Rrp47p Is an Exosome-Associated Protein Required for the 3′ Processing of Stable RNAs

Philip Mitchell,1* Elisabeth Petfalski,1 Rym Houalla,1 Alexandre Podtelejnikov,2 Matthias Mann,2 and David Tollervey1

Wellcome Trust Centre for Cell Biology, Institute for Cell and Molecular Biology, University of Edinburgh, Edinburgh EH9 3JR, United Kingdom,1 and Centre for Experimental Bioinformatics, University of Southern Denmark, DK-5230 Odense M, Denmark2

Received 7 April 2003/Returned for modification 23 May 2003/Accepted 3 July 2003

The eukaryotic 18S, 5.8S, and 25S rRNAs (yeast nomenclature is given) are generated from a single large RNA polymerase I transcript by a series of endonucleolytic and exonucleolytic processing reactions (reviewed in reference 39). The earliest detectable transcript in yeast, the 35S precursor rRNA (pre-rRNA), also undergoes extensive posttranscriptional modification involving predominantly pseudouridine formation and ribosyl-2′-O-methylation. These modifications are directed to specific nucleotides within the ~7-kb-long 35S pre-rRNA via complementary base-pairing mechanisms involving ~70 different small nuclear RNAs (snRNAs).

The snRNAs can be divided into two major functional groups; the box C/D snRNAs direct methylation of ribosyl-2′-hydroxyl groups, whereas the H/ACA snRNAs direct the conversion of uridine to pseudouridine (for reviews, see references 4 and 21). Genes encoding snRNAs have a varied organization, but in yeast and mammals all are transcribed by RNA polymerase II. Most yeast snRNA genes are expressed as individual transcripts from their own promoters, whereas several are processed from common primary transcripts and a few are encoded within the introns of protein-coding genes. Gene clusters are the predominant organization of snRNA genes in plants, whereas the majority of mammalian snRNAs are intron encoded.

The synthesis of the mature 3′ ends of all characterized snRNAs requires endonucleolytic cleavage of the transcript, followed by 3′→5′ exonucleolytic processing. Endonucleolytic cleavage is by Rnt1p, the yeast RNase III homologue, or by cleavage factor 1A (CF1A), which is also required for the 3′ end processing of mRNA transcripts (15). Maturation of intron-encoded snRNAs involves linearization of the excised intron lariat, either by the debranching enzyme Db1lp or endonucleolytic cleavage, followed by exonucleolytic processing (30, 31).

The 3′ processing of snRNAs involves the exosome (1, 37), a complex of 9 to 10 distinct 3′→5′ exonucleases that functions in both RNA processing and degradation pathways. Nuclear and cytoplasmic forms of the exosome complex have been characterized that share 10 common components and differ by the presence of the RNase Rrp6p and the putative GTPase Ski7p, respectively (3). The 10 common components are all essential for cell viability. In contrast, rrp6Δ mutants are viable but temperature-sensitive lethal (ts-lethal) and specifically impaired in exosome-mediated pathways in the nucleus (1, 8, 9, 19, 35, 37). In rrp6Δ strains, most box C/D snRNAs have short 3′ extensions, indicating a specific role for Rrp6p in the final trimming step. Longer, 3′-extended snRNA precursors also accumulate in both rrp6Δ mutants and in strains mutant for other exosome components and these species are polyadenylated by poly(A) polymerase.

The yeast spliceosomal snRNAs U1, U2, U4, and U5 are also transcribed by RNA polymerase II and are cleaved in their 3′ flanking regions by Rnt1p. In the case of U1, U4, and U5, it has been demonstrated that Rnt1p cleavage provides an entry site for 3′ exonucleolytic processing by the exosome (1, 37). However, snRNA synthesis is not blocked in strains mutant for either Rnt1p or components of the exosome complex, suggesting that alternative processing pathways exist.

The 3′-end processing of mRNAs typically involves the coordinated cleavage of the nascent transcript and polyadenyl-
ation of the generated 3′ terminus. The cleavage and polyadenylation reaction is tightly coupled to transcription termination. In *mal4-1* mutants, which are defective in CF1A activity, cleavage is inefficient and readthrough transcripts are generated that extend several kilobases into downstream genes (7). These readthrough transcripts are rapidly processed by the nuclear exosome and then either polyadenylated or degraded by an Rrp6p-dependent mRNA surveillance mechanism (35).

