

Argonaute Protein in the Early Divergent Eukaryote *Trypanosoma brucei*: Control of Small Interfering RNA Accumulation and Retroposon Transcript Abundance

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Members of the Argonaute protein family have been linked through a combination of genetic and biochemical studies to RNA interference (RNAi) and related phenomena. Here, we describe the characterization of the first Argonaute protein (AGO1) in *Trypanosoma brucei*, the earliest divergent eukaryote where RNAi has been described so far. AGO1 is predominantly cytoplasmic and is found in a ribonucleoprotein particle with small interfering RNAs (siRNAs), and this particle is present in a soluble form, as well as associated with polyribosomes. A genetic knockout of *AGO1* leads to a loss of RNAi, and concomitantly, endogenous retroposon-derived siRNAs as well as siRNAs derived from transgenic double-stranded RNA are reduced to almost undetectable levels. Furthermore, AGO1 deficiency leads to an increase in retroposon transcript abundance via mechanisms operating at the transcriptional level and at the RNA stability level. Our results suggest that AGO1 function is required for production and/or stabilization of siRNAs and provide the first evidence for an Argonaute protein being involved in the regulation of retroposon transcript levels.

In a variety of eukaryotic organisms the introduction of synthetic double-stranded RNA (dsRNA), or the production of dsRNA from transgenes, transposons, viruses, or transgenic gene arrays, induces silencing of cognate genes (8, 19). Originally, the term RNA interference (RNAi) was introduced to indicate the experimental application of synthetic or transgene-derived dsRNA to down regulate a gene of interest (11). However, it has become evident that proteins involved in RNAi also function in other dsRNA-dependent gene silencing pathways operating at both the transcriptional and the post-transcriptional levels. The hallmarks of RNAi and related phenomena are small RNAs of approximately 21 to 26 nucleotides (nt), named small interfering RNAs (siRNAs), which, in association with protein factors, function as guides to trigger degradation of target transcripts (19). The search for proteins involved in RNAi through a combination of genetic and biochemical analyses has uncovered two gene families that appear to be ancient and evolutionarily conserved, namely, Dicer and Argonaute (4, 8). Whereas Dicer, an RNase III-related enzyme, is required for processing of the dsRNA to siRNAs, members of the Argonaute family have yet to be assigned a biochemical function(s).

The Argonaute gene family was first defined in *Arabidopsis thaliana* through a genetic screen (3), and proteins belonging to this family are characterized by the presence of two motifs: a PAZ domain found near the middle of the protein and a Piwi domain located close to the C terminus of the protein (6). Whereas the PAZ domain is poorly conserved, the 300-amino-acid Piwi domain of unknown function displays a high degree of similarity among Argonaute family members (4). The ge-

nomes of most multicellular organisms code for several Argonaute proteins. For instance, in *Drosophila melanogaster* there are four characterized Argonaute genes, namely, *AGO1*, *AGO2*, *Piwi*, and *Aubergine*, all of which have been implicated in RNAi and related silencing phenomena, and a fifth Argonaute member of unknown function was predicted from genomic DNA (4). In *Arabidopsis*, the Argonaute family consists of 10 members, but only three have been studied in detail, and *Caenorhabditis elegans* has more than 20 predicted Argonaute-like genes. In contrast to the complexity of AGO gene families in multicellular organisms, the genomes of single-cell eukaryotes analyzed so far encode one (*Schizosaccharomyces pombe* and *Tetrahymena thermophila*) or two (*Neurospora crassa*) Argonaute genes.

Despite the lack of a biochemical function(s) for Argonaute proteins, phenotypic analysis has implicated members of this family in a wide variety of biological processes, including silencing phenomena. For instance, RDE-1 is required for RNAi in *C. elegans* (13), QDE-2 is essential for quelling (posttranscriptional gene silencing) in *N. crassa* (5), and AGO1 and AGO2 are essential for RNAi in *Drosophila* (18, 35). At present the precise function of these proteins in the RNAi pathway remains to be elucidated, but it is known that mutations in RDE-1 or QDE-2 do not affect the accumulation of siRNAs (5, 28), and *Drosophila* AGO1 is not required for the generation of siRNAs in vitro (35). Silencing phenomena linked to Argonaute proteins include transcriptional and post-transcriptional gene silencing in *Drosophila* (27) and programmed gene rearrangements in *Tetrahymena* (24). Furthermore, RNAi genes in fission yeast, including the single member of the Argonaute family, have been shown to be required for epigenetic gene silencing at centromeres (33), the initiation of heterochromatin formation at the silent mating type region (15), and chromosome dynamics during mitosis and meiosis

