Eur. J. Biochem. 227, 780–786 (1995)

Identification by UV cross-linking of oligo(U)-binding proteins in mitochondria of the insect trypanosomatid *Crithidia fasciculata*

Peter LEEGWATER, Dave SPEIJER and Rob BENNE

E. C. Slater Institute, University of Amsterdam, Academic Medical Centre, Amsterdam, The Netherlands

(Received 12 October/29 November 1994) – EJB 94 1554/1

RNA editing in trypanosomes is the process of insertion and deletion of U residues at specific sites of mitochondrial transcripts mediated by short guide RNAs (gRNAs) that have a 3′ oligo(U) extension. Here we describe the identification by UV cross-linking of proteins present in mitochondrial extracts from *Crithidia fasciculata* with a high affinity for gRNAs, and the characterization of the binding specificity. A 65-kDa protein binds to gRNAs provided they are equipped with a U tail, to post-transcriptionally labelled mitoribosomal 9S and 12S RNAs that also possess a 3′ terminal stretch of U residues, and to free oligo(U) sequences with a minimal length of 23–29 nucleotides. It does not bind to a number of control RNAs, one of which has an internal U stretch of 13 residues. Poly(U), but not poly(C) or total yeast RNA, efficiently competes for binding to gRNA. Proteins of 88 kDa and 30 kDa also bind to gRNAs with a U tail, to miochondrial ribosomal RNAs and to oligo(U). These proteins, however, require longer oligo(U) for binding (>39 nucleotides) and they also have an affinity for other U-rich RNAs and poly(C). For comparison, part of the analysis was also carried out with a mitochondrial extract from *Trypanosoma brucei*. In this organism, gRNA-binding proteins of 83 kDa and 64 kDa were found with the same preference for 3′-terminal oligomeric U stretches as the *C. fasciculata* 65-kDa protein, whereas the binding specificity of a 26-kDa protein resembled that of the *C. fasciculata* 88-kDa and 30-kDa proteins. The possible involvement of the proteins in the editing process is discussed.

Keywords. RNA editing; guide RNA-binding proteins; kinetoplast; UV cross-linking.

RNA editing in trypanosomatids such as *Leishmania tarentolae*, *Trypanosoma brucei* and *Crithidia fasciculata* is the process of insertion and deletion of U residues at specific sites of mitochondrial (mt) mRNA (reviewed by Simpson and Shaw, 1989; Stuart, 1991; Hajduk et al., 1993; Benne, 1994). The information for the editing process is provided by short guide (g) RNAs which are partly complementary to a specific mRNA region if G:U basepairing is allowed (Blum et al., 1990; Van der Spek et al., 1991). gRNAs have a nonencoded U tail of 5–24 nucleotides (Blum and Simpson, 1990; Pollard and Hajduk, 1991) and are encoded in both the maxicircle and minicircle component of the trypanosomal mt DNA (Blum et al., 1990; Sturm and Simpson, 1990, 1991; Pollard et al., 1990). The mechanism by which gRNAs act is unknown, but current models (reviewed in Stuart, 1993; Hajduk et al., 1993; Simpson et al., 1993; Benne, 1994) propose that editing is initiated by basepairing between the anchor sequence of a gRNA and a region of the pre-mRNA immediately 3′ to the sites to be edited. In the second phase, insertion or deletion of U residues in the pre-mRNA is carried out either by enzymic cut-and-paste reactions or by RNA-mediated transesterifications, during which the duplexed region is extended until the pre-mRNA is fully edited. Chimeric RNA molecules present in trypanosomatid mt RNA that consist of a gRNA covalently linked via its 3′ end to an editing site in pre-mRNA (Blum et al., 1991; Read et al., 1992; Arts et al., 1993) may represent intermediates of the editing process, which could imply that the U tail of gRNAs functions as a source of the inserted U residues. Thus far, attempts to reconstitute RNA editing *in vitro* to verify these models have failed, although formation *in vitro* of chimeric molecules has been achieved (Koslowsky et al., 1992; Harris and Hajduk, 1992; Blum and Simpson, 1992; Arts et al., unpublished results).

The absence of an *in vitro* editing system has also precluded the identification and characterization of editing proteins. It has been proposed that the U tail of gRNAs is created by a terminal uridylyl transferase (TUTase) and that the cut-and-paste reactions mentioned above are carried out by endonuclease(s) and an RNA ligase, respectively. These activities have indeed been found in trypanosome mitochondria (Bakalara et al., 1989; Simpson et al., 1992; Harris et al., 1992) but their participation in editing remains unproven. The supposed analogy between editing and splicing (Cech, 1991; Blum et al., 1991) has led to the speculation that editing is carried out by a machinery of complexity comparable to that of the spliceosome (the 'editosome') and that, beside the proteins directly involved in the U-insertion/deletion processes, a host of other proteins is required, e.g. proteins needed for the folding of the participating RNAs, proteins participating in the correct and ordered assembly (and disassembly) of the gRNA:pre-mRNA duplexes, etc. As a first indication that complex RNP particles are involved in RNA editing, it has been inferred from glycerol gradient sedimentation analysis that two types of high molecular-mass gRNP complexes exist; complex 1 (sedimenting at 19S) containing gRNAs, RNA ligase, chimera-forming activity and TUTase and complex 2 (sedimenting at 35–40S) containing gRNAs, RNA ligase, chimera-forming activity and pre-mRNAs (Pollard et al., 1992). Putative

Correspondence to R. Benne, E. C. Slater Institute, University of Amsterdam, Academic Medical Centre, Meibergdreef 15, NL-1105 AZ Amsterdam, The Netherlands

Fax: +31 20 691 5519.

Abbreviations. FS, frameshift; gRNA (RNP), guide RNA (RNP); ND, NADH dehydrogenase; TUTase, terminal uridylyl transferase.

gRNA-protein complexes have also been characterized by native-gel-retardation assays in extracts of *L. tarentolae* (Peris et al., 1994) and. *T. brucei* (Göringer et al., 1994; Read et al., 1994). Moreover, cross-linking experiments have identified several proteins which associate with gRNA and pre-mRNA in *T. brucei* extracts (Köller et al., 1994; Read et al., 1994), which has led to the realisation that a 90-kDa protein from *T. brucei* binds specifically to the gRNA oligo(U) tail. To date, however, no clear role in the editing process could be ascribed to this or any other protein, and their relevance remains obscure.

We are in the process of identifying and characterizing proteins that may play a role in RNA editing in the insect trypanosomatid *C. fasciculata* and have initiated the analysis of proteins that display high affinity for gRNAs in UV cross-linking assays. In this report, we describe the identification of proteins of 88, 65 and 30 kDa that can be cross-linked to gRNA. We show that this binding solely depends on the presence of the gRNA U tail but that the binding is not specific for gRNA since the three proteins also bind to U-tailed mitoribosomal rRNAs and to free oligo(U). The 65-kDa protein is particularly interesting in that it has no affinity for U-rich control RNAs, not even if these possess an internal homopolymeric U stretch. In this paper, we also present a detailed comparison between the binding specificity of *C. fasciculata* proteins and that of their counterparts from *T. brucei*.

MATERIALS AND METHODS

Cell growth and preparation of mitochondrial fractions. *C. fasciculata* was grown in batches of 10 l as described by Kleisen et al. (1975), with shaking and aeration to a density of 2×10^8 cells/ml. Mt vesicles were isolated according to the method of Birkenmeyer and Ray (1986). The *T. brucei* procyclic form was grown as described (Hoeijmakers et al., 1981); mt vesicle isolation was essentially as described by Feagin et al. (1987).