The exosome was initially characterized during analyses of the pre-rRNA processing pathway. Mutation of exosome components inhibits the conversion of 7S pre-rRNA to 5.8S rRNA and the degradation of the 5′ external transcribed spacer (5′ETS) fragment, with the accumulation of heterogeneous populations of partially processed RNAs (1, 3, 12, 26). RNA analyses of *rrp6-Δ* mutants revealed a distinct defect in 7S pre-rRNA processing (9), with the accumulation of 5.8S rRNA species that are 3′ extended by ~30 nucleotides (nt). Like most mutations that inhibit the synthesis of 5.8S and 25S rRNA, exosome mutants also show indirect effects on early pre-rRNA cleavage events that are required for 18S rRNA synthesis (2, 43).

Genetic studies indicate that exosome function in vivo requires the activity of additional cofactors that are not found in exosome preparations or are present only at substoichiometric levels. All characterized nuclear functions of the exosome require the putative RNA helicase Mtr4p/Dob1p (12, 24), whereas exosome-mediated cytoplasmic mRNA turnover pathways are dependent upon Ski7p and the Ski complex, comprising the putative RNA helicase Skl2p and the proteins Skl3p and Skl8p (10, 20, 38).

Here we report that the *YHR081w* gene product is a novel exosome-associated factor that we designate Rrp47p. This protein was previously shown to be nuclear in a systematic localization study (22) (for an image, see http://ygac.med.yale.edu) and analyses of 5.8S rRNA species. The *rrp6-Δ* allele was shown to be functional by growth rate assays and copurification of proteins that TMZ-150 containing an increasing gradient of MgCl₂, and matrix-assisted laser desorption ionization–nanoelectrospray MS analyses of gel-purified proteins were performed as previously described (3, 24). Immuno precipitation from strains expressing Rrp47p-FLAG were treated with RNase A (2 μg ml⁻¹ [final concentration]) and incubated for 60 min on ice before a wash with 5 ml of TMN-150 buffer and subsequent digestion with Toronto enzyme (TEV) protease (Invitrogen). Polyclonal antisera were raised in rabbit against His₆-tagged fusion proteins expressed in *Escherichia coli* coli containing full-length Rrp4p (26) and the N-terminal 222 residues of Rrp6p after purification from cell lysates by immobilized metal ion affinity chromatography on Ni²⁺-nitrilotriacetic acid agarose (Qiagen) and SDS-PAGE. Antiserum were used at a dilution of 1:5,000 for Western analyses.

**Materials and Methods**

**Strains.** Yeast transformations were performed with plasmids or PCR-amplified DNA by using standard molecular biological techniques. Transformants were isolated by growth on selective media and integrants were screened by PCR directly on restreaked colonies. Strains were routinely grown in yeast extract-peptone-dextrose (YPD)-rich medium. The zz-Rrp44p strain (P203) was grown in rich medium containing galactose and sucrose as carbon sources. For the analysis of the *mal4-1* GAC1::mal41 mutant, the strain was pregrown in YPD medium for 24 h to deplete Rrp41p levels before transfer to 37°C.

Strains P203 (zz-Rrp44p), P414 (Rrp47p-zz), and YRH1 (Rrp6p-TAP) were generated by integration of PCR-amplified DNA by using plasmids pTL27 (23), pJE39 (a gift from J. Brown, University of Newcastle), and pBS1479 (32), respectively. The Rrp47p-zz allele was shown to be functional by growth rate assays and copurification of proteins that TMZ-150 containing an increasing gradient of MgCl₂, and matrix-assisted laser desorption ionization–nanoelectrospray MS analyses of gel-purified proteins were performed as previously described (3, 24). Immuno precipitation from strains expressing Rrp47p-zz were treated with RNase A (2 μg ml⁻¹ [final concentration]) and incubated for 60 min on ice before a wash with 5 ml of TMN-150 buffer and subsequent digestion with Toronto enzyme (TEV) protease (Invitrogen). Polyclonal antisera were raised in rabbit against His₆-tagged fusion proteins expressed in *Escherichia coli* coli containing full-length Rrp4p (26) and the N-terminal 222 residues of Rrp6p after purification from cell lysates by immobilized metal ion affinity chromatography on Ni²⁺-nitrilotriacetic acid agarose (Qiagen) and SDS-PAGE. Antiserum were used at a dilution of 1:5,000 for Western analyses.

