3’ terminal diversity of MRP RNA and other human noncoding RNAs revealed by deep sequencing

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Abstract

Background: Post-transcriptional 3′ end processing is a key component of RNA regulation. The abundant and essential RNA subunit of RNase MRP has been proposed to function in three distinct cellular compartments and therefore may utilize this mode of regulation. Here we employ 3′ RACE coupled with high-throughput sequencing to characterize the 3′ terminal sequences of human MRP RNA and other noncoding RNAs that form RNP complexes.

Results: The 3′ terminal sequence of MRP RNA from HEK293T cells has a distinctive distribution of genomically encoded termini (including an assortment of U residues) with a portion of these selectively tagged by oligo(A) tails. This profile contrasts with the relatively homogenous 3′ terminus of an in vitro transcribed MRP RNA control and the differing 3′ terminal profiles of U3 snoRNA, RNase P RNA, and telomerase RNA (hTR).

Conclusions: 3′ RACE coupled with deep sequencing provides a valuable framework for the functional characterization of 3′ terminal sequences of noncoding RNAs.

Keywords: RNase MRP RNA, 3′ RACE deep sequencing, Oligo(U), Oligo(A), Telomerase RNA

Background

The addition of non-templated nucleotides to the 3′ ends of RNA molecules is a widespread mechanism for their regulation. Beyond the familiar long poly(A) tails of messenger RNAs, short 3′ tailing of uridine [1-4] and adenosine [5-7] nucleotides to noncoding RNAs is gathering increasing appreciation. These simple oligonucleotide additions (one to ~20 identical bases) can alter the stability, binding partners or activity of the enzymatic reactions in which these RNAs participate. Further, many of these 3′ terminally extended noncoding RNAs, including U6 spliceosomal RNA [8], tRNAs [4] and several snoRNAs [9,10], have annotated termini flanked by a stretch of genomically encoded U’s. The detailed interplay of transcriptional termination, trimming and post-transcriptional oligonucleotide addition has been elegantly characterized for a few systems [11], but the precise 3′ processing cascade and functional termini for many other critical noncoding RNAs remain unclear.

RNase MRP is a ribonucleoprotein complex with a single RNA component (MRP RNA) transcribed by RNA polymerase III [12]. Mutation of the sole MRP RNA genomic locus results in inviable yeast [13] and a spectrum of pleiotropic human diseases [14], supporting the assertion that MRP RNA is essential to eukaryotic life. In association with at least 10 proteins in humans [15,16], MRP RNA is implicated in the specific endoribonucleolytic cleavage [17,18] of several vital RNA substrates [19-24] found in the nucleolus [25,26], cytoplasm [24,27] and possibly mitochondria [28,29] of the eukaryotic cell. All of the MRP proteins also associate with the RNase P RNA [15,30] to form the enzyme responsible for the cleavage of tRNA 5′ leader sequences. Thus, RNase MRP requires tight regulation to discern its proper RNA subunit and cleave its many substrates.

Because 3′ end processing is a prevalent and potent means of regulation for other noncoding RNAs and because one instance of dramatic 3′ extension of MRP RNA was previously reported [31], we sought to...
thoroughly examine the 3′ ends of MRP RNA present in human cells. Combining aspects of various protocols [32-34], we employed a modified 3′ RACE with deep sequencing protocol and found a distribution of genomically encoded 3′ ends including variable U’s beyond the annotated 3′ nucleotide. Modest oligo(A) addition was also observed, particularly after more than one uridine. This profile contrasted with distinct distributions of U’s and A’s on other noncoding RNAs and the relatively homogenous 3′ terminus of an in vitro transcribed control MRP RNA.

Results

To comprehensively define the 3′-hydroxyl ends of endogenous RNA molecules in HEK293T cells, we adapted an RNA ligase-mediated 3′ RACE strategy coupled to deep sequencing (Figure 1). While similar methods have been previously reported [33], our protocol incorporated a few modifications. Precise 3′ terminal nucleotides were demarcated by ligation of whole cell RNA preparations with four distinct oligoribonucleotide appendices, each containing a different 5′ terminal base and internal barcode to minimize structural bias during this reaction [32,35]. Further, to ensure signal from low abundance RNA species, a library amplification step was included after the RACE selection [34].