***In vitro* RNA synthesis.** cDNAs of gRNAs and pre-mRNA were cloned behind the T7 promotor (Arts et al., 1993 and unpublished results). The DNA clones were linearized with appropriate restriction enzymes (*Dra*I for ND7 [FS] and [5′]gRNA; *Apo*I to obtain a version of ND7 [FS]gRNA that has no U tail; *Bam*HI for chimeric RNA; *Hin*dIII for vector-derived RNA and *Sau*3A for the pre-mRNA fragment). T7 RNA polymerase reactions (15 µl) contained DNA template (1 µl respective plasmid), 40 mM Tris/HCl, pH 7.9, 6 mM $MgCl_2$, 2 mM spermidine, 10 mM dithiothreitol, 0.5 mM each ATP, GTP and CTP, 0.1 mM UTP, 60 µCi [α-^{32}P]UTP (Amersham), 5U RNAsin (Promega) and 5U T7 RNA polymerase (home made). After 1 h at 37°C, plasmid DNA was removed by DNase I digestion at 50 µg/ml.

The sequences of *in vitro* synthesized RNA substrates are as follows: ND7 [FS]gRNA, GGAACAGCAUUAGUCUAAUCUAUCAGAAUGCUACUCAAAAAUUUAUAUUAU$_{23}$; ND7 [FS]gRNA without U tail, GGAACAGCAUUAGUCUAAUCUAUCAGAAUGCUACUCAAAAAUU; ND7 [5′]gRNA, GGACGGCUGAUAUAAGUGCAAAAAGGCAAUAAAGACAAAAUAAAUAUAU$_{15}$; vector-derived RNA, GGGAGACCGGAAUUCGAGCUCGGUACCCGGGGAUCCUCUAGAGUCGACCUGCAGGCAUGCAAGCU; ND7 chimeric RNA, GGAACAGCAUUAGUCUAAUCUAUCAAAAUGCU$_{13}$AGAUUAGAUUAUGUUAGUGUUGUUUGUAAUGAACAUUUGCUAUCCUUAUGGAUUAGCUG*GUUUUACAGCUGGAUC*.

All RNAs contain two G residues at the 5′ end, derived from the T7 promoter.

The chimeric RNA was cloned as described in Arts et al. (1993). The PCR amplification procedure followed resulted in the addition of 16 nucleotides to the 3′ end of the RNA (italics) that are not present in ND7 RNA.

The sequence of the ND7 pre-mRNA fragment is mainly that of the corresponding gene fragment [coordinates 2861−3779 in Sloof et al. (1987)], from which the region 3383−3706 was deleted; in the final construct, a vector-derived segment is fused to the 5′ end, GGGAGACCCAAGCUUGCAUGCCUGCAGGUC.

UV cross-linking assay. The mt fractions of *C. fasciculata* and *T. brucei* (5−10 µg protein) were incubated with radiolabelled RNA (200 cps, 0.5−2 ng) for 30 min at room temperature in 50 µl buffer with 125 mM sucrose, 10 mM Tris/HCl, pH 7.9, 1 mM EDTA, 0.5% Triton-X-100, 2 mM dithiothreitol, 5 mM $MgCl_2$, 150 mM KCl and 100 ng yeast RNA or competitor RNA as indicated in Fig. 2. The incubations were transferred to inverted lids of 1.5-ml Eppendorf vials that were placed on ice, and irradiated with 2 J/cm² UV light of 254 nm. For this purpose, a Stratagene UV Stratalinker 1800 was used. The samples were treated with RNase A (40 µg/ml) for 30 min at 37°C, followed by the addition of an equal volume of 2×sample buffer (125 mM Tris/HCl, pH 6.8, 20% glycerol, 4% SDS, 10% 2-mercaptoethanol and 0.1% bromophenol blue) and heating to 95°C for 5 min. The proteins were separated by SDS/PAGE. Separating gels (15×13×0.15 cm) consisted of 8% polyacrylamide (acrylamide/bisacrylamide = 39:1) with 0.375 M Tris/HCl, pH 8.8, and 0.1% SDS. Stacking gels were 4% polyacrylamide with 0.125 M Tris/HCl, pH 6.8, and 0.1% SDS. Electrophoresis was carried out in 25 mM Tris, 190 mM glycine and 0.1% SDS for 16 h at 50 V. Gels were fixed in 20% methanol and 10% acetic acid, dried and autoradiographed. For quantification, gels were exposed for 4−24 h to a phosphor screen and signal intensities were analyzed with a molecular Dynamics Phosphorimager apparatus using ImageQuant version 3.0.

Fragmentation of poly(U). Poly(U) (0.5 mg/ml) was partially degraded by treatment with 50 mM Na_2CO_3 at 60°C for 1 h, after which the solution was neutralized with an equal volume of 100 mM acetic acid. The RNA was isolated by ethanol precipitation and 5′-end labelled by standard techniques (Sambrook et al., 1989) utilizing 40 µCi [γ-^{32}P]ATP (3000 Ci/mmol, Amersham) for 1 µg RNA in 10 µl. Different size classes were separated by electrophoresis on a 8% polyacrylamide gel in TBE (90 mM Tris/borate, pH 8.3, and 1 mM EDTA) with 8 M urea. Oligo(U) was eluted from gel slices in double-distilled water at 60°C for 2 h and recovered by phenol extraction and ethanol precipitation. The size of eluted oligo(U) was determined by electrophoresis on a second gel with RNA size markers.

Metabolic labelling of mt RNAs and UV cross-linking. Endogenous RNA of mt vesicles of *C. fasciculata* was metabolically labelled, essentially as described for *T. brucei* by Harris et al. (1990). The mt fraction (25 µg protein) was incubated in 50 µl buffer (5 mM Hepes, 3 mM potassium phosphate, pH 7.7, 125 mM sucrose, 6 mM KCl, 10 mM $MgCl_2$, 1 mM EDTA, 2 mM 2-mercaptoethanol and 0.1 mM ATP) for 30 min at room temperature to deplete endogenous nucleotide pools. The UTP or GTP concentrations were adjusted to the values given in Fig. 4; 20 µCi [α-^{32}P]UTP or [α-^{32}P]GTP, respectively, were added and the incubation was continued for 30 min at 28°C. The vesicles were collected by centrifugation at 10000×*g* and resuspended in 50 µl STE (250 mM sucrose, 20 mM Tris/HCl, pH 7.9, and 2 mM EDTA). In some experiments, the vesicles were irradiated with UV light as described above, lysed by adding Triton X-100 to 0.5% and treated with RNase A at 40 µg/ml. In other experiments, metabolically labelled gRNAs and 9S and 12S rRNAs were isolated from the vesicles by a gel-purification procedure. The RNA bands were sliced from a 1% low-gelling-temperature agarose gel in TBE with 5 µg/ml ethidium-bromide. The RNA was extracted and purified by standard tech-