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TABLE 1. Down regulation of AGO1 leads to a decrease in RNAi

AGOT7 cell line	% FAT cells at day of growth:			
	1	2	3	4
-TET	56	40	39	40
+TET	10	4	5	2

the protein. The very 5' end of the gene consists of five 33-nt direct repeats, and translation of these direct repeats results in a region rich in arginine and glycine residues with several arginine-glycine-glycine (RGG) repeats (Fig. 1).

AGO1 is required for RNAi. To investigate whether the *AGO1* gene product functions in the RNAi pathway, we inserted a portion of the *AGO1* coding region in the vector pZJM between opposing and TET-inducible T7 RNA polymerase promoters (34) and generated the stable cell line AGOT7. Upon induction with TET, the *AGO1* mRNA declined in abundance, without any noticeable effects on cell viability (data not shown). We then tested for RNAi by assaying the ability of dsRNA corresponding to the α -tubulin gene to produce the FAT phenotype (cells with multiple nuclei, flagella, and mitochondrial genomes [27]) following electroporation into uninduced and TET-induced cells. By the use of nonsaturating amounts of α -tubulin dsRNA, approximately 39 to 56% of the cells became FAT in the uninduced culture (Table 1). In contrast, the percentage of FAT cells was significantly decreased in induced AGOT7 cells, with only 10 and 2% of the cells exhibiting the FAT phenotype following 1 and 4 days of induction, respectively. From this we concluded that the *T. brucei* *AGO1* gene was likely to be required for the RNAi response.

To begin to examine the role that AGO1 plays in RNAi in *T. brucei*, we next generated a cell line deficient in the *AGO1* gene. We deleted both alleles by homologous recombination with PCR-generated cassettes, encoding either the BSR or the hygromycin resistance marker gene (30). As expected, we were not able to detect either the *AGO1* mRNA (Fig. 2B, lane 2) or the protein in *ago1*^{-/-} cells (Fig. 2C, lane 2). Confirming our results above (Table 1), *ago1*^{-/-} cells did not respond to challenge with α -tubulin dsRNA, i.e., the mRNA remained intact (Fig. 2D, lane 4), and no FAT phenotype was apparent following electroporation of different amounts of α -tubulin dsRNA (data not shown). These results were consistent with an essential role of the AGO1 protein in the RNAi pathway.

To validate the notion that the loss of RNAi was a specific effect of AGO1 elimination, we reintroduced a copy of the *AGO1* gene into *ago1*^{-/-} cells. By a combination of PCR and restriction fragment assembly we generated a complementation cassette designed to integrate by homologous recombination at one of the two *ago1* knockout alleles (Fig. 2A). Thus, a restriction fragment harboring the cassette was electroporated into *ago1*^{-/-} cells and Neo^r cells were selected. The resulting cells were shown to express AGO1 mRNA, which is slightly smaller than that in wild-type cells due to a different and shorter 3' untranslated region (UTR) (Fig. 2B, lane 3), as well as AGO1 protein (Fig. 2C, lane 3). Importantly, the levels of both AGO1 mRNA and protein were comparable in the complemented and wild-type cells. When the complemented cells were challenged with α -tubulin dsRNA, the RNAi response