We obtained an average of 955,000 trimmed reads (range of 53,997 – 2,235,651 for 6 libraries, see Methods) per experiment for endogenous MRP RNA. Unlike typical pipelines, alignment of sequences to the reference genome was not performed, since this would have eliminated detection of extensions not mapping to the genomic template. Instead, raw sequencing reads were filtered to obtain a rigorous set where each read contained both a 3′ region of MRP RNA (Additional file 1: Table S1) and one of the appendix oligonucleotides. Since our focus was 3′ extension, reads displaying RNA termini truncated upstream of the annotated 3′ end were excluded by this analysis.

Endogenous MRP RNA molecules displayed a distinctive profile of 3′ ends. While the majority of these termini mapped to the RMRP gene locus (Figure 2a, upper panel), we observed a clear preference in this cell type for one previously annotated end (…CUGU, ~62%) over another (…CU, ~1%). Additional uridines beyond these ends were also detected; these may arise from primary transcriptional termination beyond the annotated end, or post-transcriptional oligouridylation by 3′ uridylytransferases [36]. While these possible mechanisms cannot be distinguished by our methods, the apparent greater propensity for four or five uridines presumably indicates these endings are more frequently generated or are more stable species in this cell type. Among the ~9% fraction of 3′ ends that failed complete alignment to the genomic template, most were additions of adenosines to genomically encoded termini. Interestingly, these A’s were most likely to appear after multiple U’s (Figure 2b, upper panel), suggesting different 3′ ends have distinct propensities for the addition of oligo(A) tails. Our observation that various lengths of oligo(U) are often followed by an A, but the A termini are not followed by U’s, was noted previously for signal recognition particle RNA, 7SK RNA, 5S rRNA and U6 snRNA [5]. To test whether the observed MRP RNA 3′ ends were specific to the cell line tested, we sequenced MRP RNA from a second human cell line (K562) and found it to display similar genomically encoded and oligo(A) termini (Additional file 2: Figure S1).

To control for the possibility that our library preparation method could contribute to this profile of 3′ ends, we constructed a barcoded in vitro transcript of MRP RNA (ivt-MRP), spiked it into our cellular RNA, and prepared a single library for deep sequencing. The template for ivt-MRP was designed to have the commonly annotated …CU 3′ end produced by run-off transcription. As expected for this template, and in contrast
to endogenous MRP RNA, ivt-MRP showed no appreciable abundance of the ...CUGU ending nor a penchant for additional U’s or As (Figure 2b). Rather, 95% of the ivt-MRP ends represented the designed terminus (...CU, ~75%) or single nucleotide additions to this designed end (+A in blue; +C in green; +G in yellow; +U in red). Both cellular and ivt-MRP displayed a small portion of other simple sequences shown as white slices (i.e. ...CUCC, ...CUGC, and see Figure 3). Total trimmed reads = 1,497,440 (cellular) and 906,145 (ivt). b Reads from endogenous MRP terminate at specific nucleotides in the flanking RMRP gene with non-random abundances (black bars) and distinct probabilities of oligo(A) addition (light blue caps). As an example, the relative frequency of different numbers (n) of A’s found on one of the genomically encoded termini is illustrated in the inset. The major genomically encoded end is not observed on ivt-MRP (lower panel), nor is there appreciable propensity for oligo(A) addition. Although a single A is sometimes added to the designed terminus, C and G are added with similar frequency.

