Nucleolar protein B23/nucleophosmin regulates the vertebrate SUMO pathway through SENP3 and SENP5 proteases

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Ubiquitin-like protein/sentrin-specific proteases (Ulp/SENP) mediate both processing and deconjugation of small ubiquitin-like modifier proteins (SUMOs). Here, we show that Ulp/SENP family members SENP3 and SENP5 localize within the granular component of the nucleolus, a subnucleolar compartment that contains B23/nucleophosmin. B23/nucleophosmin is an abundant shuttling phosphoprotein, which plays important roles in ribosome biogenesis and which has been strongly implicated in hematopoietic malignancies. Moreover, we found that B23/nucleophosmin binds SENP3 and SENP5 in Xenopus laevis egg extracts and that it is essential for stable accumulation of SENP3 and SENP5 in mammalian tissue culture cells. After either codepletion of SENP3 and SENP5 or depletion of B23/nucleophosmin, we observed accumulation of SUMO proteins within nucleoli. Finally, depletion of these Ulp/SENP causes defects in ribosome biogenesis reminiscent of phenotypes observed in the absence of B23/nucleophosmin. Together, these results suggest that regulation of SUMO deconjugation may be a major facet of B23/nucleophosmin function in vivo.

Introduction

Small ubiquitin-like modifier proteins (SUMOs) are ubiquitin-related proteins that act in many processes through covalent linkage to cellular proteins (Johnson, 2004). Mammalian cells express three major SUMO paralogues: mature SUMO-2 and SUMO-3 are ~95% identical to each other and each is ~45% identical to SUMO-1. (Where they cannot be distinguished, SUMO-2 and -3 will be collectively called SUMO-2/3.) SUMO-1 localizes within the nucleoplasm, nuclear envelope, and nucleolus, whereas SUMO-2 and SUMO-3 are predominantly found in the nucleoplasm (Ayaydin and Dasso, 2004). All newly synthesized SUMOs are processed by ubiquitin-like protein/sentrin-specific proteases (Ulp/SENP), and Ulp/SENP also deconjugate SUMOylated species (Hay, 2007; Mukhopadhyay and Dasso, 2007). Saccharomyces cerevisiae has two Ulp/SENP, Ulp1p and Ulp2p (Li and Hochstrasser, 1999, 2000). Ulp1p is essential and localizes to nuclear pores, whereas Ulp2p is dispensable for growth and localizes to the nucleoplasm. Ulp1p has been particularly implicated in ribosome biogenesis (Panse et al., 2006).

The nucleolus is the site of ribosome synthesis, including preribosomal RNA transcription, ribosomal RNA (rRNA) processing, and ribosomal subunit assembly (Boisvert et al., 2007). B23/nucleophosmin is an abundant 37-kD phosphoprotein that shuttles between the granular component of the nucleolus and cytoplasm. B23/nucleophosmin can become SUMOylated under some circumstances (Liu et al., 2007). It has been implicated in many cellular processes, including ribosome biogenesis and export, centrosome duplication, and maintenance of genomic integrity through the Arf–MDM2–p53 pathway (Grisendi et al., 2006; Sherr, 2006). Consistent with these diverse roles,
granular component (dsRed-B23/nucleophosmin). The signal from GFP-SENP3 and GFP-SENP5 overlapped poorly with UBF staining and only partially with dsRed-fibrillarin, suggesting that they were not concentrated in either the fibrillar centers or the dense fibrillar component (Fig. 1A, top). In contrast, both proteins showed distributions that were very similar to B23/nucleophosmin, which could be observed either by immunostaining or by coexpression of B23/nucleophosmin as a fusion with the dsRed fluorescent protein (Fig. 1A, bottom). We conclude that SENP3 and SENP5 are concentrated within the granular component.

The presence of SUMO-2/3-specific proteases within nucleoli suggested that the absence of these SUMO paralogues might be the result of their ongoing removal from nucleolar targets. To test this idea, we depleted SENP3 and SENP5 individually and together by oligonucleotide-mediated RNA interference (RNAi) from HeLa cells (Fig. 2A). Depletion of either protease did not substantially alter the distribution of SUMO proteins. However, nucleolar SUMO-1 increased after codepletion of SENP3 and SENP5 (Fig. 2B and Fig. S1, available at http://www.jcb.org/cgi/content/full/jcb.200807185/DC1). Significantly, SUMO-2/3 also became concentrated within nucleoli in the absence of both enzymes. Depletion of nuclear pore–associated SENP/Ulps (SENP1 and SENP2) did not increase nucleolar levels of SUMO proteins (unpublished data), arguing that such accumulation is not a general result of SUMO pathway manipulation or of RNAi machinery activation.

