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Both endonucleolytic and exonucleolytic cleavage mediate ITS1 removal during human ribosomal RNA processing

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Introduction

The 18S, 5.8S, and 28S (25S in yeast) ribosomal RNAs (rRNAs) are transcribed as a single precursor by RNA polymerase I in the eukaryotic nucleus. This precursor rRNA (pre-rRNA) undergoes processing and assembly steps to produce the large (LSU) and small (SSU) ribosomal subunits (Henras et al., 2008). Ribosome biogenesis requires more than 200 trans-acting factors including nucleases, helicases, small nucleolar RNPs, and 80 ribosomal proteins (Henras et al., 2008). This process consumes a large percentage of cellular energy and the rate of ribosome biogenesis determines the proliferative potential of the cell (Warner, 1999). Ribosome production is regulated in a cell cycle–dependent manner being down-regulated during differentiation and up-regulated in cancer. Ribosome biogenesis is down-regulated by tumor suppressor p19ARF and plays a direct role in activating the tumor suppressor p53 (Lessard et al., 2010; Chakraborty et al., 2011). Furthermore, several genetic diseases, including cartilage-hair hypoplasia (CHH), alopecia, neurological defects, and endocrinopathy syndrome, and Diamond Blackfan anemia, are linked to defects in ribosome production (Nousbeck et al., 2008; Narla and Ebert, 2010).

Human ribosome production is up-regulated during tumorigenesis and is defective in many genetic diseases (ribosomopathies). We have undertaken a detailed analysis of human precursor ribosomal RNA (pre-rRNA) processing because surprisingly little is known about this important pathway. Processing in internal transcribed spacer 1 (ITS1) is a key step that separates the rRNA components of the large and small ribosomal subunits. We report that this was initiated by endonuclease cleavage, which required large subunit biogenesis factors. This was followed by 3′ to 5′ exonucleolytic processing by RRP6 and the exosome, an enzyme complex not previously linked to ITS1 removal. In contrast, RNA interference–mediated knockdown of the endoribonuclease MRP did not result in a clear defect in ITS1 processing. Despite the apparently high evolutionary conservation of the pre-rRNA processing pathway and ribosome synthesis factors, each of these features of human ITS1 processing is distinct from those in budding yeast. These results also provide significant insight into the links between ribosomopathies and ribosome production in human cells.
cleavage in the human ITS1 processing (Rouquette et al., 2005). It has, however, been speculated that the endonucleolytic cleavage at site 2a in mammals, which generates 18SE, is equivalent to the A2 cleavage in yeast (Carron et al., 2011; Wang and Pestov, 2011). It is also unclear whether site 2 is equivalent to the A3 site, which in yeast is cleaved by RNase MRP (Lygerou et al., 1996). Processing of mammalian 5.8S rRNA, which involves the removal of ITS1 sequences from the 5′ end, is influenced by knockdown of Dicer or Drosha, the endonucleases linked to miRNA production, although neither protein appeared important for the primary ITS1 cleavages (Liang and Crooke, 2011).

Human ribosome production is coupled to cellular growth rate and linked to both cancer and genetic disease (Narla and Ebert, 2010). Despite this, several fundamental questions remain about the early pre-rRNA processing steps in humans and, in particular, the processing pathway and the enzymes involved in ITS1 processing need to be determined. To address these points, we have systematically analyzed factors linked to ITS1 processing in human cells.

Results

The cleavage sites in human ITS1

The potential additional step in the 3′ processing of the 18S rRNA raises several important questions about human ITS1 processing (Rouquette et al., 2005). In particular, it was suggested...
that 18SE can be generated by either endonucleolytic or exonucleolytic processing of 21S (Carron et al., 2011). Northern blotting was therefore used to recharacterize the pre-rRNA intermediates containing ITS1 sequences and better define the cleavage sites. HeLa cell RNA was separated by glyoxal gel electrophoresis, transferred to nylon membrane, and then hybridized with a variety of probes recognizing ITS1, 5.8S, and ITS2. For each probe, the ratio of the smaller RNAs (30S, 32S, 21S, and 12S) to 45S/47S was calculated and plotted.

All of the probes recognized the 47S/45S pre-rRNAs (Fig. 1, C and D; and Fig. S1 A). Interestingly, three ITS1 probes (6396, 6448, and 6508) failed to detect the smaller pre-rRNAs (32S, 30S, 21S, and 12S), suggesting this region is missing from both the LSU and SSU precursors. The 30S and 21S precursors of 18S rRNA were detected by probes hybridizing between 5520 and 6318, although weaker signals were reproducibly seen using probes between nucleotides 6121 and 6318. The 3’ ends of 30S and 21S pre-rRNAs are therefore very heterogeneous. The 32S and 12S pre-rRNAs were consistently detected using 5.8S and ITS2 probes. In contrast, probe 6603, at the 3’ end of ITS1, only weakly detected 32S and did not recognize 12S (Figs. 1 D and S1 A). We conclude that the majority of 32S and all 12S pre-rRNAs lack ITS1 sequence, with site 2 cleavage occurring in the region between nucleotides 6396 and 6508.