Figure 2 RACE sequencing reveals a distribution of 3’ termini for MRP RNA. a The majority of HEK293T cellular MRP RNA 3’ ends are genomically encoded (black pie slice), with a modest portion of these containing oligo(A)n additions to these genomically encoded ends (range of n=1-10, light blue slice). In contrast, while nearly three quarters of the reads from in vitro transcribed MRP (ivt-MRP) are the exact target sequence (grey slice), the remaining reads consist of single nucleotide additions to this designed end (+A in blue; +C in green; +G in yellow; +U in red). Both cellular and ivt-MRP displayed a small portion of other simple sequences shown as white slices (i.e. ...CUCC, ...CUGC, and see Figure 3). Total trimmed reads = 1,497,440 (cellular) and 906,145 (ivt). b Reads from endogenous MRP terminate at specific nucleotides in the flanking RMRP gene with non-random abundances (black bars) and distinct probabilities of oligo(A) addition (light blue caps). As an example, the relative frequency of different numbers (n) of A’s found on one of the genomically encoded termini is illustrated in the inset. The major genomically encoded end is not observed on ivt-MRP (lower panel), nor is there appreciable propensity for oligo(A) addition. Although a single A is sometimes added to the designed terminus, C and G are added with similar frequency.

This argues that the presence of these endings on the endogenous RNA directly reflects the MRP termini in vivo.

About 1% of ivt-MRP endings were strikingly complex (Figure 3a). These extensions beyond the designed 3’ end were complementary to nearby regions of the MRP RNA sequence (Figure 3b). An attractive mechanism for generation of these observed termini is 3’ end loopback or duplex RNA-dependent RNA polymerase extension by T7 RNA polymerase [37] analogous to that observed for mouse B2 RNA by RNA polymerase II [38]. The three examples shown demonstrate distinct registers of 3’ end loopback that would explain the observed extension sequences. Because such complex termini were conspicuously present only on ivt-MRP when compared...
directly with endogenous MRP, we conclude that these complex 3’ termini were likely to have been produced during T7 transcription and then faithfully retained through library preparation and sequencing.

One key advantage to this 3’ RACE sequencing method is the transcriptome-wide scope of the ligated cDNA library. Thus, with this library in hand, any RNA of interest can be amplified and subjected to deep 3’ terminal profiling (Figure 4). We found that RNase P RNA, which is structurally similar to MRP RNA and also transcribed by RNA polymerase III, had a distribution of additional genomically encoded U’s beyond its annotated 3’ end and virtually no propensity for oligo(A) addition. U3 snoRNA, transcribed by RNA polymerase II [11], was comparatively homogeneous with 99.5% of reads yielding the annotated 3’ terminus. In contrast, the RNA component of human telomerase, also transcribed by RNA polymerase II [39], had a greater propensity for oligo(A) addition, with each genomically encoded terminus being more likely to have multiple A’s than none (n = 5 A’s, average mode for endings shown) (Figure 4b, lowest panel).

To assess whether similar 3’ termini are captured in other published datasets, we used our bioinformatic pipeline to reanalyze raw poly(A)-depleted RNA sequencing data [4,40,41] and compared our profiles with theirs. Of course, the read depth for any particular RNA was much lower in the published whole-transcriptome datasets, e.g. an average of 1000 reads for MRP RNA per dataset compared with the average of 955,000 obtained here. On the noncoding RNAs analyzed for this study, we found a similar range of genomically encoded sequences with templated and non-templated oligo(U) and oligo(A) additions (Additional file 4: Table S2). Complex 3’ ends were also observed at very low abundance, though with properties distinct from those presented in Figure 3. Such endings included attachment of micro-RNAs, ribosomal RNA fragments and short sense or longer antisense regions of the RNA being analyzed (Additional file 5: Figure S3) and were idiosyncratic to
Discussion

The information content of the eukaryotic genome is greatly expanded in the transcriptome through post-transcriptional processing events. Well-studied examples include alternative splicing, RNA editing, and modifications including methylation and pseudouridylation. Recently, Li et al. characterized extensive differences between RNA and DNA sequences within protein coding genes that produce corresponding peptides with sequences that deviate from the genomic template [42]. The RNA 3’ end is another site at which post-transcriptional modification occurs and increases the information content of the transcriptome. Here, we analyze MR RNA and other human noncoding RNAs at a much greater sequencing depth than usual, and find a limited repertoire of sequence additions.