SENP3 and SENP5 show robust enzymatic activities against SUMO-2/3–containing substrates (Di Bacco et al., 2006;...
that defects in ribosome biogenesis were specifically caused by depletion of SENP3 and SENP5. Our results show that SENP3 and SENP5 individually play important roles in ribosome biogenesis (Fig. 3), but depletion of both proteases is required for elevation of SUMO-conjugated species within nucleoli (Fig. 2). Together, these results might suggest that although both SENP3 and SENP5 can act on the bulk of nucleolar substrates, they may each specifically regulate a subset of conjugates that are critical for particular events in the biogenesis pathway.

We were unable to extract SENP3 and SENP5 from mammalian nucleoli under conditions that would allow analysis of protein–protein interactions. As an alternative, we used Xenopus laevis egg extracts (XEEs) to look for binding partners. XEEs offer major advantages for these experiments because most nuclear and nucleolar proteins are stored in soluble forms (Powers et al., 2001). Human SENP3 and Xenopus SENP3 (xSENP3) proteins are 85% identical within their catalytic domains and 50% identical throughout their entire sequences. Human SENP5 and xSENP5 proteins are 87% identical within their catalytic domains and 43% identical throughout their entire sequences. There was little xSENP5 in Xenopus eggs (unpublished data), which is perhaps consistent with the more specialized tissue distribution of mammalian SENP5 (Fig. S2 C). Antibodies against xSENP3 recognized a protein of the appropriate size in XEEs. Analysis using vinyl sulfone derivatives of different SUMO paralogues demonstrated that xSENP3 shared the same enzymatic specificity as mammalian SENP3 (Fig. S2 D).

We observed a protein that strongly and specifically co-precipitated with xSENP3, which mass spectrometric analysis revealed to be the Xenopus homologue of B23/nucleophosmin (xB23/nucleophosmin). We confirmed this interaction by Western blotting of anti-xSENP3 immunoprecipitates (Fig. 1 B). Given the low levels of xSENP5 within XEEs, we used an alternative strategy to determine whether SENP5 might likewise
Depletion of SENP3 or SENP5 cause defects in ribosome biogenesis. (A) HeLa cells were transfected with control oligonucleotides (Control) or siRNAs directed against SENP3 (ΔSENP3) and SENP5 (ΔSENP5) or both SENP3 and SENP5 (ΔSENP3/5). 72 h later, the cells were pulsed with [3H]uridine for 25 min, followed by washing and incubation with fresh media supplemented with 1 mg/ml of cold uridine for the indicated times (in hours). At each time point, equal numbers of cells were harvested for analysis of rRNA synthesis and processing. (Bottom) Western blots of cell extracts to monitor SENP3 and SENP5 and Western blotting of actin as a loading control. Ethidium bromide staining shows the amount of total RNA loaded in each lane. (B) The amounts of 28S and 32S RNAs were quantitated for each experiment. Bars represent the mean of normalized values from the three experiments ± SD. (C) The amount of 47S pre-rRNA transcript was quantitated at the initiation of the chase period (0 h) within three independent experiments as in A after 2 h. Ratios of 32S to 28S RNAs were calculated for each experiment. Bars represent the mean values calculated from the three experiments ± SD. At each time point, equal numbers of cells were harvested for analysis of rRNA synthesis and processing. (Bottom) Western blots of cell extracts to monitor SENP3 and SENP5 and Western blotting of actin as a loading control. Ethidium bromide staining shows the amount of total RNA loaded in each lane. (B) The amounts of 28S and 32S RNAs were quantitated for each experiment. Bars represent the mean of normalized values from the three experiments ± SD. (C) The amount of 47S pre-rRNA transcript was quantitated at the initiation of the chase period (0 h) within three independent experiments as in A after 2 h. Ratios of 32S to 28S RNAs were calculated for each experiment. Bars represent the mean values calculated from the three experiments ± SD.

