The trans-Spliceosomal U4 RNA from the Monogenetic Trypanosomatid Leptomonas collosoma

CLONING AND IDENTIFICATION OF A TRANSCRIBED tRNA-LIKE ELEMENT THAT CONTROLS ITS EXPRESSION

Liu Li‡, Leo R. Otake§, Yu-xin Xu¶, and Shulamit Michaeli‡

From the ‡Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan 52900, Israel the §Department of Molecular Biophysics and Biochemistry, Howard Hughes Medical Institute, Yale University School of Medicine, New Haven, Connecticut 06536-0812, and the ¶Department of Biological Chemistry, The Weizmann Institute of Science, Rehovot 76100, Israel

U4 small nuclear RNA is essential for trans-splicing. Here we report the cloning of U4 snRNA gene from Leptomonas collosoma and analysis of elements controlling its expression. The trypanosome U4 RNA is the smallest known, it carries an Sm-like site, and has the potential for extensive intermolecular base pairing with the U6 RNA. Sequence analysis of the U4 locus indicates the presence of a tRNA-like element 86 base pairs upstream of the gene that is divergently transcribed to yield a stable small tRNA-like RNA. Two additional tRNA genes, tRNAPro and tRNAGly, were found upstream of this element. By stable expression of a tagged U4 RNA, we demonstrate that the tRNA-like gene, but not the upstream tRNA genes, is essential for U4 expression and that the B box but not the A Box of the tRNA-like gene is crucial for expression in vivo. Mapping the 2′-O-methyl groups on U4 and U6 small nuclear RNAs suggests the presence of modifications in canonical positions. However, the number of modified nucleotides is fewer than in mammalian homologues. The U4 genomic organization including both tRNA-like and tRNA genes may represent a relic whereby trypanosomatids “hired” tRNA genes to provide extragenic promoter elements. The close proximity of tRNA genes to the tRNA-like molecule in the U4 locus further suggests that the tRNA-like gene may have evolved from a tRNA member of this cluster.

In trypanosomes all pre-mRNAs are produced by trans-splicing. In this process a common short spliced leader (SL) derived from a small RNA, the SL RNA, is added to each mRNA. trans-splicing is mechanistically related to cis-splicing (1).

As in cis-splicing, U snRNAs are required. Trypanosome counterparts to U2, U4, and U6 have been characterized and shown to function in trans-splicing (2, 3). Trypanosome snRNAs are generally smaller than their cis-splicing counterparts. Only recently was the trypanosome U5 homologue identified and its gene cloned and sequenced (4, 5). Evidence supports the presence of a trypanosome tri-snRNP complex carrying the U4/U6/U5 snRNAs (5). However, the trypanosome U5 snRNA may have a unique role in trans-splicing based on its potential to interact with the SL RNA intron region by base pairing, as supported by in vivo cross-linking experiments (4) and phylogenetic conservation (5).

The majority of trypanosome snRNAs carry a divergent Sm site. The Sm site was shown in other eukaryotes to bind core proteins that are common to all snRNPs and are recognized by sera from autoimmune patients (6). The trypanosome snRNPs are the only ones so far that are not recognized by anti-Sm sera that recognize Sm proteins from yeast to man. Surprisingly, however, trypanosomes do possess Sm proteins, because recently an SmE homologue was identified among the core proteins that bind the SL RNA (7).

In mammals and yeast, U snRNA genes, except U6, are transcribed by RNA polymerase II (8). The promoters of these genes include distal and proximal elements and TATA boxes. In trypanosomes, in contrast, all small RNAs including U2, U3, U6, and 7SL RNA are transcribed by polymerase III (9). In the last three cases, A and B box elements located upstream of the gene were shown to be essential for transcription in vivo. These control elements are part of the internal control regions of divergently oriented tRNA genes or in the case of the U2 snRNA, of a tRNA-like gene (10).

To study further the assembly of trypanosome U snRNAs in vivo, we have cloned and sequenced the U4 gene from the monogenetic trypanosomatid Leptomonas collosoma. This completes the set of spliceosomal RNAs from this trypanosomatid species. The U4 gene locus represents a new mode of genomic organization, harboring both tRNA-like and tRNA genes upstream of the coding region. Like U2 snRNA, but unlike U6 snRNA, the B box sequence of the tRNA-like molecule plays a major role in the expression of the gene.