High-throughput sequencing is a powerful technology with continually emerging and illuminating applications.
The coupling of deep sequencing to the classic RACE technique has provided unprecedented insights into low abundance functional 3′ termini heretofore underappreciated [33]. General appendix-tagged cDNA libraries such as the ones produced in this study contain whole transcriptome information that can be specialized (Figure 1c) to amplify any RNA of interest. Even RNAs with non-ligatable 3′ modifications, such as the 2′,3′-cyclic phosphate on U6 snRNA [43], could be analyzed by comparison of libraries with and without enzymatic 3′-end deprotection (i.e. HCl followed by shrimp alkaline phosphatase treatment [44]). A further asset of the RACE sequencing technique is the ability to multiplex this general protocol at several stages, as demonstrated by orthogonal barcoding on the appendices, the control ivt-MRP RNA and the gene-specific RACE primer. Thus, comparison of 3′ terminal profiles across fractionated cellular compartments, associated protein partners, time courses or stress conditions enables the regulation of 3′ terminal extension to be comprehensively defined.

Our 3′ RACE sequencing analysis of the steady-state populations of four noncoding RNAs indicates that each RNA has a distinct repertoire of 3′ termini. Like MRP RNA, RNase P RNA is transcribed by RNA polymerase III and also has additional uridines beyond the annotated 3′ end. However, oligoadenylation is much less prominent with RNase P than with MRP RNA. Turning to the RNA polymerase II transcripts, we find U3 snoRNA to have a very homogeneous end. While processing in-
using T4 DNA ligase (NEB) following the manufacturer’s instructions. Insert sequences were confirmed by direct sequencing. Index-containing template for in vitro transcription was produced by PCR in 100 μL reactions using 300 ng of MRP plasmid, 1X GC buffer, 400 nM primers (mrpF1, mrp_index1_R2), 2 mM dNTPs, and 5U Phusion polymerase in the following program: 98C for 2 min, 30 cycles of 98C for 30 s, 55C for 30 s, 72C for 1 min, and final extension at 72C for 10 min. Template PCR products were then purified on agarose gels (Qiagen) and the entire eluate was used as template for in vitro transcription in 500 μL reactions containing 20 mM MgCl₂, 5 mM NTPs, 10 mM DTT, 4 mg/mL yeast pyrophosphatase (Sigma) and T7 RNA polymerase. In vitro transcription proceeded for 30 min at 37C and was stopped by phenol extraction with ethanol precipitation. Precipitated RNA was treated with 50U RQ1 DNase (Promega) and stopped by phenol extraction with ethanol precipitation according to the manufacturer’s instructions. DNase-treated RNA was then PAGE purified and stored in water at -80C.

**Cellular RNA preparation**

HEK293T cells were cultured in DMEM augmented with 10% FBS and pen/strep. 90% confluent cells were harvested in trypsin, washed twice with PBS and flash frozen in liquid nitrogen in aliquots of approximately 50 million cells. Cell pellets were extracted for whole cell RNA with Trizol reagent (Ambion) according to the manufacturer’s instructions, and quantified for total RNA by absorbance at 260 nm (via Nanodrop) and MRP RNA by northern blot comparison with ivt-MRP. 50 μg whole cell RNA containing approximately 15 ng endogenous MRP with or without 15 ng ivt-MRP was subjected to 50U of RQ1 DNase (Promega) and phenol extracted with ethanol precipitation according to the manufacturer’s protocol. Four 5 μg aliquots of each sample were then depleted of ribosomal RNA using the RiboZero rRNA Removal Kit (Epicentre), and 800 ng rRNA-depleted sample were subsequently treated with 2U alkaline phosphatase (Roche) and phenol extracted with ethanol precipitation as per the manufacturer’s instructions.