We next investigated whether fragments of ITS1 were generated by serial endonucleolytic cleavages. Yeast ITS and ETS fragments released by endonuclease cleavage are degraded by either the exosome or the 5’ to 3’ exonuclease Xrn2 (Ratl1; Petfalski et al., 1998). XRN2 and the exosome component RRP6 were therefore depleted from HeLa cells using RNAi (Fig. S2 A) and the accumulation of ITS1 fragments analyzed by Northern blotting. Depletion of XRN2 resulted in the accumulation of an ~800-nt fragment of ITS1 that extended from site 2a to position 6318 (Fig. 1 E). This fragment was barely detectable in control cells and no other fragments were detected after depletion of XRN2 and/or RRP6 (unpublished data). This indicated that there are two early endonucleolytic cleavages in ITS1 (at sites 2 and 2a), which together release the ~800-nt fragment.

Only a small fraction of the 32S species extended to site 2, indicating rapid processing to the mature 5’ end of 5.8S. In yeast, cleavage upstream of 5.8S is very rapidly followed by 5’ to 3’ exonucleolytic digestion. Knockdown of XRN2 resulted in an increase of 32S containing the 3’ end of ITS1, indicating that this is also the case in humans (Fig. S1 B). The heterogeneity observed in the 3’ ends of 30S and 21S suggested that these precursors might be processed by 3’ to 5’ exonucleases acting from site 2, in addition to endonucleolytic cleavage at 2a.

### RRP6 is required for 18S rRNA accumulation in human cells

The accumulation of the ~800-nt ITS1 fragment clearly indicates that the 18SE precursor can be generated by endonucleolytic cleavage at 2a. However, previous analyses after depletion of the small subunit biogenesis factor ENP1 indicated that 18SE can be produced by both endonucleolytic and exonucleolytic processing pathways (Carron et al., 2011). The 3’ to 5’ exonucleolytic activity of the exosome is a likely candidate for carrying out this step. We therefore depleted ENP1, XRN2, or the exonucleolytic component RRP6 from HeLa cells using RNAi (Fig. S2 A), and then analyzed the levels of rRNA processing intermediates by Northern blotting (Fig. 2 A).

As in mouse cells, depletion of XRN2 in HeLa cells caused the accumulation of 47S and 30SL5’, a 30S precursor with an additional 5’ fragment of the 5’ETS detected if the A’ cleavage is affected (Fig. 2 A), relative to the control cells (Fig. 2 B; Wang and Pestov, 2011). In addition, a significant increase in 26S was seen in some, but not all, experiments, implying that the order of cleavages in the 5’ETS is altered by depleting XRN2. Reproducible accumulation of 36S pre-rRNA was observed relative to control cells (Fig. 2 B, ITS1 probe) as previously reported in mouse cells (Wang and Pestov, 2011), indicating increased initial cleavage of ITS1 at site 2a before processing at site 2. Notably, depletion of XRN2 changed the levels of several pre-rRNA intermediates without significantly slowing down rRNA processing, suggesting that only the balance between competing pathways is altered. Depletion of ENP1 resulted in increased levels of 21S pre-rRNA, the appearance of 21SC, a shortened form of 21S (Carron et al., 2011), and significantly decreased 18SE levels (Fig. 2 C). Depletion of RRP6 did not alter the accumulation of the longer precursors but resulted in a more significant decrease in 18SE levels and the accumulation of 21SC (Fig. 2 B and C). In addition, a range of products, seen as a smear, was often observed between 21S and 18SE, indicating inefficient exonucleolytic processing of 21S pre-rRNA. Codepletion of RRP6 and ENP1 resulted in stronger accumulation of 21SC and more significant reduction in 21S and 18SE than either single knockdown (Fig. 2 C). This indicates that RRP6 functions together with certain rRNA processing factors in the processing of ITS1.

We next used metabolic labeling experiments to determine the effect of depleting RRP6 on the accumulation of mature rRNAs. HeLa cells were transfected with control siRNAs or siRNAs targeting the RRP6 mRNA. The cells were metabolically labeled using [3H] methyl-methionine (Fig. 2 D) or [32P] orthophosphate (Fig. S3, A and B) and harvested at various time points after the addition of unlabeled media. Total RNA was separated by glyoxal gel electrophoresis, transferred to nylon membrane, visualized using a phosphorimagery, and quantified.