EXPERIMENTAL PROCEDURES

Oligonucleotides—Oligonucleotides 424, 5′-GCACCTAAATGAACAAT-CACTGAGG-3′; 425, 5′-ATACTAAAAATCCACTGACTCC-3′; 25005, 5′-CCCCACCTTGTGTCGATCGA-3′ antisense to positions 94–113 of the U4 RNA; 25002, 5′-GGGAATCGAACCCGGGCCTC-3′ antisense complementary to positions –140 to –120; 25003, 5′-GGCCGTCTGCCGCCTGCCCT-3′ antisense to positions –120 to –140 in the tRNA gene; 24427, 5′-AGGCTTACCCCGCCCTAGCTTCCTCAAGGGCAGG-3′ sense complementary to positions 1–20 of U4; 26264, 5′-GGCCGTCTGCCGCCTGCCCT-3′ antisense complementary to positions –120 to –140 in the tRNA-like RNA; 24772, 5′-CAGTAC-TCCTAATCCATGCCGAGGAAATTGTGCA-3′ carrying insertion (underline) of NOI site in position 52; 24422, 5′-AGGCTTACCCCGCCCTAGCTTCCTCAAGGGCAGG-3′ sense complementary to positions –144 to –171 carrying substitutions (underlined) in the B box positions –153 to –162; 24427, 5′-TTCCCCTGGCGCTCATAAGGAGGGCGAGCCG-3′ sense complementary to positions –102 to –129 carrying substitutions.
Trypanosomatid U4 snRNA

1. DNA sequence of the U4 gene locus. The sequence of a 1.2-kilobase AluI fragment is presented. The coding region of U4 snRNA is underlined, bold, and indicated by uppercase lettering with its +1 position indicated; tRNA Pro, tRNA Gly and tRNA-like genes in the upstream region of U4 are underlined in bold letters. The direction of transcription of the U4 and tRNA genes is marked with arrows. The conserved boxes A and B of the tRNA and tRNA-like genes are indicated by boxes and uppercase letters.

2. Comparison of the clusters of tRNA or tRNA-like genes found upstream of L. collosoma and T. brucei snRNAs (9). The coding regions of the snRNAs are marked by frames with inside arrows indicating the direction of transcription. The tRNAs or tRNA-like sequences are represented by black arrows. The distance between the RNAs is indicated.

RESULTS AND DISCUSSION

The U4 Gene Is Linked to tRNA-like and Two tRNA Genes—By inverse PCR using primers derived from the Trypanosoma brucei U4 snRNA sequence (2), a Sau3AI 600-bp genomic fragment was cloned and sequenced. An RNA probe synthesized from this clone was used to screen a genomic library. A 1.2-kilobase AluI fragment carrying the gene was subcloned and sequenced. The sequence contains the U4 coding region 432 bp upstream and 253 bp downstream of sequences found upstream of the U4 gene, analogous to that described previously (10). tRNA Pro and tRNA Gly (5'-TTTGCTAGTGG-3', the most conserved positions are underlined) are consistent with the box B consensus (13, 14). Cloning of the Gene Encoding the U4 RNA—L. collosoma DNA (10 µg) was digested to completion with Sau3AI, and the digest was electrophoresed on 1% agarose gel and electroeluted. The eluted DNA was extracted with phenol-chloroform and precipitated in ethanol. The concentrated bases were excised and electroeluted. The eluted DNA was extracted from the gel, treated with AluI, and the digest was electrophoresed on 1% agarose gel. Fragments between 0.5 and 1.2 kilobases were excised and electroeluted. The concentrated DNA (0.25 µg) was ligated in 500 µl of buffer containing 50 mM Tris-HCl, pH 7.4, 10 mM MgCl2, 10 mM dithiothreitol, 1 mM ATP, 10 µg/ml gelatin, and 1 unit/ml ligase (New England Biolabs) at a DNA concentration of 0.5 µg/ml. The ligation mixture was further treated with phenol-chloroform, precipitated in ethanol, and used as inverse PCR template. The PCR was performed with the primers, 424 and 425, at 22-23°C in T5X-HF buffer containing 50 mM concentrations of dNTPs using 50 ng DNA as template. The direction of transcription was marked with arrows. The tRNA Pro and tRNA Gly transcript was sequenced by the dideoxynucleotide method and by primer extension reaction performed with the same primer. Primer extension reaction for mapping of 2'-O-methylations was performed at 0.02 and 5 µM concentrations of dNTPs using 5'-end-labeled oligonucleotides complementary to the 3'-end of U4, U5, and U6 snRNAs (13, 14).