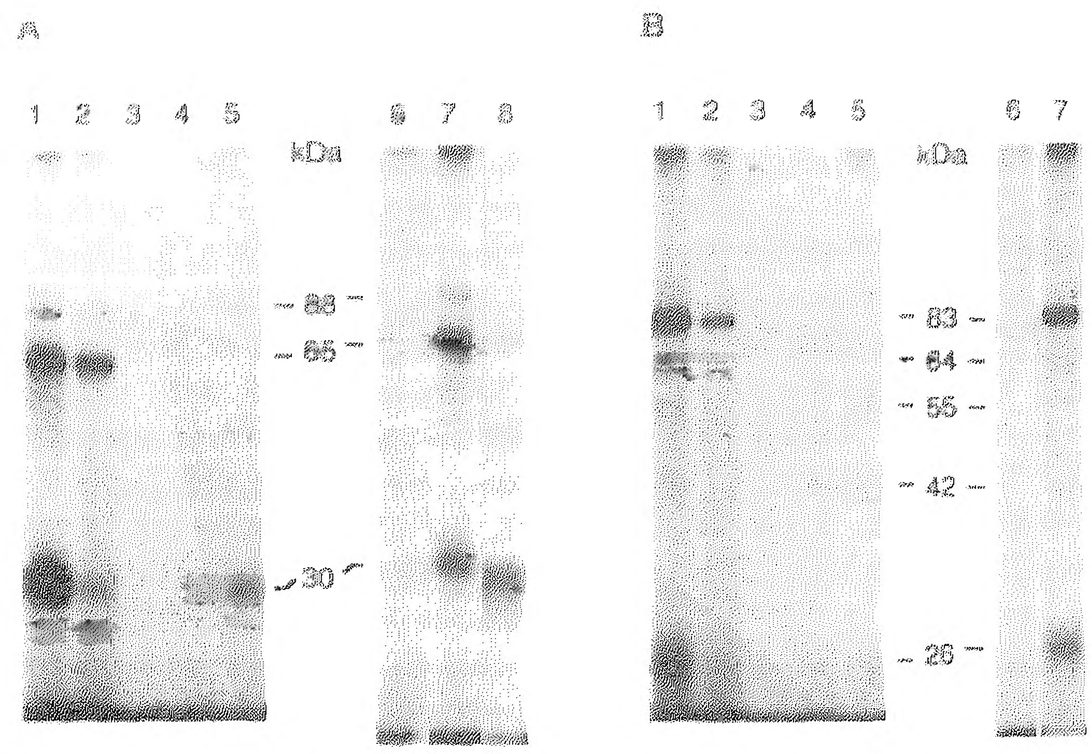

Fig. 1. UV cross-linking of mt proteins to synthetic (g)RNAs. Aliquots of mitochondrial lysate of *C. fasciculata* (A) and *T. brucei* (B) were incubated with radiolabelled synthetic *C. fasciculata* ND7 [FS]gRNA (lanes 1 and 7), ND7 [5′]gRNA (lanes 2), a truncated ND7 [FS]gRNA that has no 3′ U tail (lanes 3), a chimeric molecule of ND7 [FS]gRNA and part of the ND7 pre-mRNA (lanes 4), a fragment of ND7 pre-mRNA (lanes 5) and a vector transcript of 65 nucleotides (lanes 6). (A) Lane 8 ND7 [FS]gRNA was incubated with an aliquot of total cellular extract from *C. fasciculata*. Details of the substrate RNA preparation and sequence and of the UV cross-linking procedure are given in Materials and Methods.

niques (Sambrook et al., 1989), checked by electrophoresis on a denaturing polyacrylamide gel with RNA size markers, and added to a standard UV cross-linking assay. After cross-linking, labelled proteins were analysed as described.

RESULTS

UV cross-linking of mt proteins to synthetic RNA substrates. Recently, UV cross-linking has evolved as a powerful technique to identify RNA-binding proteins (Piñol-Roma et al., 1989). Since our objective is to identify gRNA-binding proteins from mitochondria of *C. fasciculata*, we have applied this method to mt lysates to which synthetic, uniformly radiolabelled gRNA(derivative)s and control RNAs were added, obtained from *in vitro* transcription. UV cross-linking was carried out in the presence of 150 mM KCl to eliminate low-affinity protein-RNA interactions. The cross-linked complexes were treated with RNAse A to minimize the retarding effect of the RNA during gel electrophoresis. For comparison, the experiments were also performed with mt extracts from *T. brucei*.

The results of representative experiments are shown in Fig. 1. In Fig. 1, lanes 1 and 7, cross-linking patterns are shown obtained with a synthetic version of the gRNA involved in the editing of the frameshift region (FS) of *C. fasciculata* NADH dehydrogenase (ND) subunit 7 mRNA (see Van der Spek et al., 1991; Arts et al., 1993). The ND7 [FS]gRNA used measures 73 nucleotides, including a U tail of 23 nucleotides and two G residues at the 5′ end derived from the T7 promotor (see Materials and Methods). With mt lysates of *C. fasciculata*, we detected major cross-linking proteins migrating at 65 kDa and 30 kDa and a minor band at 88 kDa (Fig. 1A). The pattern was different when this (heterologous) gRNA was used in a cross-linking experiment with *T. brucei* mt lysates, however, in which we observed prominent bands of 83 kDa and 26 kDa and minor bands at 64, 55 and 42 kDa (Fig. 1B). Cross-linking patterns were not affected by treatment of the mt lysates with micrococcal nuclease, suggesting that no RNAs other than the added gRNA are required. Cross-linking was abolished, though, by addition to the lysates of 0.1% SDS or proteinase K, demonstrating the involvement of proteins (data not shown).

In order to identify the *cis*-acting elements of the ND7 [FS]gRNA important for the binding to the various proteins, other RNA substrates were tested in the UV cross-linking assay (Fig. 1, lanes 2–5). First, another gRNA was used, i.e. a synthetic version of the gRNA involved in the editing of the 5′ editing region of ND7 mRNA of *C. fasciculata* with an encoded length of 63 nucleotides, including a U tail of 15 residues (see Materials and Methods). This gRNA also cross-links to the *C. fasciculata* 65-kDa and 30-kDa proteins, albeit less efficiently than ND7 [FS]gRNA (Fig. 1A, compare lane 2 to lane 1). Binding by the 88-kDa polypeptide is barely above background. In experiments in which gRNAs with U tails of still shorter length were tested, the 65-kDa *C. fasciculata* protein bound efficiently to gRNAs equipped with a U tail of 7–11 residues (data not shown). Also, the *T. brucei* 83-, 64-, 55-, 42- and 26-kDa polypeptides bind to *C. fasciculata* ND7 [5′]gRNA less efficiently than to [FS]gRNA (Fig. 1B, lane 2). Next, a truncated ND7 [FS]gRNA version that lacks the U tail was made by performing *in vitro* transcription with a [FS] cDNA template restricted by *ApoI*. This enzyme cuts the template strand seven nucleotides upstream of the encoded oligo(U) tail, resulting in a 43-nucleotide product with two U residues at its 3′ end (see Materials and Methods). None of the proteins recognized this gRNA (Fig. 1A and B, lanes 3). Three other RNA substrates used were a chimeric RNA consisting of a [FS]gRNA moiety of 31 nucleotides linked through a 13-nucleotide U stretch to editing site 1 of the frameshift region of a 75-nucleotide ND7 pre-mRNA fragment (see Materials and Methods and Arts et al., 1993); a 625-nucleotide 5′ fragment of ND7 pre-mRNA, which contains the 5′ and [FS] pre-edited regions and is U rich (overall 40% U, containing short stretches of more than 50% U; see Sloof et al., 1987) and an unrelated control RNA of 65 nucleotides that was transcribed from the vector (see Materials and Methods). The 30-kDa and 88-kDa (visible on longer exposure of the autoradiogram) polypeptides from *C. fasciculata* and the 26-kDa protein from *T. brucei* bound weakly to the chimeric RNA (Fig. 1A and B, lanes 4). These proteins also became cross-linked to the ND7 pre-mRNA fragment, as did the 55-kDa and 42-kDa proteins of *T. brucei* (Fig. 1A and B, lanes 5, visible on longer exposure). No proteins could be cross-linked in significant amounts to vector-derived RNA (Fig. 1A and B, lanes 6). These experiments lead to the conclusion that the 65-kDa protein of *C. fasciculata* and the 83-kDa and 64-kDa proteins of *T. brucei* bind specifically to gRNA, provided it has a U tail. The other proteins also require a U tail for binding to gRNA but, in addition, they have affinity for chimeric RNA and/or ND7 pre-mRNA, but not for vector-derived RNA.