Several observations indicated that SENP3 and SENP5 loss was caused by increased degradation rather than decreased expression. First, GFP-SENP3 and GFP-SENP5 were not transcribed from the native SENP3 and SENP5 promoters, so the drop in their levels upon B23/nucleophosmin depletion (Fig. 4 B) argues that repression of those promoters cannot account for changes in protein levels. Second, the concentrations of SENP3 and SENP5 mRNAs were not substantially altered by B23/nucleophosmin depletion in HeLa cells, as measured by RT-PCR (unpublished data), further arguing against B23/nucleophosmin control of SENP3 and SENP5 transcription or mRNA stability. Third, B23/nucleophosmin-depleted cells did not show a substantial drop in overall protein translation, as measured by incorporation of [3H]methionine (unpublished data), indicating that preexisting ribosomes were sufficiently sufficient to maintain protein synthesis levels. Notably, depletion of a key ribosomal assembly factor, Rrp9 (Venema et al., 2000), did not destabilize SENP3 and SENP5 or cause substantial nucleolar accumulation of SUMO proteins (unpublished data), demonstrating that their loss was not a simple consequence of ribosome synthesis inhibition but may be more specifically linked to the function of B23/nucleophosmin.

Finally, SENP3 and SENP5 levels in B23/nucleophosmin-depleted cells showed substantial, albeit incomplete, recovery upon treatment with the proteasome inhibitor MG132, which is consistent with the notion that they are subject to degradation in the absence of B23/nucleophosmin (Fig. 4 D). Stable cell lines expressing GFP-SENP3 and SENP5 showed a partial redistribution of GFP signals after B23/nucleophosmin depletion and MG132 treatment, with an increase in the ratio of nucleoplasmic to nucleolar distribution of both fusion proteins (unpublished data). This observation might indicate a role for B23/nucleophosmin in retention of these Ulp/SENPs within the nucleolus. However, we noted that the distribution of many other nucleolar proteins was rearranged after MG132 treatment, so it is also possible that relocalization of GFP-SENP3 and GFP-SENP5 may reflect alterations of nucleolar structure.

We hypothesized that failure to deconjugate some SUMO species might disrupt ribosome biogenesis in the absence of SENP3 and SENP5. We therefore examined the SUMOylation of mammalian homologues of ribosomal proteins or ribosome assembly factors that have been implicated as SUMO conjugation targets in yeast (Panse et al., 2004, 2006; Wohlschlegel...
argued that SENP3 acts upstream of B23/nucleophosmin, causing inhibition of ribosome biogenesis through increased B23/nucleophosmin SUMOylation. In our hands, depletion of SENP3 and SENP5 by RNAi, either singly (not depicted) or in combination (Fig. 5), did not cause a substantial SUMOylation of B23/nucleophosmin. We do not know why our results differ from those of et al., 2004; Denison et al., 2005; Hannich et al., 2005). Using cells that stably expressed His6-tagged SUMO-1 (His-SUMO1F) or SUMO-2 (His-SUMO2F) proproteins, we examined changes in electrophoretic mobility of potential conjugation targets by Western blotting after codepletion of SENP3 and SENP5. We also purified the SUMO-conjugated fraction from each cell line by affinity chromatography and examined whether SUMOylated forms of the proteins could be found by Western analysis.

A subset of proteins showed clearly altered SUMOylation patterns under these circumstances: GNL2, the mammalian homologue of a 60S preribosomal export factor, showed a supershifted form upon depletion of SENP3/5 (Fig. 5), which was verified as a SUMOylated form through its preferential retention on nickel–nitrilotriacetic acid (Ni-NTA) agarose beads. We observed a supershifted form of the 60S ribosomal subunit RPL37A that was retained on Ni-NTA agarose beads in the absence of SENP3/5 (Fig. 5, top), suggesting that it was likewise subject to enhanced modification. Other nucleolar proteins (fibrillarin, DDX3, DDX17, and NVL2; unpublished data) did not show evidence of SUMOylation in this assay. Although this is an incomplete survey of potential conjugation targets within the 60S ribosomal biogenesis pathway, it demonstrates that multiple pathway components are SUMOylation targets, as in yeast. More importantly, enhanced RPL37A and GNL2 SUMOylation after depletion of SENP3 and SENP5 implicates these proteases in the control of ribosome biogenesis through this modification.

While this manuscript was under revision, Haindl et al. (2008) reported that SENP3 and B23/nucleophosmin physically interact and that loss of SENP3 disrupts rRNA processing. They argued that SENP3 acts upstream of B23/nucleophosmin, causing inhibition of ribosome biogenesis through increased B23/nucleophosmin SUMOylation. In our hands, depletion of SENP3 and SENP5 by RNAi, either singly (not depicted) or in combination (Fig. 5), did not cause a substantial SUMOylation of B23/nucleophosmin. We do not know why our results differ from those of
Haindl et al. (2008), but suspect that the relatively low levels of His-tagged SUMO proteins expressed in our stable cell lines may mimic physiological conditions more closely than conditions of transient expression. In any case, our results do not suggest that B23/nucleophosmin is itself the primary target of SENP3 or SENP5. As an alternative model, we note that B23/nucleophosmin interacts with ribosomes (Grisendi et al., 2006), so that it might act as an adaptor for targeting of SUMO proteases to ribosomal proteins. Consistent with this idea, 60S ribosomal components Rpl26 and RplP0 are coprecipitated from XEEs with xSENP3 in a xB23/nucleophosmin-dependent manner (Fig. 1 C).