**Ligase mediated 3′ RACE with deep sequencing**

Library preparation was performed with a protocol similar to methods previously reported [33] with modifications. Pre-ligation reactions (23 μL) contained 10% PEG8000, 125 ng of RQ1, RiboZero, AP-treated whole cell RNA prepared as above and 40 pmol of one RNA appendix from the four listed in Additional file 7: Table S4, so that four separate reactions were carried out for each RNA sample. Pre-ligation reactions were heated to 85C for 5 min and immediately transferred to 37C. 10U of T4 RNA Ligase 1 were added to the melted RNAs along with final concentrations of 1X T4 RNA Ligase Reaction Buffer and 1 mM ATP. Ligation reactions (30 μL) were incubated at 37C for 30 min and stopped by phenol extraction with ethanol precipitation. Half of each ligation reaction was annealed with 10 pmol RT_primer and 25 nmol dNTPs for 5 min at 65C (35 μL reaction volume) and immediately transferred to 55C for reverse transcription in 50 μL reactions performed with 35 mM Tris, 52.5 mM KCl, 5 mM MgCl₂, 10 mM DTT and 200 U of Superscript III (Invitrogen). Reverse transcription lasted 50 min followed by heat inactivation at 85C for 5 min. 5 μL RT reaction was used as template for RACE and addition of Illumina adapters with 1X GC Buffer, 2 mM MgCl₂, 10% DMSO, 400 nM primers X_RACEF/3′universal_R1, 400 μM dNTPs and 1.25U Phusion polymerase in 25 μL final volume with the following program: 98C for 2 min, 18 cycles of 98C for 30 s, 65C for 30 s, 72C for 1 min, and final extension at 72C for 10 min. The entire RACE reaction was loaded on 2.5% agarose gels and amplicons of ~150-600 bp were excised for purification (Qiagen). Purified RACE products (30 μL) were used as template for library amplification in 100 μL reactions containing 1X HF Buffer, 2 mM MgCl₂, 400 nM primers Gen_primer-F2/Gen_primer-R2, 400 μM dNTPs and 5U Phusion polymerase with the following program: 98C for 2 min, 14 cycles of 98C for 30 s, 58C for 30 s, 72C for 1 min, and final extension at 72C for 10 min. These nested amplicons were subjected to PCR cleanup (Qiagen), quantified by Qubit and Bioanalyzer, diluted to 2 nM in 10 mM Tris-HCl, pH8.5, and combined for sequencing. 3–3.2 pM pooled libraries containing 30% phiX control V3 (Illumina) were run on the Illumina MiSeq following the manufacturer’s instructions.

**Data analysis**

300 basepair reads were assessed for quality using FASTX software and trimmed from adapters to isolate relevant insert content (Figure 1f) using a custom python script. Briefly, reads containing both a perfect appendix sequence and perfect search primer (Additional file 1: Table S1) for the RNA of interest were selected for processing, and this set was further trimmed to yield reads containing the 5′ end of the search primer through the 5′ end of the appendix (indicated region in Figure 1f). Identical trimmed reads were then collapsed to assess the abundance of each terminus and the depth of variation in 3′ terminal sequences.

**Additional files**

Additional file 1: Table S1. Search primers for bioinformatics assessment of 3′ ends.
Additional file 2: Figure S1. 3′ termini of MRNP RNA from human K562 cells.

Additional file 3: Figure S2. Northern analysis of ivt-MRP and total RNA from HEK293T cells.

Additional file 4: Table S2. Summary of 3′ termini from publicly available datasets [4,40,41].

Additional file 5: Figure S3. Examples of complex “extensions” found in publicly available datasets.

Additional file 6: Table S3. Primers used in this study.

Additional file 7: Table S4. Appendix RNA oligonucleotide sequences.

Competing interests
The authors declare they have no competing interests.

Authors’ contributions
KCG and TRC conceived the study and wrote the manuscript. KCG carried approved the final manuscript for publication.

