residual proteolysis of Cse4 observed in psh1Δ slx5Δ strains suggests that additional pathways/regulators that have yet to be identified also mediate Cse4 proteolysis. This is perhaps not surprising, given that degradation of excess of histone H3 is also regulated by at least five E3 ubiquitin ligases (Singh et al., 2012). In addition, non–ubiquitin-mediated pathways partially contribute to Cse4 proteolysis because mutant cse4 1KR, in which all lysines are changed to arginine, is still degraded (Collins et al., 2004; Au et al., 2013). Endogenously expressed Cse4 is enriched in chromatin fractions and mislocalized to euchromatin in slx5Δ and psh1Δ strains, and these phenotypes are further exacerbated in the slx5Δ psh1Δ double mutant. Previous studies examined Cse4 turnover only in the context of the kinetochore, where it is stably incorporated into chromatin (Pearson et al., 2004). Although the signal is low, the increased levels of noncentromeric Cse4 present in slx5Δ and psh1Δ strains (the “haze”) enable analysis by FRAP. The apparent stability of mislocalized Cse4 observed by FRAP suggests that ectopically localized Cse4 is stably incorporated in the euchromatin; however, it is also possible that the ectopic Cse4-containing nucleosomes are dynamic, in equilibrium with (non–fluorescently tagged) H3 in the nucleus (Verdaasdonk et al., 2012). The latter explanation would require that the exchange mechanism uses a different Cse4/H3 pool than that under which the Cse4 was initially misincorporated.

We propose a model (Figure 6) in which sumoylation and ubiquitination regulate Cse4 proteolysis to prevent its stable incorporation into euchromatin. At least two independent pathways regulate Cse4 proteolysis. One is dependent on the interaction of Psh1 with Cse4, which is potentiated by the nucleosome-stabilizing activity of the FACT complex. This suggests that Psh1 is primarily responsible for removing nucleosomal Cse4 at noncentromeric chromatin, even though the interaction of Psh1 and soluble Cse4 is also reduced in the absence of FACT (Deyter and Biggins, 2014). The second pathway, identified here, requires sumoylation of Cse4 by Siz1/Siz2 and subsequent ubiquitination of Cse4 by Slx5 to regulate cellular levels of Cse4 and prevent its mislocalization to euchromatin. Although we do not yet know whether the Siz1/2/Slx5 pathway acts on soluble Cse4 or chromatin-bound Cse4, together the two pathways act to regulate cellular levels of Cse4 and prevent its mislocalization to euchromatin. Given that mislocalization of Cse4 leads to chromosome segregation defects, it is not surprising that these cells use multiple ubiquitination pathways for proteolysis of high levels of Cse4.

Unlike Psh1, Slx5 and Slx8 are evolutionarily conserved, and depletion of the human STUbL orthologue, RNF4, results in defects in chromosome segregation (van de Pasch et al., 2013). Similar to Slx5, it is possible that RNF4 also regulates the localization of CENP-A and that defects in this pathway lead to chromosome missegregation. Previous studies showed that mislocalization of centromeric histone H3 variants Cse4, Cnp1, and CID contribute to chromosome segregation defects in flies and budding/fission yeast (Heun et al., 2006; Au et al., 2008; Gonzalez et al., 2014). Thus we propose that the mislocalization of CENP-A contributes to chromosome segregation defects in slx5Δ and RNF4-depleted cells. These studies are important, as we do not fully understand how overexpression and mislocalization of CENP-A observed in many cancers contribute to tumorigenesis. Our studies on the role of STUbLs in ubiquitin-mediated proteolysis of Cse4 provide mechanistic insights into pathways that prevent mislocalization of CENP-A and aneuploidy in human cancers.
Degraded by the proteasome

Cse4

Cse4

Cse4

Cse4

Cse4

Cse4

Psh1

Psh1

Psh1

Psh1

Siz1/2, Siz5/8

Siz1/2

Siz1/2, Siz5/8

GST pull-down assay

The ubc4Δ ubc6Δ (YOK 2501) strain was transformed with pGAL-GST-SLX5 (BOK 629, Open Biosystems Yeast GST Collection YSC4515202484078), pGAL-3HA-CSE4 (pMB 1515), or both pGAL-GST-SLX5 and pGAL-3HA-CSE4. Transformants were grown in appropriate selective medium with proline as nitrogen source and 2% sucrose to logarithmic phase, and then 2% galactose and 0.003% SDS were added to the cultures and incubation continued for another 6 h. MG132, 75 μM, was added ½ h before harvesting of the cells. We assayed 200 OD units of yeast cells as described previously (Westerbeck et al., 2014). Whole-cell extracts (2 OD) and pull down (20 OD) were analyzed by Western blot analysis.