Finally, we checked whether the gRNA-binding proteins identified so far in *C. fasciculata* have a mitochondrial localisation by comparing the cross-linking patterns of a mt extract to those of a total cellular extract. The results shown in Fig. 1A, lanes 7 and 8 indeed show a marked decrease in the intensities of the 88-, 65- and 30-kDa bands in the total cellular extract, suggesting that these proteins are of mitochondrial origin. The band in the 30-kDa area obtained with total extract (Fig. 1A, lane 8) stems from a protein different from the mt 30-kDa protein, since it migrates slightly faster and displays a completely different dependence on KCl (results not shown).

Competition experiments. The importance of the oligo(U) tail for interaction between gRNA and proteins is further illustrated by competition experiments. The *in vitro* UV cross-linking assay was performed in the presence of increasing quantities of po-

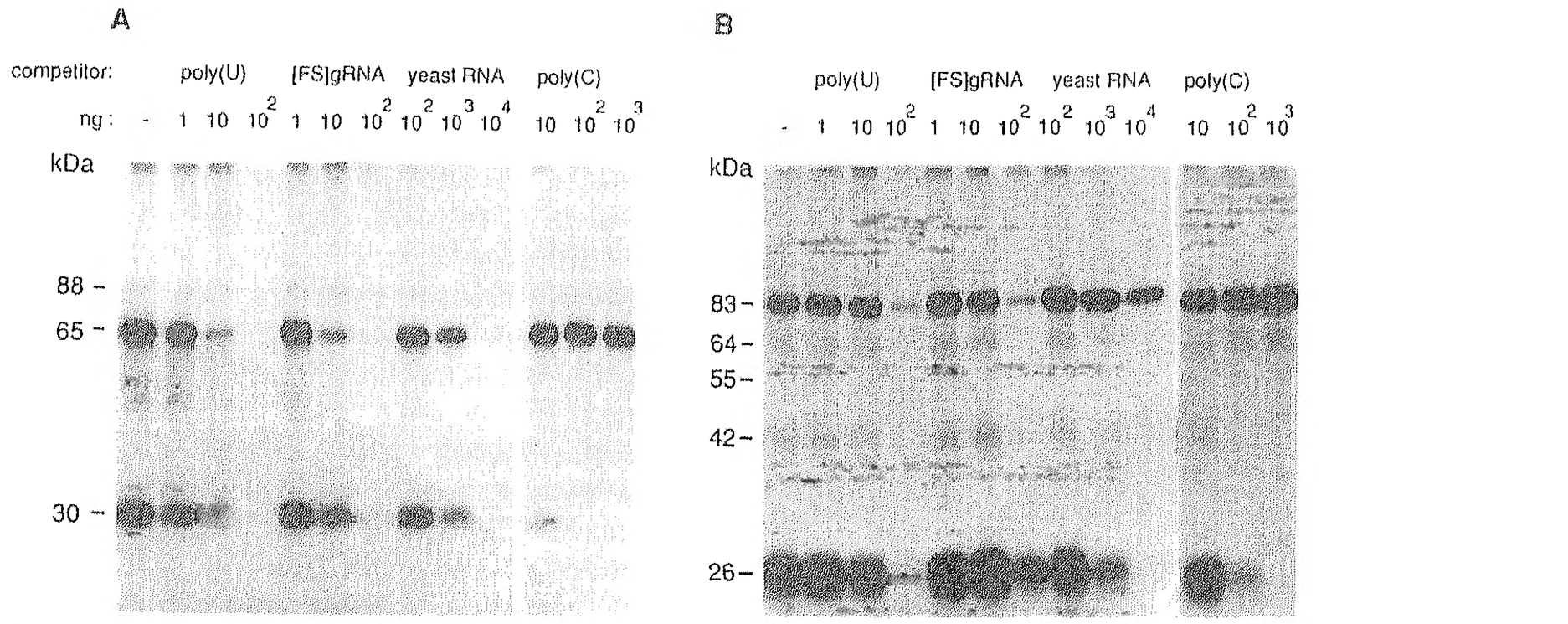

Fig. 2. Competition for ND7 [FS]gRNA cross-linking by poly(U), poly(C) and yeast RNA. Mitochondrial lysates of *C. fasciculata* (A) and *T. brucei* (B) were incubated with 1 ng radiolabelled ND7 [FS]gRNA and increasing amounts of competitor, as indicated. For further details, see Materials and Methods.

ly(U), poly(C), unlabelled ND7 [FS]gRNA or total yeast RNA (Fig. 2) and of poly(A) and poly(G). The addition of poly(U) in a 10-fold excess over labelled gRNA indeed significantly reduced gRNA binding to the 65-kDa protein of *C. fasciculata* (Fig. 2A), comparable to the effect of similar amounts of unlabelled ND7 [FS]gRNA, as determined from quantification with a Phosphorimager apparatus. In contrast, the addition of a 1000-fold excess of other competitor RNAs only had a marginal effect (yeast RNA) or none at all [poly(C)] (Fig. 2A). The effects of the addition of poly(U), unlabelled ND7 [FS]gRNA and yeast RNA on the binding of radiolabelled gRNA to the 30-kDa and the 88-kDa polypeptides of *C. fasciculata* were essentially similar to those observed for the 65-kDa protein, although the results varied slightly between experiments. The effect of poly(C) addition was markedly different, though, since for the 30-kDa and the 88-kDa protein, only 3–10-fold more poly(C) than poly(U) was required to obtain approximately the same reduction of binding. Finally, although poly(A) and poly(G) also behaved as relatively inefficient competitors, substantially smaller amounts of these homopolymers than of total yeast RNA were required for complete inhibition of gRNA binding to any of these proteins (10–20-fold less depending on the experiment, data not shown). This result does not necessarily contrast with the hypothesis that the proteins in question preferentially bind to U stretches, given the fact that both poly(A) and poly(G) can basepair with gRNA U tails, which could interfere with their capacity to interact with proteins.

The effect of addition of the different competitor RNAs in the *T. brucei* system is shown in Fig. 2B. The 83-kDa polypeptide from *T. brucei* appeared to be the counterpart of the *C. fasciculata* 65-kDa protein, since its binding to labelled gRNA was also efficiently competed away by the addition of poly(U) and ND7 [FS]gRNA, albeit that higher amounts of competitor were required, and not by poly(C) or yeast RNA (Fig. 2B). The minor bands of 64-kDa and 55-kDa were affected by the addition of the competing RNAs in a similar fashion. The binding specificity of the 26-kDa and 42-kDa proteins, in contrast, resembled that of the *C. fasciculata* 30-kDa and 88-kDa proteins, the most prominent characteristic being the fact that poly(C) is only a marginally less efficient competitor for gRNA binding than poly(U).