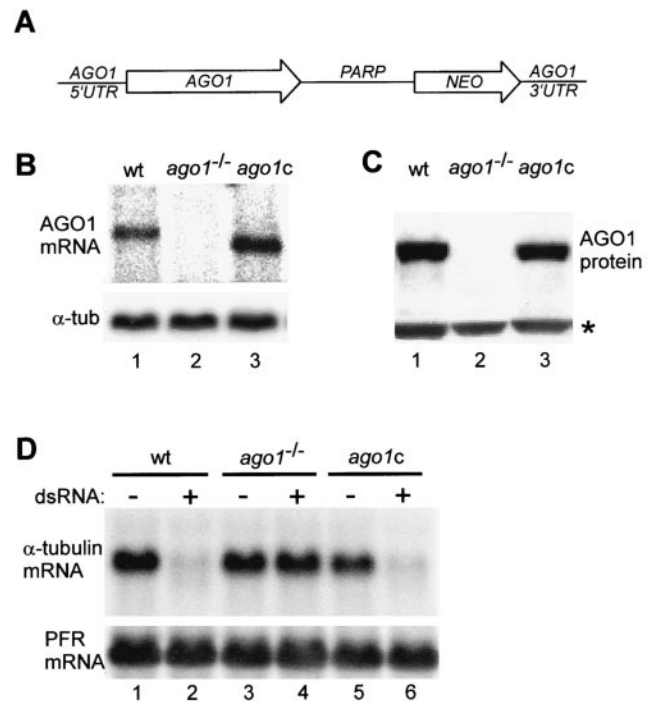


FIG. 2. The *AGO1* gene is essential for RNAi. (A) Schematic representation of the complementation cassette, which contains in a 5'-to-3' direction 330 nt of *AGO1* 5'-flanking sequences including processing signals for 5'-end formation of the *AGO1* mRNA (*AGO1* 5'UTR), the *AGO1* open reading frame of 2,712 bp (*AGO1*), the procyclic acidic repetitive protein intergenic region of 990 bp (*PARP*), the neomycin resistance gene (*NEO*), and finally 780 bp of *AGO1* 3'-flanking sequences (*AGO1* 3'UTR). (B) Northern blot analysis. RNA isolated from wild-type cells (wt; lane 1), *AGO1*-knockout cells (*ago1*^{-/-}; lane 2), and *ago1*^{-/-} cells complemented with the *AGO1* gene (*ago1c*; lane 3) was probed for *AGO1* mRNA (upper panel). α -Tubulin mRNA served as a control for RNA recovery and loading (lower panel). (C) Western blot. Total cell extracts from wild-type cells (wt; lane 1), *AGO1*-knockout cells (*ago1*^{-/-}; lane 2), and *ago1*^{-/-} cells complemented with the *AGO1* gene (*ago1c*; lane 3) were analyzed by Western blotting for the level of AGO1 protein by using anti-AGO1 polyclonal antibodies. An immunologically cross-reacting protein was used as a loading control (indicated by an asterisk). (D) Assay for RNAi. Wild-type cells (wt; lanes 1 and 2), *AGO1*-knockout cells (*ago1*^{-/-}; lanes 3 and 4), and *ago1*^{-/-} cells complemented with the *AGO1* gene (*ago1c*; lanes 5 and 6) were challenged with poly(dI-dC) (lanes 1, 3, and 5) or α -tubulin dsRNA (lanes 2, 4, and 6), and the level of α -tubulin mRNA was monitored by Northern blotting (upper panel). Paraflagellar rod (PFR) mRNA served as a control for RNA recovery and loading (lower panel).

was restored, since the α -tubulin mRNA was degraded (Fig. 2D, lane 6), and the FAT phenotype was manifested in the majority of the cells (data not shown). Taken together, these results unequivocally established an essential role for AGO1 in the *T. brucei* RNAi pathway.

AGO1 is cytoplasmic and is found both soluble and cosedimenting with polyribosomes. To analyze the cellular distribution of AGO1, we epitope tagged the AGO1 protein by inserting in the N-terminal RGG domain of the complementation cassette either a BB2 tag (BB2-AGO1) or a triple tag (TAP-AGO1), namely, the BB2 tag followed by the TAP tag, consisting of two protein A domains and a calmodulin binding domain (29). After transfection of the corresponding con-