**RESULTS**

**Purification of exosome-associated factors.** To identify novel exosome cofactors, cell lysate from a strain expressing an epitope-tagged form of the exosome component Rrp4p (zz-Rrp44p), which contains two copies of the “zz” domain of protein A fused to the N terminus, was passed over an IgG-Sepharose column. After being washed, associated proteins were eluted in a gradient of 0 to 2 M MgCl₂, resolved by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), and identified by mass spectrometry (Fig. 1A).

In addition to Rrp6p (Fig. 1A, lanes 3 to 4), two polypeptides identified by mass spectrometry in the eluate fractions were recovered at substoichiometric levels, as judged by visual inspection of Coomassie-stained gels (Fig. 1A). A ~25-kDa protein that dissociated from zz-Rrp44p at ~0.2 to 0.4 M MgCl₂ (Fig. 1A, lanes 1 to 2) was identified as the product of the *YHR081w* gene. A similarly sized protein was observed in the equivalent eluate fractions from zz-Rrp4p retained material in our previous analyses (3) but not identified. We designated this protein Rrp47p on the basis of its role in rRNA processing (see below) and copurification with the exosome (which contains Rrp4p, Rrp40p-Rrp46p, and Rrp6p). An ~80-kDa protein that dissociated from zz-Rrp44p with the other...
exosome components (Fig. 1A, lanes 3 to 4) was identified as Ski7p (YOR076c), an exosome cofactor required for cytoplasmic 3′→5′ mRNA decay (38).

To confirm the interaction between Rrp47p and the exosome, a strain was constructed that expressed a C-terminal fusion protein linked by a TEV protease cleavage site (Rrp47p-zz). Lysate from the Rrp47p-zz strain was passed over an IgG-Sepharose column, and bound proteins were eluted by digestion with TEV protease. The eluate was assayed for the presence of Rrp4p by Western blot analyses, by using an antiserum specific to Rrp4p (B and C) were done. Rrp47p-zz immunoprecipitates were eluted with or without prior digestion with RNase A. As controls for the specificity of the Rrp4p antiserum, cell extracts were loaded from strains expressing wild-type Rrp4p (B, lane 5) or epitope-tagged His(6)-Rrp4p (B, lane 6). Cleaved Rrp6p-TAP was included as a positive control for the Rrp6p Western analysis (C, lane 5). This protein is predicted to migrate slower than endogenous Rrp6p in SDS-PAGE gels due to the presence of the calmodulin-binding domain.
formed in buffer containing 0.5 M NaCl, and the coimmunoprecipitation of Rrp47p-zz with Rrp4p therefore reflects a stable interaction.

The relative intensities of Rrp47p and the other exosome components observed in Coomassie blue-stained gels (Fig. 1A) suggests that Rrp47p is present in ~20% of the exosome complex. Similarly, ~20% of the immunoprecipitated exosome complex is associated with Rrp6p (3). To assess whether Rrp4p and Rrp6p are associated with the same exosome fraction, the Rrp4p-zz immunoprecipitates were assayed for the presence of Rrp6p with an anti-Rrp6p antiserum (Fig. 1C, see Materials and Methods). Western blot analyses strongly decorated a single band of the predicted size in the Rrp4p-zz immunoprecipitate (Fig. 1C). This band was absent from total protein extracted from an rrp6-Δ strain (data not shown).

The RRP47 gene is known to be nonessential for cell viability (17). To analyze the requirement for Rrp47p in exosome function, we generated an rrp47Δ null allele (see Materials and Methods). The rrp47Δ mutant exhibited a slow-growth phenotype at 25, 30, and 37°C, with a doubling time of 6.3 h at 37°C compared to 2.4 h for the isogenic wild-type strain (data not shown). Western blot analyses demonstrated that Rrp6p levels were not significantly altered in the rrp47Δ mutant and that the coimmunoprecipitation of Rrp6p with an epitope-tagged Rrp4p fusion protein (zz-Rrp4p) was unaffected in the absence of Rrp47p (data not shown). We conclude that Rrp47p is not required for the expression of Rrp6p or its association with the exosome.