UV cross-linking to oligo(U). From the results obtained so far, we conclude that trypanosome gRNA-binding proteins interact with oligo(U) sequences, albeit with a different degree of specificity. In order to investigate whether oligo(U) by itself is sufficient for binding, the UV cross-linking assay was performed with gel-purified, 5′-end-labelled poly(U) RNA of varying size. The results of this experiment (Fig. 3) demonstrate that the 65-kDa protein from *C. fasciculata* and the 83-kDa and 64-kDa proteins from *T. brucei* efficiently bind to an oligo(U) size class of 23–29 residues or more (Fig. 3, lanes 2–5). The decrease of the signal observed with larger RNA species is most likely due to the fact that the labelled 5′ end of these longer RNAs is not efficiently protected by bound protein against treatment with RNase A. The 30-kDa and the 83-kDa proteins from *C. fasciculata* bound strongly only to oligo$(U)_{39-49}$ (Fig. 3, lane 4), oligo$(U)_{30-38}$ giving a weak signal (Fig. 3, lane 3), while the signal for these proteins also decreases in intensity with longer RNAs. Finally, the *T. brucei* 55-, 42- and 26-kDa proteins displayed weak binding only to oligo$(U)_{39-49}$.

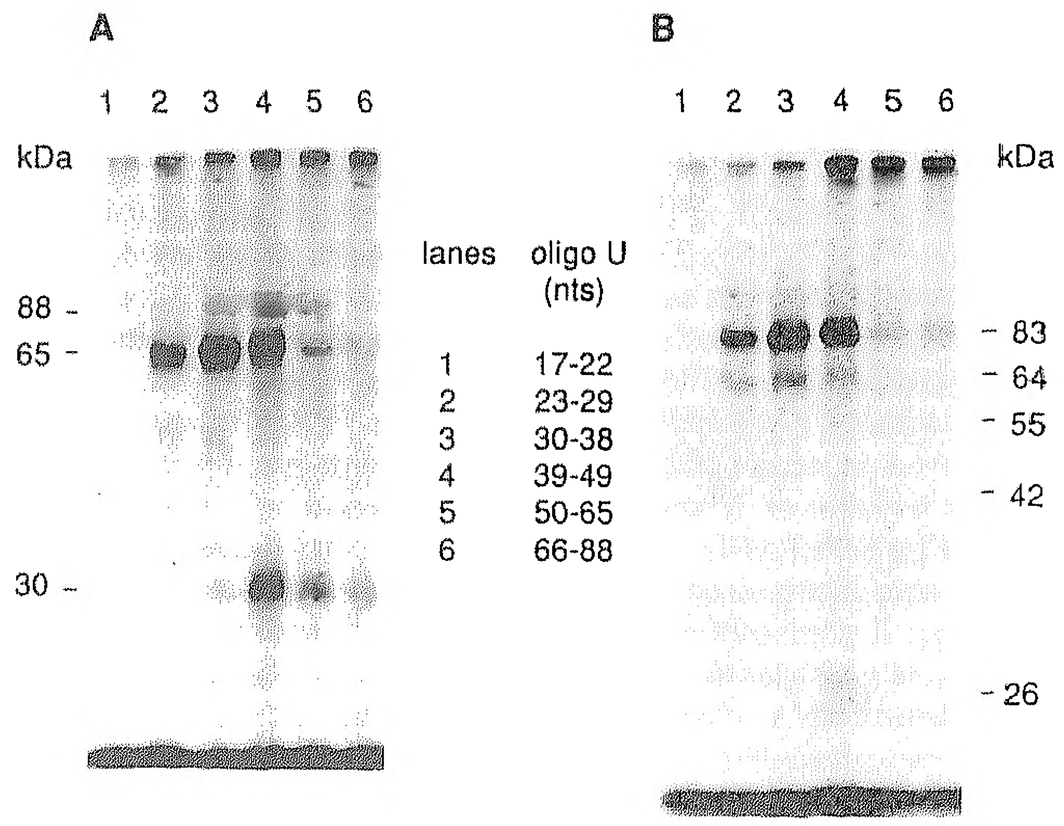

Fig. 3. UV cross-linking with different size classes of oligo(U). Poly(U) was partially degraded by mild alkaline hydrolysis and the resulting oligo(U) molecules were 5′-end labelled. Different size classes of the RNA, as indicated in the figure, were isolated from a denaturing polyacrylamide gel and used in UV cross-linking assays with *C. fasciculata* (A) and *T. brucei* (B) mitochondrial lysates. For further details, see Materials and Methods. nts, nucleotides.

These results show that all candidate oligo(U)-binding proteins can indeed be cross-linked to radiolabelled oligo(U) in the presence of an excess amount of yeast RNA.