Subcellular fractionation and chromosome spreads

Subcellular fractionation to assay chromatin enrichment of Cse4 was performed as described previously (Au et al., 2008). Cells were grown to logarithmic phase of growth in 1% yeast extract, 2% bactopeptone, and 2% glucose (YPD) at 25°C. Chromosome spreads were performed as described previously (Collins et al., 2004; Crotti and Basrai, 2004) with some modifications. 16B12 mouse anti-HA antibody (MMS-101P; Covance, Emeryville, CA) was used as primary antibody at 1:2500 dilution. Cy3-conjugated goat anti-mouse (115165003; Jackson ImmunoResearch Laboratories, West Grove, PA) was used as secondary antibody at 1:5000 dilution. Cells were visualized by DAPI staining (1 μg/ml in phosphate-buffered saline) mounted in antifade mountant (P36935; Molecular Probes, Eugene, OR). Cells were observed under an Axioskop 2 (Zeiss) fluorescence microscope equipped with a Plan-Apochromat 100× (Zeiss, Thornwood, NY) oil immersion lens. Image acquisition and processing were performed with the IP Lab version 3.9.9 r3 software (Scanalytics, Fairfax, VA).

Antibodies

Antibodies for experiments were as follows: rabbit polyclonal anti-Cse4 (Strunnikov laboratory), anti-Tub2 antibodies (Basrai laboratory), anti-HA (12CA5; Roche, Indianapolis, IN), anti-HA (ab9110; Abcam, Cambridge, MA), anti-myc (A-14; Santa Cruz Biotechnology), and anti-HA (ab9110; Abcam). Anti-Cse4 was used as primary antibody at 1:2500 dilution. Cy3-conjugated goat anti-mouse antibody (MMS-101P; Covance, Emeryville, CA) was used as primary antibody at 1:2500 dilution. Cy3-conjugated goat anti-mouse antibody (MMS-101P; Covance, Emeryville, CA) was used as primary antibody at 1:2500 dilution. Cy3-conjugated goat anti-mouse antibody (MMS-101P; Covance, Emeryville, CA) was used as primary antibody at 1:2500 dilution. Cy3-conjugated goat anti-mouse antibody (MMS-101P; Covance, Emeryville, CA) was used as primary antibody at 1:2500 dilution.

FRAP

Strains YMB9430 (Cse4-GFP, psh1Δ) and YMB9429 (Cse4-GFP, sld5Δ) were grown in YPD to mid logarithmic growth phase before imaging. Both YMB9430 and YMB9429 were grown at 24°C, but YMB9429 was shifted to 37°C 6 h before imaging. Cells were imaged using a Nikon Eclipse Ti wide-field inverted microscope with a 100×/1.49 numerical aperture Apo total internal reflection fluorescence objective (Nikon, Melville, NY) and Andor Clara charge-coupled device camera (Andor, South Windsor, CT) using Nikon NIS Elements imaging software. Photobleaching was performed with a Sapphire 488-50 CDRH laser (Coherent, Santa Clara, CA). A seven-step Z-series with

MATERIALS AND METHODS

Yeast strains and plasmids

Supplemental Tables S1 and S2 describe the genotype of yeast strains and plasmids used for this study, respectively.

Sumoylation assay in vivo and in vitro

In vitro sumoylation was assayed in crude yeast extracts using NiNTA agarose beads to pull down His-HA–tagged Cse4 or His-Flag–tagged Smt3 (HF-Smt3) under denaturing condition, as described previously (Ohkuni et al., 2015). In vitro sumoylation assays were carried out as described previously (Takahashi et al., 2003). Briefly, the components of the conjugation reaction—Smt3gg, GST-Uba2, GST-Aos1, Ubc9, and Siz1-Δ440 proteins—were expressed and purified from Escherichia coli and then used in the reaction mixture containing Cse4 as a substrate. Cse4 was produced in E. coli and purified by Sephacryl-S200 chromatography as described (Luger et al., 1997). Substrate (Cse4), E1 (GST-Uba2, GST-Aos1), E2 (Ubc9), and SUMO (Smt3gg) were incubated in a total volume 20 μl for 60 min in the presence of 10 mM ATP, 50 mM Tris-HCl (pH 8.0), 5 mM MgCl2, and 2 mM dithiothreitol at 37°C. The reaction was stopped by adding 2× Laemmli buffer.

Protein stability and ubiquitin pull-down assays

Protein stability assay was performed as described previously (Ohkuni et al., 2014) with some modifications. Cells were grown in appropriate selective medium with proline as nitrogen source and 2% sucrose to logarithmic phase, and then 2% galactose and 0.003% SDS were added to the cultures and incubation continued for another 6 h. MG132, 75 μM, was added ½ h before harvesting of the cells. We assayed 200 OD units of yeast cells as described previously (Westerbeck et al., 2014). Whole-cell extracts (2 OD) and pull down (20 OD) were analyzed by Western blot analysis.