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References
1. Jones MR, Quinton LJ, Blahna MT, Neilson JR, Fu S, Ivanov AR, Wolf DA, Mizgerd JP. Zcchc1-dependent uridylation of microRNA directs cytokine expression. Nat Cell Biol 2009, 11:1157–1163.
2. Chang HR, Schoenfeld LW, Ruby JG, Auyeung VC, Spies N, Baek D, Johnston WK, Russ C, Luo S, Babarz J, et al. Mammalian microRNAs: experimental evaluation of novel and previously annotated genes. Genes Dev 2010, 24:902–1009.
3. Heo I, Ha M, Lim J, Yoon MJ, Park JE, Kwon SC, Chang H, Kim VN: Mono-uridylation of pre-microRNA as a key step in the biogenesis of group II 5′-mer microRNAs. Cell 2012, 151:51–32.
4. Choi YS, Patena W, Levent AD, McManus WR. Mammal RNA 3′-end oligouridylation in mammals. RNA 2012, 18:394–401.
5. Chen Y, Sinha K, Perumal K, Reddy R. Effect of 3′ terminal adenyl acid residue on the uridylation of human small RNAs in vitro and in frog oocytes. RNA 2000, 6:1277–1288.
6. Kato T, Sakaguchi Y, Miyoshi K, Suzuki T, Kashwara S, Baba T, Suzuki T. Selective stabilization of mammalian microRNAs by 3′ adenylation mediated by the cytoplasmic poly(A) polymerase GL2-2. Genes Dev 2009, 23:433–438.
7. Burroughs AM, Ando Y, de Hoon MJ, Tomaru Y, Nishibu T, Ukekawa R, Fukuok T, Kurkoka T, Suzuki H, Hayashiizaki Y, Da CO: A comprehensive survey of 3′ animal miRNA modification events and a possible role for 3′ adenylation in modulating miRNA targeting effectiveness. Genome Res 2010, 20:1398–1410.
8. Lund E, Dahlberg JE. Cyclic 2′,3′-phosphates and nontemplated nucleotides at the 3′ end of spleenosomal Us small nuclear RNAs. Science 1992, 255:327–330.
9. Grzechnik P, Kufel J. Polyadenylation linked to transcription termination directs the processing of snoRNA precursors in yeast. Mol Cell 2008, 32:247–258.
10. van Hoof A, Lennertz P, Parker R. Yeast exosome mutants accumulate 5′-extended polyadenylated forms of U4 small Nuclear RNA and small nuclear RNAs. Mol Cell Biol 2000, 20:441–452.
11. Kiss T, Fayet E, Jady BE, Richard P, Weber M. Biogenesis and intranuclear trafficking of human box C/D and H/ACA RNPs. Cold Spring Harb Symp Quant Biol 2006, 71:407–417.
12. Yuan Y, Reddy R. 5′ Flanking sequences of human MRP/7-2 RNA gene are required and sufficient for the transcription by RNA polymerase III. Biochim Biophys Acta 1991, 1089:35–39.
13. Shadel GS, Muckemeyer GA, Clayton DA, Schmitt ME. Mutational analysis of the RNA component of Saccharomyces cerevisiae RNase MRP reveals distinct nuclear phenotypes. Gene 2000, 245:175–184.
14. Redjalai M, van Eetenmann H, Pilin K, Chadwick R, Johnson C, Yuan B, van Vennoo W, Prijin G, Salmea R, Rockas S, Kaidt O, de la Chapelle A. Mutations in the RNA component of RNase MRP cause a pleiotropic human disease, cartilage-hair hypoplasia. Cell 2001, 104:195–203.
15. Welting T, Kikkert BJ, van Vennoo WJ, Prijin GJ. Differential association of protein subunits with the human RNase MRP and RNase P complexes. RNA 2006, 12:1373–1382.
16. Lopez MD, Rosenblad MA, Samuelsson T. Conserved and variable domains of RNase MRP RNA. RNA Biol 2009, 6:208–220.
17. Chang DD, Clayton DA. A novel endoribonuclease cleaves at a priming site of mouse mitochondrial DNA replication. EMBO J 1987, 6:409–417.
18. Chang DD, Clayton DA. A Mammalian mitochondrial RNA processing activity contains nucleus-encoded RNA. Science 1987, 235:1178–1184.