Rrp47p is required for normal pre-rRNA processing. Previous analyses revealed that exosome mutants are delayed in the early pre-rRNA cleavages at sites A0, A1, and A2 (2, 43) (Fig. 2A). To address the role of Rrp47p in rRNA synthesis, RNA was isolated from the isogenic wild-type strain, from strains mutant for core exosome components, and from the ts-lethal rrp4-1 mutant (Fig. 2B). To assay the role of Rrp47p in snoRNA synthesis, acrylamide gels-Northern blots were hybridized with probes specific for snR8 (box H/ACA) and snoR13 (box C/D), which are transcribed from their own promoters, the dicistronic U14 snoRNA (box C/D) and the intron-encoded snoRNAs U18, snoR38 (box C/D), and snoR44 (box H/ACA) (Fig. 4).

As previously reported (1, 31), precursors to the intron-encoded snoRNAs were observed in the wild-type strain (labeled U18-3’, snoR38-3’, and snoR44-3’ in Fig. 4D to F) that have mature 5’ ends but are 3’ unprocessed. Similar 3’-extended precursors were also observed for snR8 (box H/ACA) and snoR13 (box C/D), which are transcribed from their own promoters, the dicistronic U14 snoRNA (box C/D) and the intron-encoded snoRNAs U18, snoR38 (box C/D), and snoR44 (box H/ACA) (Fig. 4).

Exosome mutants show a moderate inhibition of the endonucleolytic cleavages at sites A0, A1, and A2. However, this phenotype is also seen for many other strains defective in 60S subunit synthesis (reviewed in reference 39) and is likely to be indirect. The defects seen in these early pre-rRNA processing steps in the absence of Rrp47p are similar to those of core exosome mutations. In contrast, the role of the exosome in the endonucleolytic processing of the 5.8S rRNA and in 5’ETS degradation are very likely to be direct and here the role of Rrp47p appears to resemble closely that of Rrp6p rather than the core exosome.

Rrp47p is required for snoRNA synthesis. Mutations in the exosome complex cause the accumulation of 3’-extended and polyadenylated snoRNA precursors. In rrp6Δ mutants, but not in strains mutant for core exosome components, most box C/D snoRNA precursors also retain discrete 3’ extensions of ~3 nt (1, 37). To assay the role of Rrp47p in snoRNA synthesis, acrylamide gel-Northern blots were hybridized with probes specific for snR8 (box H/ACA) and snoR13 (box C/D), which are transcribed from their own promoters, the dicistronic U14 snoRNA (box C/D) and the intron-encoded snoRNAs U18, snoR38 (box C/D), and snoR44 (box H/ACA) (Fig. 4).
FIG. 2. Rrp47p is required for early pre-rRNA processing events. (A) Organization of the yeast pre-rRNA and processing pathway. The 18S, 5.8S, and 25S rRNAs are separated by internal transcribed spacers ITS1 and ITS2 and flanked by the external transcribed spacers 5’ETS and 3’ETS. Coding regions are indicated by thick bars; spacer regions are indicated by thin lines. Sites within the pre-rRNA complementary to probes used in the present study are indicated. Early cleavages at sites A₀, A₁, and A₂ generate the 20S and 27SA₂ pre-rRNAs. The 20S pre-rRNA is processed to 18S rRNA by cleavage at site D. 27SA₂ is processed in ITS1 and ITS2 to generate the 5.8S and 25S rRNAs. Two forms of 27SB, 7S, and 5.8S that differ by 7 nt at their 5’ ends (boxed) are generated by alternative processing pathways. The 23S and 21S pre-rRNAs arise through premature cleavage at site A₃. The 17S’ species results from 5’ degradation of pre-rRNA blocked for processing in ITS1. (B) Northern blot analyses
and snR38 + 3 species were reduced in the \( rp47-\Delta \) mutant compared to the levels observed in the \( rp6-\Delta \) mutant, whereas the U18 + 3 species appeared to be slightly shorter in the \( rp47-\Delta \) mutant after transfer to 37°C. Low levels of the snR13 + 3 species were observed in both the \( rp47-\Delta \) and \( rp6-\Delta \) mutants during growth at 30°C (Fig. 4B). In addition, a truncated fragment of snR13 (snR13T) accumulated in the \( rp47-\Delta \), \( rp6-\Delta \), and \( rp4-1 \) mutants. This probably corresponds to the 5’truncated snR13 species previously observed in \( sen1-1 \) and \( ssu72-2 \) mutants (13, 33). The reason for the appearance of this species is unclear but it strongly correlates with the generation or stabilization of snR13 readthrough transcripts, which are seen in several exosome mutant strains (A. Fatica and D. Tollervey, unpublished data).