3. Comparison of the clusters of tRNA or tRNA-like genes found upstream of L. collosoma and T. brucei snRNAs (9). The coding regions of the snRNAs are marked by frames with inside arrows indicating the direction of transcription. The tRNAs or tRNA-like sequences are represented by black arrows. The distance between the RNAs is indicated.

The genomic arrangement of the L. collosoma U4 locus does not resemble the loci of T. brucei U3 (15), L. collosoma U5 (5), and L. collosoma U6 (11, 16, 17); each of which has a divergently transcribed tRNA gene located 95–96 bp upstream of the U snRNA sequences (Fig. 2). We therefore examined a tRNA-like element upstream of the U4 RNA, analogous to that described for U2 snRNA (10). Indeed, bona fide A and B boxes were found (5'-TCCGGATGGG-3' and 5'-GGTTCATGCC-3', respectively), both of which agree with the consensus sequence (underlined). In comparing the consensus sequences with the corresponding boxes in the U2 locus (10), the A box of U2 is located at position −104 whereas the U4 A box is located at position −107. The U2 A box sequence (5'-TGCC-
CCGGGTGT-3') deviates more from the consensus sequence than the U4 A box. The U4 box A contains all the highly conserved positions (underlined), whereas the U2 A box contains two deviations at positions 8 and 12 with G and T instead of A and G. The B box in the U2 locus (5'-GGTTCGAGCCT-3') is located at position 2155 and that of U4 is located at position 2153; both the U2 and U4 B boxes agree well with the consensus. Thus, the tRNA-like boxes of U2 and U4 are positioned similarly with respect to the snRNA coding regions.

The U4 gene organization is unique when compared with other U snRNAs (Fig. 2), because it not only contains a tRNA-like element like the T. brucei U2 locus, but also carries two additional upstream tRNA genes, similar to U3, 7SL RNA, U6, and U5 snRNA gene loci. However, the companion tRNA located 95–98 bp upstream of the snRNAs is always divergently transcribed, whereas the tRNA gene adjacent to the tRNA-like sequence is transcribed from the same strand as the U4 gene. The presence of tRNA-like and tRNA sequences suggests that the former may have originated from a bona fide tRNA gene that had accumulated major changes and lost its identity. This tRNA may have been part of a tRNA cluster because most tRNA genes in trypanosomatids are clustered. In the case of 7SL, U5, U6, and U3, the identity of tRNA gene was kept, whereas in the case of U2 and U4, tRNA gene mutations accumulated but the identity of the A and B boxes was preserved including their proper spacing (Fig. 3A).

Because the tRNAs upstream of small RNA genes are transcribed (16, 18), it was of interest to examine whether the tRNA-like gene is also transcribed. Primer extension analysis was performed using an oligonucleotide (26264), and a discrete extension product was obtained, suggesting the presence of tRNA-like RNA transcript (Fig. 3B). Comparison of the tRNA-like structure to the tRNA Pro secondary structure is presented in Fig. 3A. Deviations of the tRNA-like structure from the canonical are mainly in the D stem and TcC stem-loops. The acceptor stem is extended at the 5'-end and the anti-codon loop is composed of 5 instead of 7 nt. However, the RNA can still be folded into the cloverleaf structure, and the A and B boxes are located in their conserved positions.

To examine the genomic organization of the U4 gene, L. collosoma DNA was subjected to Southern blot analysis. A single hybridization band was observed after digesting the DNA using restriction enzymes with 4-bp and 6-bp recognition sites, suggesting that the U4 gene, like all other U snRNA genes in trypanosomatids (2), is a single copy gene (Fig. 4A).
Northern blot analysis indicates a single transcript of 114 nt (Fig. 4).

The U4 RNA and the Relatedness to Its Homologues—The U4 coding sequence is highly conserved among trypanosomatid species: 87% identity with *T. brucei* (2) and 89% with *Leishmania* *ternatolae* (GenBank™/EBI Data Bank Accession no. X97621) U4 RNA (Fig. 5). The RNA is shorter (114 nt) compared with metazoans (142–145 nt) (20), higher plants (150–154 nt) (21), and budding yeast (160 nt) (22). The predicted secondary structure of U4 snRNA contains four stem-loop structures (I-IV) similar to higher eukaryotic U4 snRNAs. Unlike other unicellular organisms such as *Physarum polycephalum, Saccharomyces cerevisiae,* and *Schizosaccharomyces pombe,* the trypanosomatid U4 snRNAs possess a full stem-loop (IV) at the 3'-end (Fig. 5) (21). The position of the U4 and tagged U4 are indicated with arrows. Lanes 1, 2, 3, and 4 are as in A. DNA sequencing with the same oligonucleotide is shown on the right. Primer extension with a neo antisense oligonucleotide was the control. The primer extension products are indicated. WT, wild type; PE, primer extension.