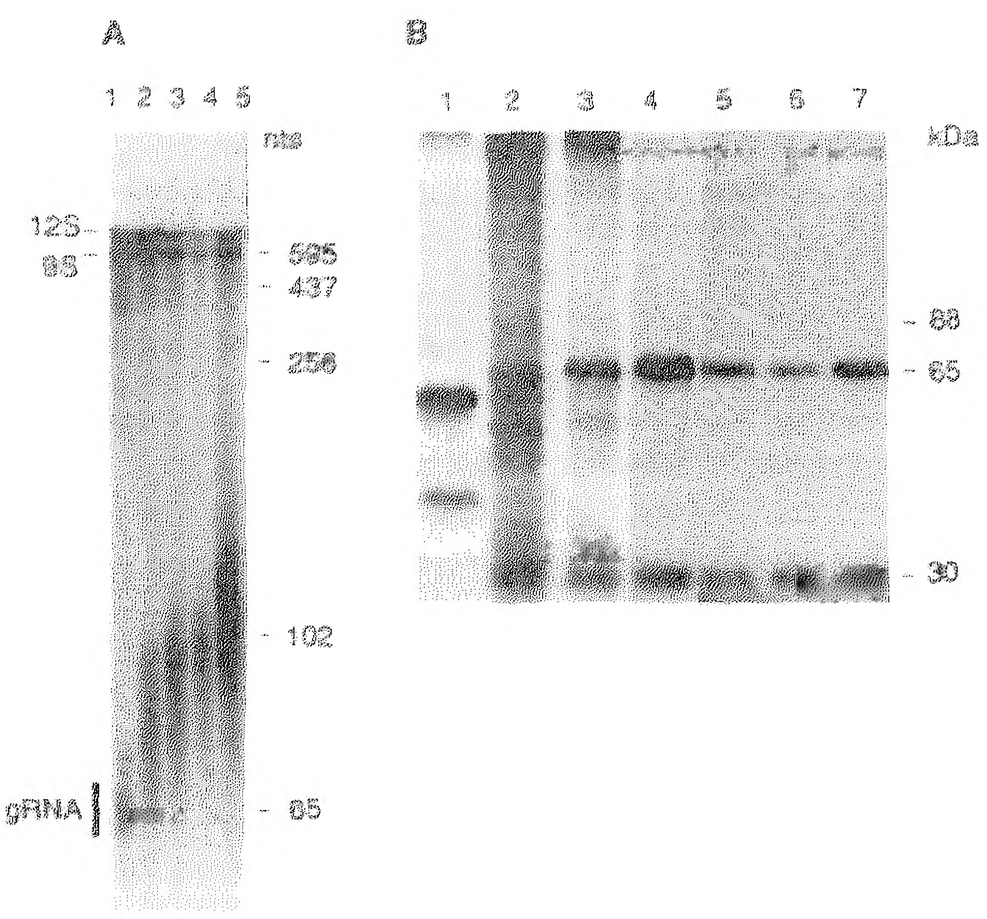

Fig. 4. UV cross-linking to metabolically labelled RNAs. (A) Analysis of metabolically labelled RNA. Purified mitochondrial vesicles from *C. fasciculata* were incubated as described in Materials and Methods, after which a fixed amount of [α-^{32}P]UTP and varying amounts of unlabelled UTP were added and the incubation continued. RNA was isolated and analyzed on a denaturing 8% polyacrylamide gel which was calibrated with marker RNAs, the sizes of which are indicated in nucleotides (nts). The UTP concentrations tested were 0.1, 1, 2, 4 and 8 μM (lanes 1–5, respectively). The positions of 9S, 12S rRNAs and gRNAs are indicated. (B) UV cross-linking. Mitochondrial vesicles of *C. fasciculata* were incubated with 0.1 μM [α-^{32}P]GTP (lane 1) or [α-^{32}P]UTP (lanes 2, 5–7) as described. In lanes 1 and 2, the vesicles were irradiated with UV light, lysed by addition of Triton X-100 to 0.5%, treated with RNAse A and analyzed by SDS/PAGE. In lane 4, a standard cross-linking experiment with *in vitro* synthesized, radiolabelled ND7 [FS]gRNA is shown. In lane 3, equal parts of the incubations of lanes 2 and 4 were mixed to demonstrate comigration of bands. For the experiments shown in lanes 5–7, labelled RNA was isolated from the vesicles by gel-purification procedures as described in Materials and Methods and added to standard cross-linking assay mixtures, in lieu of synthetic gRNA. Lane 5, 12S rRNA; lane 6, 9S rRNA; lane 7, gRNA.

UV cross-linking to endogenous, metabolically labelled mtRNAs. The experiments described thus far have been performed with *in-vitro*-produced gRNAs and other synthetic substrates. In order to establish whether the polypeptides that bind to these gRNAs also bind to endogenous gRNAs and other mtRNAs that possess U tails, we applied the UV cross-linking technique to intact mt vesicles from *C. fasciculata*. RNAs present in these vesicles become labelled by the action of endogenous TUTase when [α-^{32}P]UTP is added after the depletion of the endogenous nucleotide pool by an incubation step, essentially as described by Bakalara et al. (1989) for *L. tarentolae* and Harris et al. (1990) for *T. brucei*. The labelling patterns obtained are shown in Fig. 4A. No labelling of RNA is found with [α-^{32}P]GTP under these conditions, which confirms that transcription is arrested (data not shown). A large part of the label is incorporated into RNA species of 60–120 nucleotides, migrating in a pattern very similar to that of gRNAs from *L. tarentolae*, *T. brucei* and *T. equiperdum* (Bakalara et al., 1989; Harris et al., 1990; Blum and Simpson, 1990; Pollard and Hajduk, 1991). Interestingly, the size of these RNAs (and therefore the length of the U tail added) is proportional to the UTP concentration used (Fig. 4A), suggesting that, *in vivo*, the UTP concentration may be one of the determinants of the length of the U tail of gRNAs. As in the other trypanosomatids, under these conditions two large RNAs which comigrate with mt 9S and 12S rRNA when electrophoresed on a native agarose gel (data not shown), also become labelled. It has indeed been reported that mt 9S and 12S rRNA of *T. brucei* possess a U tail of 11 and 2–17 residues, respectively (Adler et al., 1991).

To investigate whether mt proteins are associated with the labelled RNAs, the vesicles were irradiated with UV light, lysed with Triton and treated with RNase A followed by gel electrophoresis and autoradiography (Fig. 4B, lane 2). For comparison, proteins UV cross-linked to synthetic ND7[FS]gRNA in our standard assay system were electrophoresed in Fig. 4B lane 4, whereas in lane 3, samples as applied to lanes 2 and 4 were mixed. The results demonstrate that the 88-, 65- and 30-kDa proteins become labelled by this procedure. Slight shifts in the electrophoretic mobility observed when comparing lanes 2 and 4 (Fig. 4B) are due to differences in salt concentrations of the samples (Fig. 4B, lane 3). A third prominent band of 60-kDa was also labelled when [α-^{32}P]GTP was used (Fig. 4B, lane 1) and already present when the RNA was not treated with RNase A (not shown). This band probably represents a nucleotide-binding protein. A fourth band of approximately 54-kDa was not formed reproducibly. Finally, gel-purified metabolically labelled RNAs were added to standard assay systems. As shown in Fig. 4B lane 7, *C. fasciculata* proteins of 88 (visible upon long exposure of the autoradiogram), 65 and 30-kDa can indeed be UV cross-linked to gRNA isolated from the 60–80-nucleotide region of the gel obtained from metabolic labelling at the lowest UTP concentration (see Fig. 4B, lane 1). However, the same bands are radioactively labelled when RNAs isolated from the 12S and 9S region were added (Fig. 4B, lanes 5 and 6), indicating that these proteins also have affinity for the mt rRNAs (see discussion).

DISCUSSION

Proteins in mt extracts from *C. fasciculata* and *T. brucei* that bind to oligo(U). We have studied the binding specificity of proteins of 88, 65 and 30 kDa from mitochondria of *C. fasciculata* and of 83, 64, 55, 42 and 26 kDa from *T. brucei* that can be UV cross-linked to synthetic gRNAs from *C. fasciculata*. The results clearly show that the 65-kDa protein of *C. fasciculata* and the 83-kDa and 64-kDa proteins of *T. brucei* are oligo(U)-binding proteins and that short stretches of U are sufficient for binding (Figs. 1–3). Moreover, the failure of these proteins to bind to chimeric gRNA:pre-mRNA, in spite of the presence of an internal stretch of 13 U residues (Fig. 1), suggests that the U residues must have a 3′-terminal location. In addition, we showed that the *C. fasciculata* 65-kDa protein efficiently cross-links to 12S and 9S mitoribosomal RNAs that were post-transcriptionally labelled by incubating mt vesicles with [α-^{32}P]UTP (Fig. 4). It has been reported that mt 9S and 12S rRNA from *T. brucei* possess 3′ terminal U tails of 11 nucleotides and 2–17 residues, respectively (Adler et al., 1991) and, in *C. fasciculata*, tails of a similar length can be expected. The length of the tails of the rRNAs that we used in the experiment was not measured, but it is most likely not dissimilar from that *in vivo*, considering the fact that low UTP concentrations were used in the labelling procedure that did result in gRNAs of normal size (see Fig. 4A, lane 1). Together, these observations strongly suggest that the presence of a short 3′-terminal U tail is by itself sufficient for binding of this class of proteins to an RNA and that no other sequences are involved.

The RNA-binding specificities and efficiencies of the 65-kDa protein of *C. fasciculata* and the 83-kDa protein of *T. brucei*

are very similar, making it attractive to assume that they are homologues. If so, their different size is somewhat surprising given the overall similarity of the editing processes in these closely related trypanosomes (for evolutionary distance between trypanosomatids, see Fernandes et al., 1993; Landweber et al., 1994; Maslov et al., 1994; Lukes et al., 1994). Interestingly, the *T. brucei* protein of 64-kDa has binding characteristics identical to those of the 83-kDa protein, although the amount of cross-linked protein is considerably lower. These observations could reflect species-specific differences in the number and size of these oligo(U)-binding proteins, but it could also be hypothesized that in both trypanosomes a shorter version is generated by proteolysis of a longer form with a considerable species-specific difference in the extent of the cleavage reaction. If so, it is not likely that the 88-kDa protein of *C. fasciculata* is the longer form of the 65-kDa protein, given its rather different binding specificity. Instead, one would have to assume that the long form is virtually completely cleaved in this organism. Detailed characterisation and (gene)sequence analysis of all the relevant proteins would be required, however, to settle this issue.