We conclude that Rrp47p and Rrp6p play related roles in the initial processing of 3’-extended snoRNA precursors. However, the lack of Rrp47p has milder effects on the removal of the last few nucleotides than the absence of Rrp6p.

**Rrp47p is required for normal synthesis of U4 and U5 snRNAs.** The absence of Rrp6p or mutations in core components of the exosome complex also causes defects in the 3’ processing of snRNAs (1, 37). We therefore analyzed the levels of the U4 and U5 snRNAs and their processing intermediates in the \( rp47-\Delta \) mutant (Fig. 5).

Two 3’-extended pre-U4 species are detected in wild-type cells (1), denoted U4-3’I and U4-3’II (Fig. 5A). The U4-3’I intermediate has a short 3’ extension of \( \sim 6 \) nt, whereas the larger U4-3’II precursor is a pair of similarly sized RNAs \( \sim 140 \) nt longer than the mature U4 snRNA. Higher levels of the U4-3’II intermediate were observed in the \( rp47-\Delta \) mutant than in the wild-type strain (Fig. 5A). Shorter 3’-extended species were also observed in the \( rp6-\Delta \) and \( rp4-1 \) mutants (1, 37). No clear effect was observed on the levels of the U4-3’I or mature U4 snRNA in the \( rp47-\Delta \) mutant compared to the isogenic wild-type control strain.

In wild-type cells, mature U5 snRNA is present as a major, long form (U5L) and a less-abundant short form (U5S) that differ by \( \sim 35 \) nt at their 3’ ends. Precursor species with short extensions are observed in wild-type strains for both U5L and U5S (denoted U5L-3’ and U5S-3’, respectively), as well as a longer precursor denoted U5-3’I (Fig. 5B). The U5L-3’, U5S-3’, and U5-3’I precursors accumulated in the \( rp47-\Delta \), \( rp6-\Delta \), and \( rp4-1 \) mutants compared to the wild-type strain (Fig. 5B). Mutants in the exosome complex lead to increased levels of U5S, while having little effect on the levels of U5L (1). Comparable levels of the minor U5S and major U5L snRNA were observed in the \( rp47-\Delta \) mutant, whereas the U5L form was the more abundant form in the \( rp6-\Delta \) and \( rp4-1 \) mutants (Fig. 5).

Quantitative analyses revealed that the U5L/U5S ratio increased in the \( rp47-\Delta \), \( rp6-\Delta \), and \( rp4-1 \) mutants by 1.6-, 3.1-, and 2.9-fold, respectively, compared to the wild-type control.

**FIG. 3. Rrp47p is required for 7S pre-rRNA processing and 5’ETS degradation.** (A) Northern blot analyses of 5.8S rRNA species in a wild-type strain and in exosome mutants. RNA was recovered from wild-type and mutant strains, as in Fig. 2. (Upper panel) Hybridization with a probe specific for 5.8S species extended into ITS2; (lower panel) hybridization with probe specific for the mature 5.8S rRNA. (B) Hybridization with a probe specific for the 5’ETS species. Probes used are indicated in parentheses to the left of each panel. The long and short forms of 5.8S rRNA are clearly resolved.
Strains lacking Rrp47p therefore exhibit mild defects in U4 and U5 snRNA processing similar to those seen in strains lacking Rrp6p or mutant for core components of the exosome. We conclude that Rrp47p is required for the exosome-mediated 3′ processing of U4 and U5 snRNAs.

Analysis of the *rrp47*-Δ *rrp6*-Δ double mutant. To analyze further the functional relationship between Rrp47p and Rrp6p, we generated *rrp47*-Δ *rrp6*-Δ double mutants by genetic crossing. Sister strains from full tetrads showing a tetraploid segregation for the *rrp47*-Δ and *rrp6*-Δ alleles were grown at
The double-mutant strains were viable, with a growth rate comparable to that of the rrp6-Δ single mutant strain, indicating that the proteins do not have redundant functions.