The requirement for B23/nucleophosmin in ribosome synthesis has been proposed to include both action as an endonuclease (Savkur and Olson, 1998) and as a chaperone (Szebeni and Olson, 1999). Our data show that regulation of SUMOylation through SENP3 and SENP5 is another major aspect of B23/nucleophosmin function in this process. The capacity of xB23/nucleophosmin to link xSENP3 with ribosomes suggests that it may recruit SUMO proteases to maturing ribosomal particles. Interestingly, B23/nucleophosmin has been implicated in a variety of apparently unrelated cellular processes (Grisendi et al., 2006), many of which are also dependent on the SUMO conjugation (Hay, 2005). We therefore speculate that altered SUMOylation may be a simple, unifying mechanism that underlies much of the apparent plurality of B23/nucleophosmin functions.

Materials and methods

Chemicals and reagents

Human testis QUICK-Clone cDNA, human multiple tissue cDNAs, pEGFP, and pDsRed were obtained from Clontech Laboratories, Inc. Oligofectamine, Rabbit IgG tricolor labeling kit, and geneticin were obtained from Invitrogen. siRNA oligonucleotides (SENPF1, AATTCTTTGTCATGCTGAA; SENPF2, AAATCCGCTGAACTGGTTAAT; SENPF3, AAATCCGCTGAACTGGTTAAT; SENPF5, AAGTCCACTGGTCTCTCATTA; control, AACTGTCAGTCAGTCAGTCAGT) were obtained from Qiagen. Human SENP3 (amino acids 204 – 406) and SENP5 (amino acids 1 – 237) cDNA constructs were expressed in E. coli (BL21 [DE3]) and purified over Ni-NTA agarose. Antiserum against His-SUMO1F or SUMO-2F were depleted of SENP3 and SENP5 by siRNA. 72 h later, the cells were harvested, lysed in lysis buffer (6 M guanidine-HCl, 0.1 M Na2HPO4/NaH2PO4, 0.01 M Tris-HCl, pH 8.0, and 10 mM β-mercaptoethanol), plus 5 mM imidazole, total cell lysates were mixed with 50 μl of Ni-NTA agarose beads and incubated for 2 h at 23°C. The beads were washed with lysis buffer, followed by buffer A (0.1 M urea, 0.1 M Na2HPO4/NaH2PO4, 0.1 M Tris-HCl, pH 8.0, 10 μM β-mercaptoethanol, and 0.2% Triton X-100). After washing, the beads were eluted with 200 mM imidazole in 5% SDS, 0.15 M Tris-HCl, pH 6.7, 30% glycerol, and 0.72 M β-mercaptoethanol. The eluted fraction was subjected to SDS-PAGE and Western blotting with anti-RPA37A, -GNL2, or -B23/nucleophosmin antibodies.

Interactions of B23/nucleophosmin with SENP3 or SENP5

Interphase XEEs were prepared as described previously (Orjalo et al., 2006). For Fig. 1 B (top), anti-xSENP3 and -xB23/nucleophosmin antibodies or rabbit IgG were conjugated to protein A Dynabeads (Invitrogen). The XEE was supplemented with 10 μg/ml each of leupeptin, pepstatin, and chymostatin and with 20 μM Ran-G69L (Orjalo et al., 2006) and incubated with antibody-coated beads for 1 h at 23°C. The beads were washed with buffer A (250 mM sucrose, 2.5 mM MgCl2, 1 mM DTT, 100 mM KCl, and 10 mM Heps, pH 7.7) plus 0.00001% digitonin and protease inhibitors and eluted with 25 μl of 0.1 M glycine, pH 2.3. For Fig. 1 B (bottom), pT7-FLAG-Trx-xSENP5 mRNA was made using an mMessage mMachine T7 kit (Applied Biosystems) and translated in XEEs (Boyarchuk et al., 2007). 25 μl of the reaction was mixed with 25 μl of interphase XEE and 20 μM Ran-G69L. The mixture was diluted 10-fold with buffer B (250 mM sucrose, 2.5 mM MgCl2, 1 mM DTT, 50 mM KCl, 100 mM Heps, pH 7.7, and 0.00001% digitonin) and incubated for 1 h at 23°C. Mouse anti-FLAG antibody (M2; Sigma-Aldrich), rabbit anti-xB23, non-specific mouse IgG, or non-specific rabbit IgG were added to aliquots of the clarified supernatant and incubated for 1 h on ice before addition of 15 μl of preblocked protein G-Sepharose (GE Healthcare). After 1 h at 4°C with rotation, the beads were pelleted, washed with buffer A plus 0.00001% digitonin, and eluted with 25 μl of 0.1 M glycine, pH 2.3.