The majority of changes between the trypanosomatid U4 RNAs are in the central domain and central loop (Fig. 6). The central domain and 3'-stem-loop in the yeast U4 RNA is quite tolerant to mutation (24). Interestingly, however, when the *T. brucei* stem-loop structure, which is homologous to the 3'-stem-loop of the yeast RNA was used to replace this homologous domain in yeast, the chimeric RNA could not complement a null allele of the yeast U4 snRNA (25). This chimeric U4 RNA did not associate well with the U6 snRNA, suggesting that in addition to base pair interactions in stem I and II, other interactions are required to promote U4/U6 complex formation. It was found that only a single mutation in the 3'-stem-loop in yeast resulted in a cold-sensitive phenotype (24). This suggests that the overall structure of the 3'-stem-loop, rather than its particular sequence, may be important for the U4 function.

A third potential for base pair interactions between U4 and
the presence of 5 or 0.02 mM dNTPs (indicated) with specific oligonucleotides antisense to the 3'-end for each snRNA. The 5'-ends of the snRNAs are indicated by arrows. The position of the reverse transcriptase stops (one nt before the methylated site) are indicated with the number of the nt.

U6 exists in the Sm-like site of U4 positions 90–95 (Fig. 6), similar to a more stable potential interaction for the T. brucei U4 snRNA at positions 86–91 (also in the Sm-like site) (2). The significance of this potential is currently unknown. Recently, a U4 snRNA at positions 86–91 (also in the Sm-like site) (2). The similarity to a more stable potential interaction for the T. brucei U6 exists in the Sm-like site of U4 positions 90–95 (Fig. 6), suggesting the formation of a stable interaction between the U4 and U6. The potential for interaction between the U6 and U2 (helix III) also exists for the trypanosome snRNAs (27). Interestingly, the U6 sequence block involved in the formation of the stem III between U6 and U4 is also involved in the formation of the helix III between U6 and U2. So far no genetic evidence exists to support these phylogenetically conserved stem III interactions.

The central domain is the most variable region in the U4 molecule. Indeed, deletion of almost the entire region in yeast yielded only a mild cold-sensitive phenotype (24). Thus, the sequence of this domain may not be important except to serve as spacer that separates the 5’- and 3’-domains of the U4 RNA.

It has long been debated whether trypanosome snRNAs carry a bona fide Sm binding site. The L. collosoma U4 Sm-like site (positions 87–93) deviates from the canonical sequence, because the U stretch is disrupted by an A. Many trypanosomatid SL and snRNA Sm-like sites deviate from the canonical consensus. In L. collosoma U2 snRNA, the U stretch is disrupted by a C (27), whereas the U6 Sm site is very divergent with only a single U (18). The only two RNAs that carry canonical Sm sites are the SL RNA (28) and the U5 snRNA (5).

However, this property is not shared with other trypanosomatids, for instance the T. brucei SL RNA and U5 Sm sites (4, 29, 30). By compiling all the Sm-like sites a consensus trypanosome Sm site can be derived: AAAN4G (where in 71% cases N is a U). Based on the strong deviation of these sites from the consensus Sm-like sequence and the finding that trypanosomes proteins are not recognized by anti-Sm sera, it was proposed that trypanosome core proteins and their corresponding binding site may differ significantly from those in mammals. Affinity selection using antisense biotinylated oligonucleotides to T. brucei snRNP and SL RNP RNAs suggests that core proteins are shared among all these particles (31). Moreover, antibodies raised against these proteins immunoprecipitate all the spliceosomal RNAs including U6 and SL RNA (32). The recent finding of an SmE homologue in trypanosomes, which carries both Sm motifs 1 and 2, suggests that Sm proteins do exist in trypanosomes (7). Yet, the lack of recognition of these proteins by anti-Sm sera is intriguing. Changes in both the Sm-like site and the core proteins may have co-evolved. These deviations may stem from the need of these snRNAs to interact with different capping enzymes, because SL RNA has a unique cap structure and U5 unlike U2 and U4 does not possess a trimethylguanosine cap (5), whereas the U6 most probably possesses an inverted cap, like in all other eukaryotes (2).