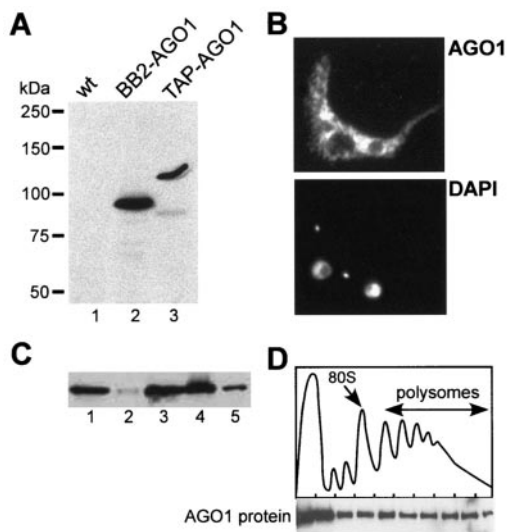


FIG. 3. Cellular localization of AGO1. (A) Western blot with anti-BB2 antibodies of extracts from wild-type (lane 1), BB2-tagged AGO1 (lane 2), and TAP-tagged AGO1 (lane 3) cells. (B) Cells expressing TAP-tagged AGO1 were processed for indirect immunofluorescence as described previously (26) by staining with a rabbit anti-protein A antibody (subpanel AGO1). DNA was stained with 4',6'-diamidino-2-phenylindole (subpanel DAPI). The small dots represent the kinetoplast DNA. (C) Western blot of TAP-tagged AGO1 with a rabbit anti-protein A polyclonal antibody of equivalent amounts of total extract (lane 1), postnuclear pellet (lane 2), supernatant (lane 3), S100 fraction (lane 4), and ribosomal pellet (lane 5). (D) Sucrose density gradient analysis of a cytoplasmic extract from *T. brucei* cells expressing TAP-tagged AGO1 (9). The upper panel shows the absorbance profile at 254 nm, and the positions of the 80S monosome and polyribosomes are indicated. The lower panel shows a Western blot analysis of the sucrose density gradient fractions using a rabbit anti-protein A polyclonal antibody.

structs into *ago1^{-/-}* cells, the expression of BB2- or TAP-AGO1 was confirmed by Western blot analysis with an anti-BB2 antibody (Fig. 3A). Moreover, both tagged AGO1 proteins were functional in RNAi, since challenging the cells with α -tubulin dsRNA resulted in the degradation of α -tubulin mRNA (data not shown).

Trypanosomes expressing TAP-AGO1 were then used for immunofluorescence analysis (Fig. 3B) with a rabbit anti-protein A antibody. AGO1 was predominantly cytoplasmic but was not homogeneously distributed in the cytoplasm. In particular, the fluorescence signal appeared more intense in the perinuclear region and there were "clusters" of fluorescence superimposed on a diffuse cytoplasmic signal.

Next, we analyzed the distribution of TAP-AGO1 in cell extracts. Figure 3C shows the results of a fractionation by differential centrifugation of a whole-cell extract prepared by detergent lysis. By this analysis TAP-AGO1 was mostly found in the postnuclear supernatant (lane 3) and in the S100 fraction (lane 4). However, there was a proportion of AGO1 that sedimented at $100,000 \times g$ as large complexes (lane 5). To further evaluate the sedimentation characteristics of these large AGO1 complexes, a cytoplasmic extract was centrifuged through a 15 to 50% sucrose gradient and individual fractions were analyzed by Western blotting with the anti-protein A antibody (Fig. 3D). AGO1 was found near the top of the

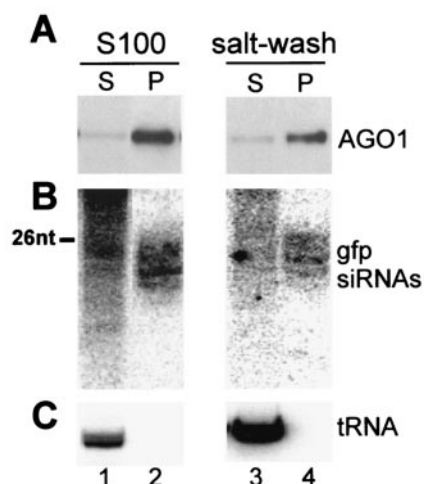


FIG. 4. AGO1 is associated with siRNAs. S100 and ribosome salt-washed fractions from cells expressing BB2-tagged AGO1 and GFP dsRNA were subjected to immunoprecipitations with anti-BB2 antibodies, and supernatant (S) and pellet fractions (P) were processed for Western blot analysis for AGO1 (A) and for Northern blot analysis for GFP siRNAs (B), as well as for initiator methionyl tRNA to control for immunoprecipitation specificity (C). A DNA size marker of 26 nt is indicated in panel B.

gradient, where soluble material and small ribonucleoprotein particles sediment, as well as heterodispersed throughout the gradient fractions, where polyribosomes sediment. A similar distribution of the AGO1 protein was detected in wild-type cells by using a polyclonal anti-AGO1 antibody (data not shown).