Also, the *C. fasciculata* 88-kDa and 30-kDa proteins and the *T. brucei* 26-kDa protein bind to gRNAs with a U tail and to oligo(U), although longer U stretches are required for efficient binding (Figs. 1 and 3). In addition, they bind to other RNAs provided that they are U rich. The ensuing suggestion that U residues, albeit not necessarily 3′-terminally located, are essential for binding of RNA to these proteins also, is supported by the competition experiments shown in Fig. 2. Clearly, however, they are a bit more promiscuous in their binding specificity since poly(C) is an only slightly less efficient competitor than poly(U). Finally, most of the binding characteristics of the *T. brucei* 55-kDa and 42-kDa proteins resemble that of the 26-kDa protein. It is difficult, however, to assess their binding specificity with more precision, due to the fact that the amounts of these proteins that can be cross-linked are rather low and the intensity of the signals varies between experiments (compare Figs 1 and 2).

Proteins that bind to homologous *T. brucei* gRNAs. The *T. brucei* proteins described in this paper that have a high affinity for (heterologous) *C. fasciculata* gRNAs, almost certainly correspond to proteins of similar size that have been recently identified by other groups as high-affinity gRNA-binding proteins in assays utilizing homologous *T. brucei* gRNAs. For example, there can be little doubt that our 83-kDa protein is identical to the 90-kDa protein described by Read et al. (1994) and Köller et al. (1994), the difference in the estimated size resulting from differences in the gel systems used. Like the 83-kDa protein, the 90-kDa protein strongly binds to gRNA at high KCl concentrations, its binding depends on the presence of a U tail and poly(U) is an efficient competitor. The fact that identical results can be obtained with heterologous *C. fasciculata* gRNAs lend further support to the assumption that the U tail by itself is both essential and sufficient for binding of a gRNA to this protein. The suggestion made by Köller et al. (1994) that a tail of one U residue would suffice for binding to the 90-kDa and other proteins is not supported by our data, however, because a truncated *C. fasciculata* ND7[FS]gRNA that has two U residues at its 3′ end does not bind. It could be possible that the truncated gRNA of 43 nucleotides that we used is too small to be recognized, but we consider this to be unlikely given the fact that oligo(U) of 23–29 nucleotides, is already efficiently bound. The apparent discrepancy may result from the fact that Köller et al. (1994) used an ill-defined gRNA preparation, obtained by reducing the UTP concentration in the *in vitro* synthesis reaction mixtures, in which the presence of gRNA species with longer U tails was not rigourously excluded.

In the lower molecular-mass range, Read et al. (1994) and Köller et al. (1994) find high-affinity gRNA-binding proteins with sizes and binding characteristics similar to those of our 64-, 55- and 42-kDa proteins. It is not immediately obvious, however, that our 26-kDa protein corresponds to the 21-kDa protein of Köller et al. (1994) and the 25-kDa protein of Read et al.(1994). Although in all cases the protein is the major high-affinity gRNA-binding protein in that size range, differences in binding specificity appear to exist. For example, the other groups report that the binding of gRNA to the 21-kDa and 25-kDa proteins is only marginally affected by the removal of the gRNA U tail or not at all, which is in contrast with our finding that the protein does not bind to a tailless ND7[FS]gRNA. In the hands of Köller et al. (1994), nevertheless, poly(U), but not poly(A), is still an efficient competitor, which is essentially what we found for the 26-kDa protein. Although we cannot exclude the possibility that we are dealing with different proteins, we prefer the view that the use of gRNAs with a different sequence and a considerable difference in (tail) length may account for most of the apparent discrepancies: whereas Köller et al. (1994) used a 62-nucleotide *T. brucei* ATPase subunit 6 gRNA with 3–9 U residues at the 3′ end, we used a 50-nucleotide *C. fasciculata* ND7 [FS]gRNA with 23 U residues. Most of the data could be explained by assuming that the short U tail of the ATP6 gRNA is not essential for the formation of the binding motif recognized by this protein and that other, as yet unidentified, pyrimidine-rich regions can take its place. In line with this, our 26-kDa protein also binds to RNAs that do not possess long homopolymeric U stretches (Fig. 1 B); it binds to oligo(U) rather weakly (Fig. 3) and it also has affinity for poly(C) (Fig. 2). Clearly, more work is required to identify with more precision the RNA sequence elements that determine the binding of this protein.

Concluding remarks. Evidently, affinity for gRNA U stretches is, by itself, no guarantee that the proteins described in this work have a role in the editing process and more experimental evidence is required. Interestingly, glycerol gradient analysis of mt extracts from *C. fasciculata* indicates that the 30-kDa and 65-kDa proteins are present in high molecular-mass complexes, which also contain gRNA but no rRNA (data not shown). It has further been reported that the *T. brucei* 25-kDa and 90-kDa proteins associate with gRNP complexes *in vitro* (Read et al., 1994). Oligo(U)-binding proteins therefore appear to be part of large, gRNA-containing (editosomal?) complexes. In addition, it should be emphasized that if the editing machinery contains proteins that recognize all gRNAs, the U tail is likely to be at least a part of the binding site since it is the only sequence element that gRNAs have in common. All these observations make the trypanosomatid oligo(U)-binding mt proteins prime candidates for further investigation. One of our current research projects is, therefore, to purify and further characterize these proteins and the mt components (proteins/RNAs) with which they interact.

We thank Gert Jan Arts, Daniël Blom, Janny van den Burg, Paulette Groenevelt, Annett de Haan, Paul Sloof and Rob Wolthuis for their contributions at various stages of the work and for stimulating discussions. The research is supported by the Netherlands Foundation for Chemical Research (SON) and the Foundation for Medical and Health Research (MW), which are subsidized by the Netherlands Foundation for Scientific Research (NWO).

REFERENCES

Adler, B. K., Harris, M. E., Bertrand, K. I. & Hajduk, S. L. (1991) Modification of Trypanosoma brucei mitochondrial rRNA by post-

transcriptional 3′ polyuridine tail formation, *Mol. Cell. Biol. 11*, 5878–5884.

Arts, G. J., Van der Spek, H., Speijer, D., Van den Burg, J., Van Steeg, H., Sloof, P. & Benne, R. (1993) Implications of novel guide RNA features for the mechanism of RNA editing in *Crithidia fasciculata*, *EMBO J. 12*, 1523–1532.

Bakalara, N., Simpson, A. G. & Simpson, L. (1989) The Leishmania kinetoplast mitochondrion contains terminal uridyl-4-transferase and RNA ligase activities, *J. Biol. Chem. 264*, 18679–18686.

Benne, R. (1994) RNA editing in trypanosomes, *Eur. J. Biochem. 221*, 9–23.

Birkenmeyer, L. & Ray, D. S. (1986) Replication of kinetoplast DNA in isolated kinetoplasts from *Crithidia fasciculata*, *J. Biol. Chem. 261*, 2362–2368.

Blum, B., Bakalara, N. & Simpson, L. (1990) A model for RNA editing in kinetoplast mitochondria: 'guide' RNA molecules transcribed from maxicircle DNA provide the edited information, *Cell 60*, 189–198.

Blum, B. & Simpson, L. (1990) Guide RNAs in kinetoplast mitochondria have a nonencoded 3′ oligo(U) tail involved in recognition of the preedited region, *Cell 62*, 391–397.

Blum, B., Sturm, N. R., Simpson, A. M. & Simpson, L. (1991) Chimeric gRNA-mRNA molecules with oligo(U) tails covalently linked at sites of RNA editing suggest that U addition occurs by transesterification, *Cell 65*, 543–550.