In control cells, 47S/45S pre-rRNAs were observed at the start of the chase (Fig. 2 D). With time, the 32S intermediate accumulated and this was followed by the mature 18S and 28S rRNAs. Because of their low relative abundances, the 41S, 30S, and 21S pre-rRNAs were barely visible and difficult to follow in these experiments. In both control and knockdown cells, 32S pre-rRNA and 28S rRNA accumulated at a similar rate and to similar levels. In contrast, significantly less 18S rRNA was produced during the time course in RRP6-depleted cells (approximately two- to threefold less at 3 h relative to 28S levels). We conclude that RRP6 is required for the efficient production of the 18S rRNA in human cells and that the majority of the SSU rRNA is produced via this pathway.

### The exonuclease activity of RRP6 is required for 18SE production

To determine whether the exonuclease activity of RRP6 was required for 18SE production, stably transfected HEK293...
et al., 2011) are required for 18SE accumulation. Individual proteins were depleted from HeLa cells using RNAi (Fig. S2 A) and the effects on rRNA processing were analyzed. No significant changes in the levels of the longer, 47S to 30S, pre-rRNAs were seen. Depletion of either RRP46 or the RNA helicase MTR4 resulted in a fourfold reduction in 18SE levels (Fig. 3, C and D). However, instead of the prominent band of 21SC seen when RRP6 was depleted, a broad range of differently sized products between 21S and 18SE, often visible as a smear, were seen upon depletion of RRP46 or MTR4. Depletion of DIS3 or C1D (the human homologue of yeast Rrp47/Lrp1) had no clear effect on 21S, 21SC, and 18SE levels, whereas depletion of MPP6 resulted in a slight accumulation of 21SC but no change in 18SE levels. Each of these proteins were, however, essential for 3′ processing of 5.8S, as previously reported (Fig. S2 B; Schilders et al., 2007; Tomecki et al., 2010). These data suggest that RRP6 acts catalytically in 18SE production, functioning together with the exosome core, the MTR4 helicase, and, to a lesser extent, the exosome cofactor MPP6. The lack of effect seen on DIS3 depletion is not entirely unexpected, as little of the protein is in the nucleolus where this processing step is predicted to occur (Tomecki et al., 2010).

The majority of 18SE appears to be generated by exonucleolytic processing of 21S by RRP6 and the exosome core, whereas endonucleolytic cleavage at site 2a was only observed after the depletion of XRN2. We therefore tested whether stimulation of the endonucleolytic pathway by depletion of XRN2 would make 18SE production independent of the exosome and MTR4.

HEK293 cells contain higher levels of 47S/45S and 18SE than the other precursors relative to HeLa cells, but pre-rRNA levels were unaltered by replacement of endogenous RRP6 by FLAG-RRP6 (Fig. 3, A and B). In contrast, 18SE levels were reduced and both 21S and 21SC levels were increased in cells expressing only RRP6exo. This demonstrates that the exonucleolytic activity of RRP6 is required for efficient conversion of 21S to 18SE.

The exosome core and exosome cofactors are required for 18SE production

The exosome is a multi-subunit complex and we assessed whether the nuclease DIS3, an exosome core component (RRP46), or exosome cofactors (MPP6, C1D, or MTR4; Lykke-Andersen et al., 2011) are required for 18SE accumulation. Individual proteins were depleted from HeLa cells using RNAi (Fig. S2 A) and the effects on rRNA processing were analyzed. No significant changes in the levels of the longer, 47S to 30S, pre-rRNAs were seen. Depletion of either RRP46 or the RNA helicase MTR4 resulted in a fourfold reduction in 18SE levels (Fig. 3, C and D). However, instead of the prominent band of 21SC seen when RRP6 was depleted, a broad range of differently sized products between 21S and 18SE, often visible as a smear, were seen upon depletion of RRP46 or MTR4. Depletion of DIS3 or C1D (the human homologue of yeast Rrp47/Lrp1) had no clear effect on 21S, 21SC, and 18SE levels, whereas depletion of MPP6 resulted in a slight accumulation of 21SC but no change in 18SE levels. Each of these proteins were, however, essential for 3′ processing of 5.8S, as previously reported (Fig. S2 B; Schilders et al., 2007; Tomecki et al., 2010). These data suggest that RRP6 acts catalytically in 18SE production, functioning together with the exosome core, the MTR4 helicase, and, to a lesser extent, the exosome cofactor MPP6. The lack of effect seen on DIS3 depletion is not entirely unexpected, as little of the protein is in the nucleolus where this processing step is predicted to occur (Tomecki et al., 2010).
and Pestov, 2011). Cleavage at A2 is dependent on factors linked to 18S processing, including SSU processome components (Henras et al., 2008). We therefore used RNAi to determine whether SSU processome proteins (fibrillarin, UTP24, RCL1, BMS1, and RRP5) and other 18S rRNA processing factors (NOB1, ENP1, and RPS19) are required for ITS1 processing in HeLa cells (Fig. S2 A). The requirement of factors for 2a endonucleolytic cleavage cannot readily be assessed because 36S pre-rRNA, the only intermediate specific to this pathway, is barely detectable in control cells. However, depletion of XRN2 stimulates processing through this pathway, so each knockdown was performed both individually and in combination with XRN2 to facilitate monitoring of 2a cleavage. Pre-rRNA processing in the knockdown cells was followed by Northern blotting (Fig. 4 A) and metabolic labeling (Fig. S4).