This conclusion was supported by RNA analyses, which showed that the level of the 5.8S intermediate in the rrp47-Δ rrp6-Δ double mutant was very similar to either single mutant (Fig. 6A). The 3' processing of the U14 and snR38 snoRNAs in the rrp47-Δ rrp6-Δ double mutant resembled the rrp6-Δ single mutant rather than the rrp47-Δ single mutant, with a substantial accumulation of the short, 3'-extended species (Fig. 6B and C).

Recombinant Rrp6p has been demonstrated to have exonuclease activity (11), whereas sequence analyses do not suggest such an activity for Rrp47p. We therefore propose that Rrp47p is required for the activity of Rrp6p in 7S pre-rRNA processing and in the initial processing of snoRNA precursors. In contrast, Rrp47p promotes, but is not strictly required for, the Rrp6p-dependent final trimming of box C/D snoRNAs.

Rrp47p is not required for nuclear mRNA surveillance or cytoplasmic mRNA turnover. Rna14p is required for transcription termination of RNA polymerase II and the cotranscriptional cleavage and polyadenylation of mRNA transcripts. The absence of Rrp6p and the depletion of the core exosome component Rrp41p have distinct phenotypes in the mRNA surveillance pathways that degrade the readthrough transcripts generated in the ts-lethal rna14-1 mutant (35). To address the role of Rrp47p in nuclear mRNA surveillance, we recovered RNA from rna14-1, rna14-1 rrp6-Δ, and rna14-1 GAL::rrp41 strains at time points after transfer to 37°C and then analyzed the ACT1 and CYH2 transcripts by hybridization of agarose gel-Northern blots (Fig. 7A).

Upon transfer to 37°C, the ACT1 and CYH2 mRNAs were rapidly depleted in the rna14-1 mutant. Approximately normal length transcripts were stabilized in the rna14-1 rrp6-Δ mutant, whereas long extended transcripts accumulated in the rna14-1 GAL::rrp41 mutant, as previously reported (35). In contrast, no mRNA stabilization was observed in the rna14-1 rrp47-Δ mutant and the ACT1 and CYH2 mRNAs were depleted upon transfer to 37°C with kinetics similar to the rna14-1 single mutant. Consistent with the lack of suppression of rna14-1 by the absence of Rrp47p, the rna14-1 rrp6-Δ mutant was viable at 37°C, whereas the rna14-1 rrp47-Δ mutant was not (Fig. 7B).

These data demonstrate that Rrp47p is not required for the nuclear, exosome-mediated initial degradation of the long readthrough transcripts generated in the rna14-1 mutant or for the subsequent Rrp6p-dependent degradation of the truncated mRNAs.

Reporter constructs containing poly(G) tracts within the 3' extended U4 snRNA species; (center panels) hybridization with a probe complementary to the mature U4 snRNA; (lower panel) control hybridization with a probe complementary to SCR1. (B) Analysis of U5 snRNA. Hybridization was performed with a probe complementary to the mature U5 snRNA. (Upper panel) long exposure (2 days) to reveal the 3'-extended U5 snRNA precursors; (middle panel) short exposure (3 h) to reveal the relative levels of the U5L and U5s snRNAs; (lower panel) hybridization with a probe complementary to SCR1. The probes used are indicated in brackets on the left of each panel.
untranslated region have been extensively used to trap and analyze intermediates in the exonucleolytic decay of cytoplasmic mRNA (reviewed in reference 36). In mutants of the exosome that are defective in cytoplasmic 3′→5′ mRNA decay, the turnover of the poly(G)→3′ end fragment of the MFA2pG reporter transcript is impeded compared to wild-type strains and shorter degradation intermediates accumulate (20). Constructs encoding the MFA2pG transcript were transformed into isogenic wild-type and rrp47Δ strains, as well as a ski7Δ mutant that is specifically defective for cytoplasmic mRNA decay. RNA recovered from the transformants was resolved in 8% polyacrylamide-urea gels and analyzed by Northern hybridization by using a probe complementary to the 3′ end of the poly(G) cassette. Degradation intermediates from the poly(G)→3′ fragment were observed in the ski7Δ mutant but not in the rrp47Δ mutant or the wild-type strain (Fig. 7C). This result demonstrates that Rrp47p is not required for the exosome-mediated cytoplasmic 3′→5′ decay pathway.