AGO1 is associated with siRNAs. We have recently shown that 10 to 20% of siRNAs are associated with translating polyribosomes and that the polysome-associated siRNAs can be released by salt extraction as a ribonucleoprotein particle with an apparent molecular mass of approximately 70 kDa (9). The sedimentation profile of AGO1 in the sucrose density gradient of Fig. 3D paralleled the distribution of siRNAs in trypanosome extracts, and in preliminary experiments we found that, similarly to the siRNAs, AGO1 present in a polysomal pellet was rendered soluble upon salt extraction (data not shown). To test whether siRNAs are in a complex with the AGO1 protein, we prepared an S100 and a corresponding ribosome salt-wash fraction from a cell line expressing BB2-AGO1, as well as GFP dsRNA. Next, we immunoprecipitated BB2-AGO1 from these two fractions by using the monoclonal BB2 antibody coupled to protein A beads. Western blot analysis revealed that most of the AGO1 protein was immunoprecipitated from the S100 and the ribosome salt-wash fractions (Fig. 4A). Since Northern blot analysis showed that a significant proportion of GFP siRNAs were enriched in the respective immunoprecipitates (Fig. 4B), we concluded that AGO1 is part of a complex containing siRNAs. Further fractionation of the ribosome salt-washed material on a Superdex 200 gel filtration column revealed that the majority of BB2-AGO1 cofractionated with GFP siRNAs (Fig. 5) with an apparent molecular mass of 70 kDa, as previously described for siRNAs (9). Similar results were obtained with the S100 fraction (data not shown).

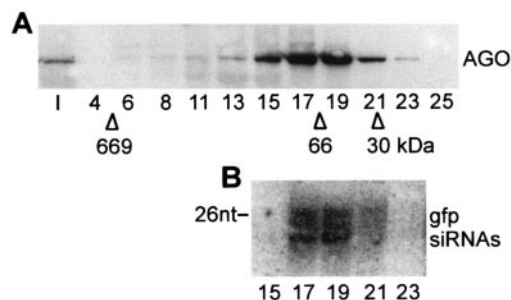


FIG. 5. AGO1 cofractionates with GFP siRNAs. The salt-extracted material from the ribosome pellet of cells expressing BB2-tagged AGO1 and GFP dsRNA was loaded onto a Superdex 200 column, and selected fractions were subjected to Western blot analysis with anti-BB2 antibodies (A) and Northern blotted for the presence of GFP siRNAs (B). The elution positions of carbonic anhydrase (30 kDa), bovine serum albumin (66 kDa), and thyroglobulin (669 kDa) are indicated. A DNA size marker of 26 nt is indicated in panel B.

AGO1 plays a role in the accumulation of siRNAs. To begin to examine the function of AGO1 in the RNAi mechanism, we analyzed the steady-state levels of siRNAs in *ago1*^{-/-} cells. First, we monitored endogenous siRNAs homologous to the Ingi retroposon transcripts by Northern blot hybridization with RNA derived from wild-type cells and four independently cloned *ago1*^{-/-} cell lines (Fig. 6A). This experiment showed that the accumulation of Ingi siRNAs was severely reduced in *ago1*^{-/-} cells compared to wild-type cells (compare lane 1 to lanes 2 to 5). Interestingly, the residual small RNAs present in *ago1*^{-/-} cells were a few nucleotides longer than the average siRNAs present in wild-type cells. Complementation of the RNAi deficiency with the BB2- or TAP-AGO1 cassette restored both the abundance and the size of Ingi siRNAs (Fig. 6B, lanes 3 and 4).

Second, we examined whether *ago1*^{-/-} cells were impaired in the accumulation of siRNAs derived from a transgene. To this end, we generated *ago1*^{-/-} cell lines constitutively expressing GFP dsRNA as a hairpin RNA. All four cell lines tested expressed transcripts diagnostic of GFP dsRNA, albeit to different levels (Fig. 6D). This variable level of expression most likely reflects integration of the GFP hairpin transgene at different and perhaps multiple sites in the tubulin gene array. In contrast, GFP siRNAs were almost undetectable in cells expressing GFP dsRNA (Fig. 6C; compare lane 1 to lanes 2 to 5). Similarly to what we observed for the retroposon-derived siRNAs, at least in one cell line the residual GFP siRNAs were of the “long” kind (Fig. 6C, lane 3). In conclusion, *ago1*^{-/-} cells are deficient in the accumulation of siRNAs derived from endogenous retroposon transcripts, as well as from a transgene, and the residual amounts of small RNAs still detected in *ago1*^{-/-} cells are of a distinct size class.