Using RNAi, RRP46 or MTR4 were depleted, alone or together with XRN2, and the effect on 18SE production was monitored by Northern blotting. As described above, depletion of XRN2 had no effect on 21S and 18SE levels, whereas depletion of RRP46 or MTR4 reduced the levels of 18SE more than fourfold (Fig. 3 E). Strikingly, codepletion of XRN2 with either RRP6 or MTR4 resulted in almost normal levels (80–90%) of 18SE.

We conclude that depletion of XRN2 favors endonucleolytic cleavage at site 2a before cleavage at site 2, reducing the requirement for the normally major pathway of exosome/MTR4 processing from site 2 to 2a.

**Human endonuclease cleavage site 2a is analogous to yeast A2.**

Our data indicate that cleavage at site 2 normally separates the human LSU and SSU pre-rRNAs. In yeast, A2 cleavage performs the same function, but this site is putatively suggested to be homologous to the human 2a site (Carron et al., 2011; Wang and Pestov, 2011).
In yeast, Rrp5 is important for both A2 and A3 cleavages (Venema and Tollervey, 1996). In HeLa cells, depletion of RRp5 led to a major increase in 45S and a reduction in 30S and 18S levels (Fig. 4 A). Decreasing RRp5 levels had a greater impact on 18S levels than on 21S, suggesting that it is also important for exonucleolytic processing to site 2a. Metabolic labeling experiments confirmed that 45S pre-rRNA accumulated in cells depleted of RRp5, whereas maturation to both 18S and 28S rRNAs was severely inhibited (Fig. S4). In Northern blots, novel bands above both 30S and 21S were also seen, which we termed 30SLL3 and 21SLL3, respectively. The 30SLL3 intermediate, which unfortunately runs at the same position as 30SLS5 and LSU 32S, lacked the 5’ end of the 5’ETS (present in 30SLS5; Fig. 4 C). It was not possible to map the 3’ end of 30SLS5 because of the overlap with the LSU intermediate 32S, but 21SLL3 contained the 3’ end of ITS1 and 5.8S (Fig. 4 B) and from this we infer that 30SLL3 also includes the complete ITS1 and 5.8S regions. When RRp5 was codepleted with XRN2, 36S pre-rRNA and the ITS1 fragments were not detected. We conclude that decreasing the levels of RRp5 significantly affects both cleavages in ITS1, with some precursors produced in which both ITS1 cleavages are bypassed and cleavage of the primary transcript occurs in ITS2. Collectively, these data are consistent

**Figure 4.** SSU processome components are required for endonuclease cleavage at site 2a in ITS1. (A) RNA extracted from control HeLa cells or cells depleted of ribosome biogenesis factors either alone or together with XRN2 (indicated at top) was analyzed by Northern blotting using probes that recognized either the middle or 5’ end of ITS1 (indicated on the right). RNA loading was monitored by methylene blue staining of 18S and 28S rRNAs (MB). FIB., fibrillarin. The presence (+) or depletion (−) of XRN2 is indicated at the top of the relevant lanes. (B) RNA from control cells or cells depleted of RRp5 was analyzed by Northern blotting using probes specific for the 5’ETS and ITS1 as indicated. The positions of the mature and pre-rRNAs are indicated. (C) Schematic representation of the full-length pre-rRNA transcript and relevant pre-rRNAs. Positions of Northern probes are indicated. Black lines in A and B indicate intervening lanes that have been removed.
with the human 2a site being equivalent to the A2 cleavage site in yeast. Furthermore, the impairment of cleavage at both ITS1 sites on depletion of human RRP5 appears analogous to the inhibition of both A2 and A3 cleavages after depletion of yeast Rrp5 (Venema and Tollervey, 1996).