Extragenic Sequence Elements Controlling the Expression of the U4 Gene—To investigate the elements that control expression of the U4 gene, the coding region was tagged in the internal loop III by inserting 6 bp between position 82 and 83 (Figs. 5 and 7). The marked gene carrying 210 bp of upstream sequence carrying the tRNA-like coding region and 91 bp of downstream sequence was cloned into the pX expression vector (Fig. 7A). RNA prepared from transfected cell lines was analyzed by primer extension using oligonucleotide (25000) complementary to the 3'-end of the U4 snRNA. The results indicate that the tagged gene was expressed efficiently (Fig. 7B, lane 2), suggesting that the tRNA-like element, but not the tRNAPro and tRNAProGlu, is important for the U4 expression. To further explore elements essential for the expression, we mutated the A and B boxes separately and established cell lines. Analysis of U4 expression (Fig. 7B) demonstrated that mutation of the A box had no effect, whereas mutation of the B box completely inactivated the gene. To control for gene dosage (plasmid copy number), the level of the neo mRNA encoded by the pX vector was examined by primer extension and found to be almost identical in all cell lines (Fig. 7B, bottom). This pattern of dependence on the tRNA-like extragenic A and B box elements is identical to that obtained for the U2 gene, except that mutation in the T. brucei box A also had a slight effect on expression (10). The T. brucei U2 B box was identified as a binding site for a nuclear protein (33). The protein might be involved in chromatin organization. Indeed, a B box located downstream to the yeast U6 coding region was shown to affect chromatin organization (34).

Mapping 2'-O-Methyl Modifications on the L. collosoma U4, U5, and U6 snRNAs—An important characteristic of U snRNAs is their specific modification in regions highly conserved in evolution. In the vertebrate U4 and U6, modifications are clustered in the 5'-terminal region of U4 and the central region of U6 (35). Modifications are less numerous in yeast (36). We therefore examined the modifications of snRNAs from trypanosomes, which diverged much earlier than yeast from the eukaryotic lineage. The position of the 2'-O-methyl groups was determined by primer extension in the presence of low dNTP concentration (14), which causes the reverse transcriptase to pause one nt before the methylated site (13). The presence of specific stops in low (0.02 mM) but not high (5 mM) dNTP concentrations (Fig. 8) suggests 2'-O-methylation at positions A63 and A72 of U4. The A63 position is conserved in vertebrates and is the nearest nt to the potential stem I of the U4/U6

FIG. 8. Mapping of the ribose methylated sites in L. collosoma U4, U5 (5), and U6 (18) snRNAs. Primer extension was performed in the presence of 5 or 0.02 mM dNTPs (indicated) with specific oligonucleotides antisense to the 3'-end for each snRNA. The 5'-ends of the snRNAs are indicated by arrows. The position of the reverse transcriptase stops (one nt before the methylated site) are indicated with the number of the nt.
duplex. A72 is in the vicinity of U4/U6 stem III (see Fig. 6), but this position is not modified in vertebrates (35). In U6 snRNA 2′-O-methyls can be assigned to positions G42, G47, U50, C53, and U56, located in stem I and stem II of the U4/U6 duplex (Figs. 6 and 8). The modified nt of trypanosome U6 RNA agree well with their positions in vertebrate U6 (35), where they appear in regions involved in intramolecular base pairing and are expected to be at or near the spliceosome catalytic center. Interestingly, U5 is modified (Fig. 8) in position A19 of the invariant loop, which is the one position that deviates from the canonical U5 invariant loop sequence (5). We have suggested that this position interacts with the SL RNA +2 position by base pairing (4, 5). Another U5 modification appears in position A28, which seems to be specific to trypanosome, because no modified nt were found in other eukaryotes downstream of the invariant loop.

Recent study has shown that 2′-O-methylation of vertebrate U6 snRNA is guided by box C+D snRNAs (37), suggesting that modification may take place in nucleolar or coiled bodies that have a close relationship with the nucleoli. Indeed the modification of U6 position U47 was shown to be guided by a guide RNA that also guides the methylation of 28 S rRNA. So far, no snRNAs that have potential to guide modification of trypanosome U4 or U6 snRNAs have been discovered, although a guide that directs modification of 5.8 S rRNA has been described (19).

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