DISCUSSION

The exosome complex functions in a wide range of RNA processing and degradation pathways. It remains largely unclear how different classes of exosome substrates are initially identified and subsequently targeted to the very distinct fates of either accurate 3′ end processing or rapid and complete degradation. This differentiation is likely to be largely dependent upon additional cofactors that are predicted to be present at substoichiometric levels in exosome preparations and may be only weakly associated with the complex. We used a one-step immunoaffinity chromatography procedure coupled with elution of retained proteins in an increasing MgCl2 concentration gradient to identify substoichiometric proteins associated with the exosome component Rrp44p. This allowed the identification of a novel exosome cofactor, Rrp47p. The association of Rrp47p with the exosome was insensitive to RNase treatment and therefore probably reflects a direct interaction. The substoichiometric levels of Rrp47p in exosome preparations and its electrophoretic mobility, which is similar to that of the five smallest core exosome components, presumably precluded its identification in previous analyses. Rrp47p was previously shown to be localized to the nucleus (22), suggesting that it associates with only the nuclear exosome. Consistent with this finding, Rrp47p was not required for cytoplasmic mRNA turnover. The nuclear-specific exosome component Rrp6p was efficiently coprecipitated with epitope-tagged Rrp47p, indicating that they are components of the same complex. A genome-wide analysis of protein complexes in yeast identified Rrp47p in the immunoprecipitates of the exosome components Rrp44p and Rrp46p (16). It should, however, be noted that the product of the YIR035c gene was also identified in association with exosome components in the same study, whereas a deletion mutant showed no defect in pre-rRNA or snoRNA processing or in cytoplasmic 3′→5′ mRNA decay (P. Mitchell, unpublished observations).

The RNA processing defects in the rrp47Δ mutant resembled those previously observed in strains lacking Rrp6p. For several substrates, these are distinct from the defects seen in strains mutant for core exosome components or Mtr4p. Comparison of the phenotypes of rrp47Δ, rrp6Δ, and rrp47Δ
rrp6-Δ double mutants suggested that Rrp47p functions to promote Rrp6p activity. The absence of Rrp47p did not significantly affect either the expression level of Rrp6p or its coimmunoprecipitation with Rrp4p (R. Houalla and D. Tollervey, unpublished observations), suggesting that Rrp47p is not required for Rrp6p expression or its assembly into the exosome. Although Rrp47p shares no similarity with characterized 3’→5’ exoribonucleases, the homologous human protein C1D binds strongly to nucleic acids (28). Rrp47p may therefore function in substrate recruitment and targeting to Rrp6p.

Significantly, the effects of the absence of Rrp47p and Rrp6p, although related, were not identical, and not all nuclear functions of the exosome required Rrp47p. In particular, no effect was observed in the absence of Rrp47p on the exosome-mediated degradation of readthrough transcripts observed in the ma14-1 mutant, which is defective in pre-mRNA cleavage and transcription termination (7, 42). This indicates that Rrp47p may facilitate interactions between the Rrp6p-exosome complex and specific classes of exosome substrates.

Rrp47p was previously reported to function in DNA double-strand break repair and the homologous human protein C1D binds with high affinity to free 3’ ends of DNA (14, 28). Both nonhomologous end joining and homologous recombination events involve nucleotide removal from the free ends by exonucleases. The RNase D family of 3’→5’ exonucleases, which includes Rrp6p, is closely related to the proofreading domain of RNA polymerases (27). Rrp47p may therefore regulate exonucleolytic activities required for both stable RNA processing and DNA repair.

ACKNOWLEDGMENTS

We thank Jeremy Brown (University of Newcastle, Newcastle, United Kingdom) for plasmid pJE39.
This work was supported by the Welcome Trust.

REFERENCES


12. de la Cruz, J., D. Kressler, D. Tollervey, and P. Linder. 1998. Dohlp (Mrnlp) is a putative ATP-dependent RNA helicase required for the 3’ end formation of 5.8S RNA in Saccharomyces cerevisiae. EMBO J. 17:1128–1140.