**Depletion of BOP1, RBM28, and NOL12 impair cleavage at site 2 in ITS1**

In yeast, the A3 endonuclease cleavage site is located 3’ of site A2. This suggested that human site 2 may be equivalent to yeast A3. In yeast, A3 cleavage requires Nop4 (Bergès et al., 1994; Sun and Woolford, 1994), which is homologous to human RBM28 (Nousbeck et al., 2008). Subsequent exonucleolytic digestion from A3 to the major 5’ end of 5.8S rRNA requires factors including Erb1 and Rrp17 (Oeffinger et al., 2009; Granneman et al., 2011; Sahasranaman et al., 2011), which are homologous to human BOP1 (Pestov et al., 2001) and NOL12, respectively. RBM28, BOP1, or NOL12 were depleted from HeLa cells using RNAi, either alone or in combination with XRNR2, to test whether human site 2 is analogous to the yeast A3 cleavage. The effects on pre-rRNA processing were analyzed by Northern blotting and metabolic labeling experiments. Depletion of BOP1 resulted in clear defects in 28S and 5.8S accumulation, with loss of the normally major, short form of 5.8S rRNA (5.8SS) and accumulation of the longer form (5.8SL; Fig. 5, A and B). In addition, depletion of BOP1 also resulted in a reduced rate of 18S production. Interestingly, depletion of XRNR2 had no effect on the ratio of 5.8S rRNA species (Fig. 5 B). BOP1 depletion resulted in reproducible increases in the levels of 47/45S, 41S, 36S, and 36SC pre-rRNA, a 5’ shortened form of 36S (Fig. 5, C, E, and F). Conversely, the levels of 32S, 30S, 21S, and 12S were reduced, whereas 18S levels were only mildly affected probably because this intermediate can be generated directly by 2a cleavage. This indicates that processing at site 2a is only slowed, whereas site 2 cleavage is more impaired. Consistent with this, significantly less of the ITS1 fragment was observed after the codepletion of XRNR2 (Fig. 5 D). After BOP1 depletion, 36S accumulation was greatly increased by codepletion of XRNR2. The levels of 36SC pre-rRNA appeared reduced after the codepletion of XRNR2 (Fig. 5 D). After BOP1 depletion, 36S accumulation was greatly increased by codepletion of XRNR2, suggesting that this representation of 36S to 32S pre-rRNA.

Depletion of NOL12 resulted in defects in 28S, 5.8S, and 18S rRNA production in metabolic labeling experiments, indicating a complete block in ITS1 processing (Fig. 5 A). NOL12 depletion also increased the levels of 47/45S, 41S, 36S, and 36SC pre-rRNAs, although the effect on 36S and 36SC was not as dramatic as seen after BOP1 depletion (Fig. 5, C and D). The levels of 32S, 30S, 21S, 12S, and 18S were all significantly reduced, indicating that processing at both sites 2a and 2 was severely impaired. Consistent with this, ITS1 fragment levels were significantly reduced upon codepletion of XRNR2 (Fig. 5 D). After codepletion of XRNR2 with NOL12, 36SC levels were decreased and 36S accumulation was increased, but not to the extent seen in BOP1 and XRNR2 codepletions. The presence of more 36SC than 36S in NOL12-depleted cells suggests that this probable 5’ to 3’ exonuclease is not required for the exonuclease processing at the 5’ end of 36S. Strikingly, codepletion of XRNR2 with NOL12 restored 18SE levels to near wild-type levels, suggesting that stimulating site 2a cleavage could rescue 18SE production (Fig. 5 C).

In metabolic labeling experiments, depletion of RBM28 had no effect on 18S rRNA accumulation and resulted in only a mild decrease in 5.8S and 28S levels with no change in the ratio of 5.8S species (Fig. 5, A and B). Depletion of RBM28 resulted in increased levels of 45S, 41S, 36S, and 36SC, whereas 32S and 12S levels were slightly reduced. 30S, 21S, and 18SE levels were unaffected (Fig. 5, C and D). Codepletion of RBM28 with XRNR2 caused significantly more 36S to accumulate than when only RBM28 levels were reduced. Compared with the yeast homologue of RBM28, which is essential for A3 cleavage (Bergès et al., 1994; Sun and Woolford, 1994), depletion of the human counterpart only slowed down ITS1 processing and, as seen with the depletion of XRNR2, resulted in an increase in cleavage at site 2a before site 2.

We conclude that site 2 in the human ITS1 is analogous to site A3 in the yeast pre-rRNA. Interestingly, our data therefore suggest that, in humans, the A3-like cleavage is the primary endonuclease cleavage that separates the rRNAs of the large and small subunits.