AGO1 affects the accumulation of retroposon transcripts. Our previous sequence analysis of siRNAs in *T. brucei* revealed a large proportion of siRNAs derived from Ingi and spliced leader-associated conserved sequence (SLACS) retroposon elements and suggested that RNAi down regulates the steady-state levels of retroposon transcripts (10). Consequently, we would predict that elimination of the RNAi response would result in an increased steady-state level of retroposon tran-

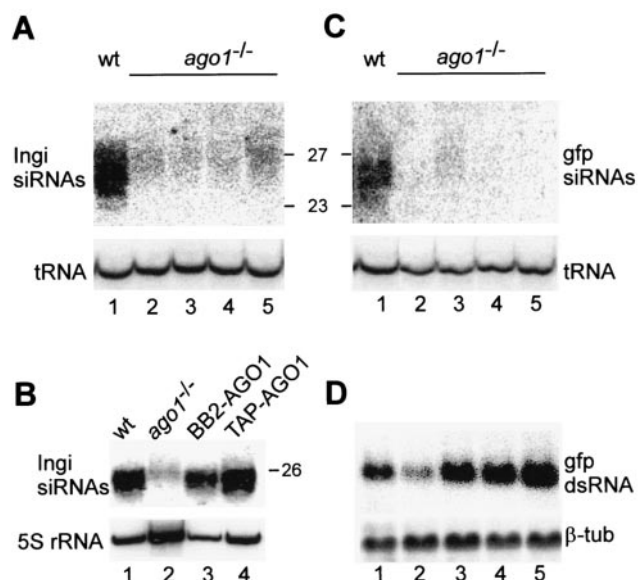


FIG. 6. siRNA accumulation is dependent on AGO1. (A) The level of Ingi siRNAs was probed by Northern blotting in wild-type cells (wt; lane 1) and four independently cloned cell lines deficient in the AGO1 protein (*ago1*^{-/-}; lanes 2 to 5). RNA size markers in nucleotides are indicated on the right. The hybridization to initiator methionyl tRNA (tRNA) served as a loading control. (B) Abundance of Ingi siRNAs in wild-type (lane 1), AGO1-deficient (lane 2), BB2-AGO1-complemented (lane 3), and TAP-AGO1-complemented (lane 4) cells. The level of 5S rRNA was used as a loading control. (C) Northern blot analysis for GFP siRNAs of RNA isolated from wild-type cells expressing GFP dsRNA (lane 1) and four independent clonal *ago1*^{-/-} cell lines expressing GFP dsRNA (lanes 2 to 5). RNA size markers in nucleotides are indicated on the left. The hybridization to initiator methionyl tRNA (tRNA) served as a loading control. (D) Detection of GFP dsRNA in the cell lines described in panel C, with β -tubulin mRNA (β -tub) serving as a loading control.

scripts. To test this, total RNA from wild-type and *ago1*^{-/-} trypanosomes was analyzed by Northern blot hybridization (Fig. 7A and B). Indeed, we found that Ingi and SLACS transcripts were approximately three- and fivefold more abundant, respectively, in *ago1*^{-/-} cells than in wild-type cells. To address the origin of this difference, we first evaluated the decay rate of Ingi (Fig. 7A) and SLACS (Fig. 7B) transcripts in wild-type and *ago1*^{-/-} cells over a period of 4 h after blocking of transcription with actinomycin D. The pattern of Ingi hybridization was quite complex with several discrete bands superimposed on a smear (Fig. 7A). This is consistent with previous reports by others (25) and reflects the highly dispersed genomic organization of the Ingi retroposon family (22). We observed that the decay rate of the majority of the discrete transcripts visible by Northern blotting was similar in *ago1*^{-/-} and wild-type cells, with the exception of one transcript, indicated by an asterisk in Fig. 7A, which appeared to be longer lived in *ago1*^{-/-} cells than in wild-type cells. In contrast, the SLACS element, which is a site-specific retroposon inserted in the spliced leader RNA gene cluster (1), generated a major transcript whose decay was at least four times slower in *ago1*^{-/-} cells than in wild-type cells (Fig. 7B). Next, we asked whether AGO1 deficiency had any effect on the transcription of Ingi or SLACS elements. To this end we synthesized radiolabeled RNA in permeabilized