19. Schmitt ME, Clayton DA. Nuclear RNase MRP is required for correct processing of pre-5′SR RNA in Saccharomyces cerevisiae. Mol Cell Biol 1993, 13:793–7941.
20. Lindahl L, Bommanianti A, Li X, Hayden L, Jones A, Khan M, Orai T, Zengel IM. RNase MRP is required for entry of 3′SR precursor RNA into the canonical processing pathway. RNA 2000, 15:1407–1416.
21. Cai T, Auld S, Gill T, Cerio M, Schmitt ME. The Saccharomyces cerevisiae RNase mitochondrial RNA processing is critical for cell cycle progression at the end of mitosis. Genetics 2002, 161:1029–1042.
22. Gill T, Cai T, Aulds J, Wierzbicki S, Schmitt ME. RNase MRP: Cleaves the CL2B RNA to promote cell cycle progression: novel method of miRNA degradation. Mol Cell Biol 2004, 24:945–953.
23. Jaag HM, Lu Q, Schmitt ME, Naya PD. Role of RNase MRP in viral RNA degradation and recombination. J Virol 2011, 85:2423–2433.
24. Mattissens S, Hinson ER, Omnellkin CK, Hermans M, Zabel B, Cresswell P, Prijin GJ: Viperni RNA is a novel target for the human RNase MRP/ RNase P endonuclease. Cell Mol Life Sci 2011, 68:2469–2480.
25. Kiss T, Marshall M, Filipowicz W. Heat shock-induced 7-2′MRP RNAs in plant and mammalian cells: association with higher order structures in the nucleolus. EMBO J 1992, 11:3737–3747.
26. Jacobson MB, Cao L, Wang Y, Pederson T. Dynamic localization of RNase MRP RNA in the nucleolus observed by fluorescent RNA cytochemistry in living cells. J Cell Biol 1995, 131:1649–1658.
27. Gill T, Auld S, Schmitt ME. A specialized processing body that is temporally and asymmetrical regulated during the cell cycle in Saccharomyces cerevisiae. J Cell Biol 2006, 173:35–45.
28. Li K, Smagula CS, Parsons WJ, Richardson JA, Gonzalez M, Hazzer HK, Williams RS. Subcellular partitioning of MRNP RNA assessed by ultrastructural and biochemical analysis. J Cell Biology 1994, 124:871–882.
29. Kiss T, Filipowicz W. Evidence against a mitochondrial location of the 7-2′MRP RNA in mammalian cells. Cell 1992, 70:1–16.
30. Rosenblad MA, Lopez MD, Piccinelli P, Samuelsson T. Inventory and analysis of the protein subunits of the ribonucleas P and MRNP provides further evidence of homology between the yeast and human enzymes. Nucleic Acids Res 2006, 34:5145–5156.
31. Maita Y, Yousakawa M, Furushio M, Lassmann T, Possenet R, Okamoto N, Kasim Y, Hayashizaki Y, Hahn WC, Nasumoto K. An RNA-dependent RNA polymerase formed by TERT and the MRNP RNA. Nature 2009, 461:230–235.
32. Zhaang F, Fuchs RT, Sun Z, Zheng Y, Robb GB: Structural bias of T4 RNA ligase-mediated 3′-adapter ligation. Nucleic Acids Res 2012, 40:554.
33. Wilusz JE, Whipple JM, Phizicky EM, Sharp PA: RNPs marked with CCACA are targeted for degradation. Science 2011, 334:817–821.
34. Newman MA, Mani V, Hammond SM. Deep sequencing of microRNA precursors reveals extensive 3′ end modification. RNA 2011, 17:795–1803.
35. Hafner M, Renvick N, Brown M, Mihaliovic A, Holoch D, Lin C, Penn JT, Nusbaum D, Morozov P, Lubikh J, et al: RNA-ligase-dependent biases in miRNA representation in deep-sequenced small RNA cDNA libraries. RNA 2011, 17:6971–6972.
36. Scott DD, Norbury CJ: RNA decay via 3′ uridylation. Biochim Biophys Acta
1829, 2013:654–665.
37. Cazenave C, Uhlenbeck OC: RNA template-directed RNA synthesis by T7 RNA