**Depletion of RNase MRP proteins does not affect cleavage in ITS1**

In yeast, A3 cleavage is performed by the endonuclease complex RNase MRP (Lygerou et al., 1996). Loss of this complex has only a minor effect on pre-rRNA processing and results in defective 5’ processing of 5.8S (Schmitt and Clayton, 1993). If human site 2, which is the major ITS1 processing site, is cleaved by RNase MRP, then we would expect that this endonuclease is far more important to pre-rRNA processing in humans than it is in yeast. The core RNase MRP/RNase P protein POP1, which is essential for the accumulation and function of both of these RNPs in yeast, was depleted from HeLa cells using RNAi, either alone or in combination with XRNR2 (Fig. 6 A). Depletion of POP1 resulted in a substantial decrease in the levels of this protein and a four- to fivefold decrease in RNase MRP and P RNA levels (Figs. 6 B and S4 B). Knockdown of POP1 also significantly increases the levels of the virem protein (Mattijssen et al., 2011). The virem mRNA is a target for either RNase MRP or RNase P and lack of proteins common to these endonucleases results in increased expression of the virem protein. Northern analyses showed that depletion of POP1 reproducibly resulted in accumulation of pre-tRNAiMet (Fig. S4 B), confirming the impaired function of RNase P, although this defect was not clearly visible using pulse chase labeling (Figs. 6 E and S4 C). A mild increase in mature tRNA levels was observed in the POP1-depleted cells, but this was substantially less than seen for the precursor. In contrast, depletion of POP1, either alone or together with XRNR2, had no noticeable effect on the levels of any of the pre-rRNA intermediates or the ratio of 5.8S and 5.8S (Fig. 6, C and D; and Fig. S4 D). In metabolic labeling experiments the levels of the mature rRNAs were also not significantly affected by the depletion of POP1 and there was no change in the ratio of 5.8S species detected (Figs. 6 E and S4 C).
These results were unexpected and we therefore also analyzed the effect of depleting additional RNase MRP/P subunits, RPP38 and RPP40. Levels of these proteins were also significantly reduced by RNAi treatment and RNase MRP/P RNA levels were decreased (Fig. 6, A and B; and Fig. S4 B). Depletion of RPP40 and, to a lesser extent, RPP38 also caused accumulation of pre-tRNAiMet, as previously demonstrated for RPP38 (Cohen et al., 2003; Fig. S4 B). Interestingly, modest increases in mature tRNA levels were also seen upon depletion of these proteins, although we cannot currently explain this observation. Consistent with the depletion of POP1, reducing the levels of either RPP38 or RPP40 had no detectable effect on pre-rRNA levels or on accumulation of the mature rRNAs (Fig. 6, D and E; and Fig. S4, C and D). Simultaneous depletion of POP1 and RPP40/RPP38 also had no clear effect on pre-rRNA processing (Fig. S4, C and D; unpublished data) and no greater impact on tRNA processing than the single depletions. Site 2 cleavage plays an important role in human pre-rRNA processing so the observation that depletion of RNase MRP/P proteins by more than 10-fold had no effect on ITS1 processing therefore questions the role of human RNase MRP in ribosome biogenesis.

Discussion

Here we have characterized alternative ITS1 processing pathways in human cells. The major pathway involves a single endonucleolytic cleavage at site 2 followed by exonucleolytic processing to both the 5' end of 5.8S and to site 2a to generate the 18SE precursor, which contains ~25 nt of ITS1 at the 3'
exosome and the TRAMP component MTR4 are also needed for the full activity/processivity of RRP6. The involvement of the RNA helicase MTR4 is not surprising given that this region of human ITS1 is \( \sim 800 \) nt long (compared with \( \sim 85 \) nt in yeast), 82% GC rich, and highly structured (Fig. S5). The requirement for RPS19, ENP1, RRP5, and RCL1 in this process indicates that the exosome also interacts with the SSU processome. Depletion of RRP6 severely reduced, but did not abolish, 18SE accumulation and 18S rRNA production. This may be a result of incomplete depletion of RRP6 but more end of 18S rRNA. The final ITS1 sequence is then removed by endonucleolytic cleavage at site 3 (Fig. 7). Alternatively, the 18SE precursor can be generated by endonucleolytic cleavage at site 2a. This minor pathway can compensate for a block in 18SE production by exonucleolytic processing after site 2 cleavage when stimulated by XRN2 depletion.