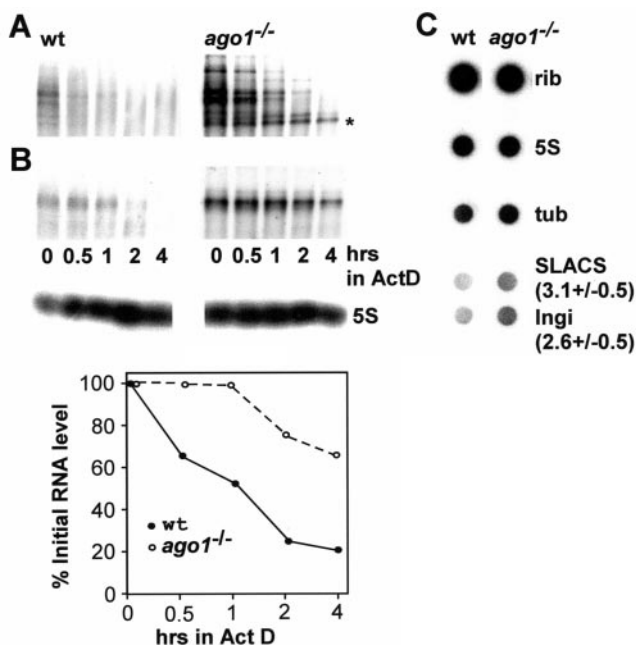


FIG. 7. AGO1 affects the accumulation of Ingi and SLACS transcripts. (A) Northern blot of Ingi transcripts in wild-type (wt) and *ago1*^{-/-} cells over a period of 4 h following the addition of actinomycin D. The asterisk indicates a transcript which appeared to be more long lived in *ago1*^{-/-} cells than in wild-type cells. (B) Northern blot of SLACS transcripts in wild-type and *ago1*^{-/-} cells over a period of 4 h following the addition of actinomycin D (upper panel). Hybridization to 5S RNA served as a loading control (middle panel). SLACS transcripts were quantitated relative to 5S RNA (lower panel). (C) Newly synthesized RNA from wild-type and *ago1*^{-/-} cells was hybridized to the following DNAs spotted onto a nitrocellulose filter: large rRNAs (rib), 5S rRNA (5S), α -tubulin (tub), SLACS, and Ingi. The numbers next to the SLACS and Ingi hybridizations indicate the fold increase in *ago1*^{-/-} cells relative to wild-type cells. The experiment was repeated three times, and the standard deviation is indicated.

trypanosome cells and analyzed the abundance of newly synthesized Ingi or SLACS transcripts by dot blot hybridization (Fig. 7C). Using the large rRNA and 5S RNA hybridization values as standards for normalizing the dot blots, we determined that transcription of Ingi and SLACS elements was increased approximately 2.6 (± 0.5)- and 3.1 (± 0.5)-fold, respectively, in *ago1*^{-/-} cells.

DISCUSSION

In this paper we describe the characterization of the first component of the RNAi machinery in *T. brucei*, namely, a member of the Argonaute gene family. Like other members of this family, the *T. brucei* AGO1 protein is a highly basic protein and contains the signature domains PAZ and Piwi (6), which at present do not have a defined function. One characteristic feature of AGO1 is the presence of an N-terminal domain rich in arginine and glycine residues with a high abundance of RGG repeats, resembling the RGG RNA binding motif. Similar repeats, although not as prevalent, are found in two members of the *Arabidopsis* Argonaute family (accession no. NP_565662 and NP_175274). Arginine residues present within RGG domains are often asymmetrically dimethylated, and it is intriguing

that the N terminus of AGO1 has several repeats that are preferred for asymmetric arginine dimethylation, namely, G/F GGRGGG/F, making it a likely candidate for this posttranslational modification (21).

Our genetic analysis demonstrated that *AGO1* is required for RNAi in *T. brucei*. Cells lacking both copies of the *AGO1* gene are deficient in sequence-specific mRNA degradation when challenged with dsRNA. These cells did not show a substantial growth defect, suggesting that the RNAi mechanism is dispensable for cell growth in the laboratory-adapted insect-form trypanosomes. However, since RNAi deficiency in *T. brucei* leads to upregulation of retroposon transcripts, it is possible that mobilization of retroelements is occurring in *ago1*^{-/-} cells, and thus, we cannot exclude the possibility that the loss of RNAi might have detrimental effects on the genome integrity in the long term.