Blum, B. & Simpson, L. (1992) Formation of gRNA/mRNA chimeric molecules *in vitro*, the initial step of RNA editing, is dependent on an anchor sequence, *Proc. Natl Acad. Sci. USA 89*, 11944–11948.

Cech, T. R. (1991) RNA editing: world's smallest introns? *Cell 64*, 667–669.

Feagin, J. E., Jasmer, D. P. & Stuart, K. (1987) Developmentally regulated addition of nucleotides within apocytochrome b transcripts in *Trypanosoma brucei*, *Cell 49*, 337–345.

Fernandes, A. P., Nelson, K. & Beverley, S. M. (1993) Evolution of nuclear ribosomal RNAs in kinetoplastid protozoa: Perspectives on the age and origins of parasitism, *Proc. Natl Acad. Sci. USA 90*, 11608–11612.

Göringer, H. U., Koslowsky, D. J., Morales, T. & Stuart, K. (1994) The formation of mitochondrial ribonucleoprotein complexes involving guide RNA molecules in Trypanosoma brucei, *Proc. Natl Acad. Sci. USA 91*, 1776–1780.

Hajduk, S. L., Harris, M. E. & Pollard, V. W. (1993) RNA editing in kinetoplastid mitochondria, *FASEB J. 7*, 54–63.

Harris, M. E., Moore, D. R & Hajduk, S. L. (1990) Addition of uridines to edited RNAs in trypanosome mitochondria occurs independently of transcription, *J. Biol. Chem. 265*, 11368–11376.

Harris, M., Decker, C., Soliner-Webb, B. & Hajduk, S. (1992) Specific cleavage of pre-edited mRNAs in trypanosome mitochondrial extracts, *Mol. Cell. Biol. 12*, 2591–2598.

Harris, M. E. & Hajduk; S. L. (1992) Kinetoplastid RNA editing: in vitro formation of cytochrome b gRNA-mRNA chimeras from synthetic substrate RNAs, *Cell 68*, 1091–1099.

Hoeijmakers, J. H. J., Snijders, A., Jansen, J. W. G. & Borst, P. (1981) Transcription of kinetoplast DNA in *Trypanosoma brucei* bloodstream and culture forms, *Plasmid 5*, *329–350*.

Kleisen, C. M., Borst, P. & Weijers, P. J. (1975) Properties of the intact multi-circular complex from *Crithidia luciliae*, *Biochim. Biophys. Acta 390*, 155–167.

Köller, J., Nörskau, G., Paul, A. S., Stuart, K. & Göringer, H. U. (1994) Different *Trypanosoma brucei* guide RNA molecules associate with an identical complement of mitochondrial proteins *in vitro*, *Nucleic Acids Res. 22*, 1988–1995.

Koslowsky, D. J., Göringer, H. U., Morales, T. & Stuart, K. (1992) *In vitro* guide RNA/mRNA chimaera formation in *Trypanosoma brucei* RNA editing, *Nature 356*, *807–809*.

Landweber, L. F. & Gilbert, W. (1994) Phylogenetic analysis of RNA editing: A primitive genetic phenomenon, *Proc. Natl Acad. Sci. USA 91*, 918–921.

Lukes, J., Arts, G. J., Van den Burg, J., De Haan, A., Opperdoes, F. Sloof, P. & Benne, R. (1994) Novel pattern of editing regions in mitochondrial transcripts of the cryptobiid *Trypanoplasma borreli*. *EMBO J. 13*, 5086–5098.

Maslov, D. A., Avila, H. A., Lake, J. A. & Simpson, L. (1994) Evolution of RNA editing in kinetoplastid protozoa, *Nature 368*, 345–348.

Peris, M., Frech, G. C., Simpson, A. M., Bringaud, F., Byrne, E., Bakker, A. & Simpson, L. (1994) Characterization of two classes of ribonucleoprotein complexes possibly involved in RNA editing from *Leishmania tarentolea* mitochondria, *EMBO J. 13*, 1664–1672.

Piñol-Roma, S., Adam, S. A., Choi, Y. D. & Dreyfuss, G. (1989) Ultraviolet-induced cross-linking of RNA to proteins *in vivo*, *Methods Enzymol. 180*, 410–418.

Pollard, V. W., Rohrer, S. P., Michelotti, E. F., Hancock, K. & Hajduk, S. L. (1990) Organization of minicircle genes for guide RNAs in *Trypanosoma brucei*, *Cell 63*, 783–790.

Pollard, V. W. & Hajduk, S. L. (1991) *Trypanosoma equiperdum* minicircles encode three distinct primary transcripts which exhibit guide RNA characteristics, *Mol. Cell. Biol. 11*, 1668–1675.

Pollard, V. W., Harris, M. E. & Hajduk, S. L. (1992) Native mRNA editing complexes from *Trypanosoma brucei* mitochondria, *EMBO J. 11*, 4429–4438.

Read, L. K., Corell, R. A. & Stuart, K. (1992) Chimeric and truncated RNAs in trypanosoma brucei suggest transesterifications at non-consecutive sites during RNA editing, *Nucleic Acids Res. 20*, 2341–2347.

Read, L. K., Göringer, H. U. & Stuart, K. (1994) Assembly of mitochondrial ribonucleoprotein complexes involves specific guide RNA (gRNA)-binding proteins and gRNA domains but does not require preedited mRNA, *Mol. Cell. Biol. 14*, 2629–2639.

Sambrook, J., Fritsch, E. F. & Maniatis, T. (1989) *Molecular cloning: a laboratory manual*, 2nd edn, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

Simpson, L. & Shaw, J. M. (1989) RNA editing and the mitochondrial cryptogenes of kinetoplast protozoa, *Cell 57*, 355–366.

Simpson, A. M., Bakalara, N. & Simpson, L. (1992) A ribonuclease activity is activated by heparin or by digestion with proteinase K in mitochondrial extracts of *Leishmania tarentolae*, *J. Biol. Chem. 267*, 6782–6788.

Simpson, L., Maslov, D. & Blum, B. (1993) in *RNA editing, the alteration of protein coding sequences of RNA* (Benne, R., ed.) pp. 53–85, Ellis Horwood, Chichester, UK.

Sloof, P., Van den Burg, J., Voogd, A. & Benne, R. (1987) The nucleotide sequence of a 3.2 kb segment of mitochondrial maxicircle DNA from *Crithidia fasciculata* containing the gene for cytochrome oxidase subunit III, the N-terminal part of the apocytochrome b gene and a possible frameshift gene; further evidence for the use of unusual initiator triplets in trypanosome mitochondria, *Nucleic Acids Res. 15*, 51–65.

Stuart, K. (1991) RNA editing in mitochondrial mRNA of trypanosomatids, *Trends Biochem. Sci. 16*, 68–72.

Stuart, K. (1993) The RNA editing process in *Trypanosoma brucei*, *Sem. Cell Biol. 4*, 251–260.

Sturm, N. R. & Simpson, L. (1990) Kinetoplast DNA minicircles encode guide RNAs for editing of cytochrome oxidase subunit-III messenger RNA, *Cell 61*, 879–884.

Sturm, N. R. & Simpson, L. (1991) *Leishmania tarentolae* minicircles of different sequence classes encode single guide RNAs located in the variable region approximately 150 bp from the conserved region, *Nucleic Acids Res. 19*, 6277–6281.

Van der Spek, H., Arts, G. J., Zwaal, R. R., Van den Burg, J., Sloof, P. & Benne, R. (1991) Conserved genes encode guide RNAs in mitochondria of *Crithidia fasciculata*, *EMBO J. 10*, 1217–1224.