After cleavage at site 2, RRP6, a 3' to 5' exonuclease component of the exosome complex, processes to site 2a. Importantly, the exosome has not been demonstrated to be involved in ITS1 processing before in any organism. The core exosome and the TRAMP component MTR4 are also needed for the full activity/processivity of RRP6. The involvement of the RNA helicase MTR4 is not surprising given that this region of human ITS1 is \( \sim 800 \) nt long (compared with \( \sim 85 \) nt in yeast), 82% GC rich, and highly structured (Fig. S5). The requirement for RPS19, ENP1, RRP5, and RCL1 in this process step indicates that the exosome also interacts with the SSU processome. Depletion of RRP6 severely reduced, but did not abolish, 18SE accumulation and 18S rRNA production. This may be a result of incomplete depletion of RRP6 but more
in the 5' exonucleolytic processing of the 36S precursor to 32S. Indeed, in either BOP1 or RBM28 knockdowns, 36S accumulation was increased relative to 36SC by codepletion of XRN2, an exonuclease likely to be involved in converting 36S to 32S. In yeast, blocking A3 cleavage or subsequent exonucleolytic processing from A3 to the 5' end of 5.8S results in loss of 5.8SS and accumulation of 5.8S L. Depletion of human BOP1 resulted in the accumulation of only 5.8SL, suggesting that this processing mechanism is conserved. Similarities and differences between the functions of these proteins in humans and yeast are outlined in Fig. 7.

The lack of effect of depleting RNase MRP on site 2 cleavage and the 5' processing of 5.8S was unexpected. The decrease in MRP/P protein levels significantly reduced RNase MRP/P RNA abundance and both inhibited cleavage of the viperin mRNA (Mattijssen et al., 2011) and affected processing of tRNAiMet (Fig. S5 A) and tRNATyr (unpublished data). It was surprising that the effect on tRNA processing, caused by depleting multiple components of the RNase P complex to this extent, was not stronger. These data are, however, consistent with previously published data analyzing RPP38 (Cohen et al., 2003). Indeed, the authors claimed that RPP38 is not essential for pre-rRNA processing after only observing very weak accumulation of 5.8S processing intermediates. We did not observe the accumulation of such precursors in RPP38, POP1, or RPP40 knockdowns (Fig. S5). As a result of the nature of RNAi knockdowns, low residual levels of proteins remained after depletion of RPP40, RPP38, or POP1 (<10% of each). In consequence, we cannot exclude the possibility that the residual RNase MRP activity is sufficient to maintain pre-rRNA processing. However, our data suggest that RNase MRP is not essential for ITS1 processing and that a distinct endonuclease is responsible for site 2 cleavage in human cells.

It is not clear why endonucleolytic cleavage at site 2a is not part of the major processing pathway in humans. In yeast, several pre-rRNA processing steps, including cleavage at A2, occur cotranscriptionally (Kos and Tollervey, 2010), whereas analyses...
of Miller spreads indicate that vertebrate pre-rRNA processing is mostly posttranscriptional. It is possible that 2a cleavage is inefficient in the absence of cotranscriptional processing. Alternatively, the close proximity of 2a to the 3' end of 18S (~25 nt) or extreme GC content of ITS1 may make this cleavage inefficient. Site 2a cleavage is affected by deletion of factors linked to cleavage at site 2, suggesting competition and/or cross talk between processing pathways. Alternative ITS1 processing pathways have also been described in Xenopus laevis oocytes (Savino and Gerbi, 1990), suggesting that this is a conserved feature of pre-rRNA processing that may aid overall cleavage efficiency. Our data indicate that the initial ITS1 cleavage is primarily linked to factors important for LSU biogenesis. Furthermore, the rRNA processing defects seen upon depletion of BOP1, RRP5, and NOL12 were strikingly similar to those seen upon ARF overexpression (Sugimoto et al., 2003) or depletion of the ARF-regulated transcription termination factor TTF-1 (Lessard et al., 1996), suggesting that this is a conserved feature of pre-rRNA processing that may aid overall cleavage efficiency.

For metabolic labeling experiments using 3H-methyl-thymine, the cells were incubated in methionine-free media (1.5 μCi/ml) and then in methionine-free media containing 50 μCi/ml 3H-labeled methionine ([3H]methionine) for 30 min. The cells were then incubated in normal media containing 10x inorganic phosphate (1 h) and then blocked in PBS/10% FCS. Cells were incubated with the anti-FLAG (rabbit; Sigma-Aldrich) and anti-fibrillarin (72B9; mouse) in PBS/10% FCS. Cells were washed with PBS and then incubated with the secondary antibody (Alexa Fluor 555-labeled donkey anti–mouse and Alexa Fluor 647-labeled donkey anti–rabbit) in PBS/10% FCS. The cells were washed with PBS containing DAPI and then mounted in Mowiol. All steps were performed at room temperature. Images were captured with an inverted microscope (Axiovert 200M; Carl Zeiss) with a Plan-Apochromat, 100x/1.4 oil DIC x/0.17 objective (Carl Zeiss) and an AxioCam MRm camera, using Axiovision software.

## Materials and methods

### RNAi

RNAi siRNA duplex (listed in Table S1) transfection was performed using Lipofectamine RNAiMAX reagent (Invitrogen). Cells were harvested 60 h after transfection and then analyzed by Western (antibodies listed in Table S2) and Northern blotting.