polymerase. Proc Natl Acad Sci USA 1994, 91:6972–6976.
38. Wagner SD, Yakovchuk P, Gilman B, Ponciano SL, Druylling LF, Kugel JF,
Goodrich JA: RNA polymerase II acts as an RNA-dependent RNA
polymerase to extend and destabilize a non-coding RNA. EMBO J 2013,
32:781–790.
39. Mitchell JR, Cheng J, Collins K: A box H/A small nuclear RNA-like
domain at the human telomerase RNA 3′ end. Mol Cell Biol 1999,
19:567–576.
40. Derrien T, Johnson R, Bussotti G, Tanzer A, Djebali S, Tilgner H, Guernec G,
Martin D, Merkel A, Knowles DG, et al: The GENCODE v7 catalog of human
long noncoding RNAs: analysis of their gene structure, evolution, and
expression. Genome Res 2012, 22:1775–1789.
41. Tilgner H, Knowles DG, Johnson R, Davis CA, Chakrabortty S, Djebali S,
Curado J, Snyder M, Gingeras TR, Guigo R: Deep sequencing of subcellular
RNA fractions shows splicing to be predominantly co-transcriptional in the
human genome but inefficient for IncRNAs. Genome Res 2012,
22:1616–1625.
42. Li M, Wang IX, Li Y, Bruzel A, Richards AL, Toung JM, Cheung VG:
Widespread RNA and DNA sequence differences in the human
transcriptome. Science 2011, 333:53–58.
43. Shchepachev V, Witschnewski H, Missiaglia E, Soneson C, Azzalin CM: Mpn1,
mutated in poikiloderma with neutropenia protein 1, is a conserved
3′-to-5′ RNA exonuclease processing U6 small nuclear RNA. Cell Rep 2012,
2:855–865.
44. Mroczek S, Krawiszcz J, Kutner I, Lazniewski M, Kucinski I, Ginalski K,
Dziembowski A: C16orf57, a gene mutated in poikiloderma with
neutropenia, encodes a putative phosphodiesterase responsible for the
terminal diversity of MRP RNA 3′-end modification. Genes Dev 2012,
26:1911–1925.
45. Verheggen C, Lafontaine DL, Samarsky D, Mouaiakel J, Blanchard JM,
Bordonne R, Bertrand E: Mammalian and yeast U3 snoRNPs are matured
in specific and related nuclear compartments. EMBO J 2002,
21:2736–2745.
46. Boulon S, Marmier-Gourrier N, Pradet-Balade B, Wurth L, Verheggen C,
Jady BE, Rothe B, Pescia C, Robert MC, Kiss T, et al: The Hsp90 chaperone
controls the biogenesis of L7Ae RNPs through conserved machinery.
J Cell Biol 2008, 180:579–595.
47. Zaugg AJ, Lingner J, Cech TR: Method for determining RNA 3′ ends and
application to human telomerase RNA. Nucleic Acids Res 1996, 24:532–533.
48. Schmid M, Jensen TR: The exosome: a multipurpose RNA-decay machine.
Trends Biochem Sci 2008, 33:501–510.
49. Schneider C, Kudla G, Wlotzka W, Tuck A, Tollervey D: Transcriptome-wide
analysis of exosome targets. Mol Cell 2012, 48:422–433.
50. Schilders G, Rajmakers R, Raats JM, Pruin GJ: MPP6 is an exosome-
associated RNA-binding protein involved in 5.8S rRNA maturation.
Nucleic Acids Res 2005, 33:6795–6804.
51. Bernadt H, Hamisch C, Rammlott C, Stohl N, Zirkel A, Doehm JC,
Himmelbauer H, Tavanez JP, Huttelman S, Wahlen E: Maturation of
mammalian H/A box snoRNAs: PAPDS-dependent adenylation and
PARN-dependent trimming. RNA 2012, 18:958–972.
52. Reddy R, Tan EM, Henning D, Nohga K, Busch H: Detection of a nucleolar
7–2 ribonucleoprotein and a cytoplasmic 8–2 ribonucleoprotein with
autoantibodies from patients with scleroderma. J Biol Chem 1983,
258:1383–1386.
53. Hashimoto C, Steitz JA: Sequential association of nucleolar 7–2 RNA with
two different autoantigens. J Biol Chem 1983, 258:1379–1382.