By immunofluorescence and cell fractionation experiments we found that AGO1 is mainly localized in the cytoplasm. However, the immunofluorescence pattern is not typical of a soluble protein. Rather, a proportion of AGO1 appears to be compartmentalized in some subcellular compartment, whose identity is at present uncertain. It is possible that a proportion of AGO1 is associated with endoplasmic reticulum-bound polyribosomes translating mRNAs coding for membrane or secretory proteins. Although we do not have biochemical evidence that AGO1 is directly associated with membranes, it is worth mentioning that EIF2C1/hAGO1, also known as GERP95, is a peripheral membrane protein that localizes primarily to the Golgi complex or to the endoplasmic reticulum, depending on the cell type (7).

Previous studies in *Drosophila* revealed that the RNA-induced silencing complex, containing AGO2 and most siRNAs, can be salt extracted from a 200,000 $\times g$ pellet fraction from S2 cell extracts (17). Moreover, affinity purification of QDE-2, a *Neurospora* AGO family member, uncovered a complex containing siRNAs (5), and affinity purification of human RNA-induced silencing complex showed that EIF2C1 and EIF2C2 are part of a complex containing siRNAs (23). Here, we have provided evidence that in trypanosomes siRNAs are also in a complex containing AGO1. This is probably not surprising, considering the AGO2-QDE-2-EIF2C results. What is quite unique to trypanosomes is the small size of about 70 kDa of the ribonucleoprotein particle, where siRNAs and AGO1 reside. We now know that this measurement, which was obtained on a gel filtration column, is an underestimate, since the particle contains at least one AGO1 molecule of about 98 kDa plus siRNAs, which contribute an additional 8 to 16 kDa depending on whether one or both strands of siRNAs are present. Notwithstanding this uncertainty about the mass of the AGO1 ribonucleoprotein particle, it is tempting to speculate, as suggested previously (18), that one of the functions of AGO1 is to bind siRNAs. Similar to what we described for siRNAs (9), we found that a proportion of the 70-kDa AGO1 RNP cosediments with polyribosomes and can be released from polyribosomes by salt extraction. It could be argued that the highly basic AGO1 protein binds to ribosomes nonspecifically. However, we think that this interpretation is unlikely, because we recently determined that a mutant protein lacking the RGG domain does not bind to polyribosomes and its calculated pI is

only slightly lower than that of wild-type AGO1 (H. Shi, A. Djikeng, C. Tschudi, and E. Ullu, unpublished data).

At the RNA level *ago1*^{-/-} cells accumulate significantly reduced amounts of endogenous siRNAs and almost undetectable levels of transgene-derived GFP siRNAs. These observations are consistent with the possibility that AGO1 is required to produce and/or stabilize siRNAs. In this respect the siRNA phenotype of *ago1*^{-/-} trypanosomes resembles that of Piwi mutant flies (27), as well as that of the *alg-1/alg-2* mutant worms (12), but is different from that of *rde-1* and *qde-2* mutations in *C. elegans* (28) and *Neurospora* (5), respectively. Thus, our results support the notion that there are functional differences between AGO family members in terms of their role in production and/or stabilization of siRNAs.

The residual small RNAs homologous to the Ingi retroposon that we detected in *ago1*^{-/-} cells had a size distribution a few nucleotides longer than that of wild-type Ingi siRNAs. These "longer" small RNAs might result from a defect in processing of dsRNA or might be produced by a different "Dicer" activity and might have a different function than siRNAs. The presence of different size classes of small RNAs has been reported previously in plants, where short (21- to 23-nt) siRNAs are required for mRNA degradation and long (25-nt) siRNAs correlate with systemic silencing (16), and their identity as bona fide siRNAs has been confirmed (32). More recently, inactivation of the *Arabidopsis AGO4* gene has been shown to control accumulation of 25-nt-long siRNAs corresponding to the retroposon AtSN1 (38).

The second RNA phenotype that we uncovered in *ago1*^{-/-} cells concerns the increased accumulation of Ingi and SLACS retroposon transcripts in steady-state RNA. Our results further suggest that retroposon transcript abundance is regulated at both the transcriptional (Ingi and SLACS) and posttranscriptional (SLACS) levels. This is to our knowledge the first report that links a member of the Argonaute gene family to the expression of retroposon transcripts. This observation ties in well with our previous results demonstrating the presence of constitutively expressed retroposon-derived siRNAs (10) and provides further evidence that RNAi is involved in regulating the abundance of retroposon transcripts in trypanosomes. It will be interesting to determine whether retroposition is activated in *AGO1*-deficient cells and in what cellular compartment RNAi-mediated degradation of retroposon transcripts takes place.

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