The cDNA for human RRP6, altered to make the mRNA resistant to the siRNAs used to deplete endogenous RRP6, was cloned into the pcDNA5/RT (Invitrogen) containing 2x FLAG tags under the control of a tetracycline-regulated promoter. A single amino acid mutation in the catalytic site of RRP6 (RRP6ex), D313A was also generated. The oligonucleotides used to make these constructs are listed in Table S3. The constructs were transfected into Flp-In T-Rex HEK293 cells and stably transfected cells selected as described by the manufacturer (Invitrogen). Cells expressing RRP6, RRP6ex, or the FLAG tag alone were incubated with 0.1 μg/ml tetracycline to induce protein expression, and then transfected with siRNAs to deplete endogenous RRP6. 48 h later, the cells were harvested and analyzed by Western and Northern blotting.

### RNA analysis

RNA was extracted from cell pellets using TRI reagent (Sigma-Aldrich) and analyzed by glyoxal-agarose gel and urea-PAGE and transferred to nylon membrane. For Northern blot analysis, oligonucleotides (Table S4) were 5' labeled with [32P]ATP using T4 polynucleotide kinase and used as probes. Random prime-labeled probes hybridizing immediately upstream and downstream of the A' cleavage in the 5'ETS (ETS1 and ETS2, respectively) were produced from PCR products (Turner et al., 2009). Random prime-labeled probes against the full-length RNase MRP RNA and the S domain of 7SL were also generated.

For metabolic labeling experiments using 3H-methyl-thymine, the cells were incubated in methionine-free media (1.5 μCi/ml) and then in methionine-free media containing 50 μCi/ml 3H-labeled methionine ([3H]methionine) for 30 min. The cells were then incubated in normal media containing 10x inorganic phosphate (1 h). Cells were then incubated in normal media and harvested at the required time points (0, 15, 30, 60, 120, and 240 min). RNA was extracted using TRI reagent and analyzed by agarose-glyoxal or urea-PAGE as appropriate. Results were visualized using a phosphorimager (Typhoon FLA9000; GE Healthcare). All quantification was normalized to the levels of mature 18S or 28S rRNA, as appropriate.

### Immunofluorescence

HEK293 cells expressing either the Flag tag only (pcDNAs [Knox et al., 2011]), Flag-RRP6, or Flag-tagged, RNAi-resistant RRP6 or RRP6exo were grown on coverslips and induced with 0.1 mg/ml tetracycline for 36 h before being fixed with PBS containing 4% paraformaldehyde. The cells were washed with PBS and permeabilized in 0.2% Triton X-100 and then blocked in PBS/10% FCS. Cells were incubated with the anti-FLAG (rabbit; Sigma-Aldrich) and anti-fibrillarin (72B9; mouse) in PBS/10% FCS. Cells were washed with PBS and then incubated with the secondary antibody (Alexa Fluor 555-labeled donkey anti–mouse and Alexa Fluor 647-labeled donkey anti–rabbit) in PBS/10% FCS. The cells were washed with PBS containing DAPI and then mounted in Mowiol. All steps were performed at room temperature. Images were captured with an inverted microscope (Axiovert 200M; Carl Zeiss) with a Plan-Apochromat, 100x/1.4 oil DIC x/0.17 objective (Carl Zeiss) and an AxioCam MRm camera, using Axiovision software.

### Online supplemental material

Fig. S1 shows Northern blot ITS1 mapping data. Fig. S2 shows RNAi depletion of ribosome biogenesis factors from HeLa cells. Fig. S3 is a characterization of HEK293 stable cells lines expressing RRP6. Fig. S4 shows the requirement for SSU proteins and RNase MRP/P subunits in the formation of the mature rRNAs. Fig. S5 is a model of human ITS1 structure. Table S1 shows ribosome biogenesis factor siRNA sequences. Table S2 contains the antibodies used in this study. Table S3 shows the primers used to make RRP6 expression constructs. Table S4 shows Northern blot probe sequences. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.201207131/DC1.

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### References

Allmang, C., Y. Henry, J.P. Morrisey, H. Wood, E. Petfalski, and D. Tollervey. 1996. Processing of the yeast pre-rRNA at sites A(2) and A(3) is linked. RNA. 2:63–73.


Mol. Cell


Schilders, G., E. van Dijk, and G.J. Prijui. 2007. CID and hMrtp6 associate with the human exosome and PMK60-100 and are involved in pre-rRNA processing. Nucleic Acids Res. 35:2564–2572. http://dx.doi.org/10.1093/nar/gkm082


Venema, J., and D. Tollervey. 1996. RRPS5 is required for formation of both 18S and 5.8S rRNA in yeast. EMBO J. 15:5701–5714.