In Fig. 1 C, interphase XEEs were depleted using protein A Dynabeads coupled with anti-xB23/nucleophosmin antibodies or mock treated with rabbit IgG-coupled control beads. Resultant XEEs were supplemented with protease inhibitors and 20 μM Ran-G69L, and immunoprecipitations with anti-xSENP3 antibodies or rabbit IgG were performed as described in the previous paragraph. Bound proteins were eluted with 0.1 M glycine, pH 2.3. In all cases, equal elution volumes were subjected to SDS-PAGE and Western blotting. In Fig. 1, protein A–HRP was used for visualization of xSENP3. Anti-mouse IgG–HRP was used for FLAG epitope visualization. Anti-rabbit HRP was used for visualization of all other antibodies.

Immunofluorescence microscopy and Western blotting

Cells were grown on Labteck coverslip-bottomed chambers or glass slide coverslips. 72 h after transfection with siRNAs, cells were fixed for 5 min with 4% formaldehyde in PBS and permeabilized for 5 min with 0.5% Triton X-100 in PBS. The cells were blocked for 1 h in PBS containing 1% bovine serum albumin. After washing with PBS, the cells were incubated with primary antibodies diluted 1:200 in blocking solution for 1 h. The coverslips were washed and incubated for 1 h with Alexa Fluor 488–conjugated anti-primary antibodies.
Serotonin- and dopamine-dependent pathways converge on the GABA receptor


good anti–rabbit or AlexaFluor 568–conjugated goat anti–mouse secondary antibodies (Invitrogen) diluted 1:500 in blocking solution. All the incubations were performed at 23°C. After antibody incubations, the cells were washed twice with PBS and Hoechst 33342 was added to the final wash solution for 1 min to stain the DNA. Coverslips were mounted in Vectorshield (Vector Laboratories). Fluorescence images were captured using a confocal microscope (LSM510 META; Carl Zeiss, Inc.) equipped with a 40x Plan Neofluar objective, with confocal microscopy software (SP2 version 3.2; Carl Zeiss, Inc.). Images were analyzed using Photoshop 7.0 (Adobe).

Western blotting was performed using standard protocols (Gallagher et al., 1998). Unless otherwise indicated, all antibodies were used at a dilution of 1:2,000 for Western blotting. Electrophoretic migration of bands in all gels was indicated with respect to molecular mass standards run on the same SDS-PAGE gels.

Metabolic labeling and analysis of [3H]uridine-labeled RNA

72 h after transfection with SENP3 or SENP5 siRNAs, Hela cells were pulsed in DME containing [3H]uridine (10 μCi/ml) for 25 min, and then chased in nonradioactive media for the indicated times in the presence of 1 μg/ml of cold uridine (EMD). At each point, the same number of cells was harvested. Total RNA was extracted with Trizol reagent (Invitrogen) and suspended with diethylpyrocarbonate-treated water. Formaldehyde loading dye (Applied Biosystems) was added before heat treatment at 65°C for 45 min. RNAs were separated on a 1% agarose-denaturing gel containing 0.55 M formaldehyde. Formaldehyde was removed by washing with water for 40 min, and the gel was treated with 7.5 mM NaOH to hydrolyze the RNA. After soaking the gel within 20x SSC buffer for 45 min, the RNA was transferred to a nylon membrane (GE Healthcare) overnight. After transfer, RNA was cross-linked to the membrane with UV light. The membrane was dried, sprayed by ENHANCE (PerkinElmer), and exposed to Biomax XR film (Kodak) at −80°C.

Online supplemental material

Fig. S1 shows the quantitation of SUMO redistribution after SENP3, SENP5, and B23/nucleophosmin depletion. Fig. S2 shows SENP3 and SENP5 paralogue preferences and expression patterns. Fig. S3 shows mislocalization of ribosomal processing factor NTV2 in the absence of SENP3 and SENP5. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200807185/DC1.

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