Subcellular fractionation and chromosome spreads

Subcellular fractionation to assay chromatin enrichment of Cse4 was performed as described previously (Au et al., 2008). Cells were grown to logarithmic phase of growth in 1% yeast extract, 2% bactopeptone, and 2% glucose (YPD) at 25°C. Chromosome spreads were performed as described previously (Collins et al., 2004; Crotti and Basrai, 2004) with some modifications. 16B12 mouse anti-HA antibody (MMS-101P; Covance, Emeryville, CA) was used as primary antibody at 1:2500 dilution. Cy3-conjugated goat anti-mouse antibody (115165003; Jackson ImmunoResearch Laboratories, West Grove, PA) was used as secondary antibody at 1:5000 dilution. Cells were visualized by DAPI staining (1 μg/ml in phosphate-buffered saline) mounted in antifade mountant (P36935; Molecular Probes, Eugene, OR). Cells were observed under an Axioskop 2 (Zeiss) fluorescence microscope equipped with a Plan-Apochromat 100× (Zeiss, Thornwood, NY) oil immersion lens. Image acquisition and processing were performed with the IP Lab version 3.9.9 r3 software (Scanalytics, Fairfax, VA).

Antibodies

Antibodies for experiments were as follows: rabbit polyclonal anti-Cse4 (Strunnikov laboratory), anti-Tub2 antibodies (Basrai laboratory), anti-HA (12CA5; Roche, Indianapolis, IN), anti-HA (ab9110; Abcam, Cambridge, MA), anti-myc (A-14; Santa Cruz Biotechnology), and anti-HA (ab9110; Abcam). Anti-Cse4 was used as primary antibody at 1:2500 dilution. Cy3-conjugated goat anti-mouse antibody (MMS-101P; Covance, Emeryville, CA) was used as primary antibody at 1:2500 dilution. Cy3-conjugated goat anti-mouse antibody (MMS-101P; Covance, Emeryville, CA) was used as primary antibody at 1:2500 dilution. Cy3-conjugated goat anti-mouse antibody (MMS-101P; Covance, Emeryville, CA) was used as primary antibody at 1:2500 dilution.

FRAP

Strains YMB9430 (Cse4-GFP, psh1Δ) and YMB9429 (Cse4-GFP, sld5Δ) were grown in YPD to mid logarithmic growth phase before imaging. Both YMB9430 and YMB9429 were grown at 24°C, but YMB9429 was shifted to 37°C 6 h before imaging. Cells were imaged using a Nikon Eclipse Ti wide-field inverted microscope with a 100×/1.49 numerical aperture Apo total internal reflection fluorescence objective (Nikon, Melville, NY) and Andor Clara charge-coupled device camera (Andor, South Windsor, CT) using Nikon NIS Elements imaging software. Photobleaching was performed with a Sapphire 488-50 CDRH laser (Coherent, Santa Clara, CA). A seven-step Z-series with

FIGURE 6: Model for how Sls5 regulates proteolysis of Cse4 and prevents its mislocalization to euchromatin. Restricting the localization of Cse4 to centromeric DNA is essential for faithful chromosome segregation. At least two independent pathways prevent the stable incorporation of Cse4 into euchromatin. One of these pathways is dependent on the interaction of Psh1 with Cse4. The second pathway requires sumoylation of Cse4 by Siz1/Siz2 and ubiquitination of sumoylated Cse4 by Sls5. The two pathways may a) regulate soluble pools of Cse4 to prevent its mislocalization and/or b) facilitate proteolysis of chromatin-bound Cse4.
200-nm step size with 600-ms exposure time was taken before a 300-ms exposure lapse from the laser. Immediately after the laser exposure, a 5-min time lapse with 30-s intervals with the same settings as the first Z-series was initiated. The Z-series was compiled into single images using maximum projection, and the integrated intensity of the bleach area was measured using MetaMorph 7.7 imaging software (Molecular Devices, Sunnyvale, CA). The integrated intensity of the bleached area had the integrated intensity of the cell background subtracted at each time point, and photobleaching was corrected for by determining the average bleaching rate of a nearby Cse4-GFP signal and adding back the average signal loss per Z-series. Photobleaching and background subtraction was performed using Excel (Microsoft, Redmond, WA).

**Chromosome transmission fidelity**

The chromosome transmission fidelity assay was performed as described previously (Spencer et al., 1990; Ohkuni et al., 2008). Strains were plated on synthetic medium with limiting adenine and incubated at 25°C for 4 d. Loss of the reporter chromosome results in red sectors in an otherwise white colony. Colonies that are at least half red indicate loss of the reporter chromosome in the first cell division.

**ACKNOWLEDGMENTS**

We thank members of the Basrai laboratory for helpful discussions and comments on the manuscript. We gratefully acknowledge Charlie Boone, Frank Holstege, and Sue Biggins for reagents and advice, Tatiana Karpova (Fluorescent Imaging Facility, National Cancer Institute) for assistance with cell biology experiments, Kathy McKinnon (Vaccine Branch FACS Core, National Cancer Institute) for assistance with FACS, and Anita Corbett, Ian Cheeseman, Michael Lichten, Tom Misteli, and Peter Kaiser for comments on the manuscript. This work was supported by the National Institutes of Health Intramural Research Program to M.B., National Science Foundation Grant MCB 1051970 to O.K., and National Institutes of Health R37 Grant GM32238 to K.B.

**REFERENCES**


