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Immunopurification of Ago1 miRNPs selects for a distinct class of microRNA targets

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microRNAs comprise a few percent of animal genes and have been recognized as important regulators of a diverse range of biological processes. Understanding the biological functions of miRNAs requires effective means to identify their targets. Combined efforts from computational prediction, miRNA over-expression or depletion, and biochemical purification have identified thousands of potential miRNA-target pairs in cells and organisms. Complementarity to the miRNA seed sequence appears to be a common principle in target recognition. Other features, including miRNA-target duplex stability, binding site accessibility, and local UTR structure might affect target recognition. Yet computational approaches using such contextual features have yielded largely nonoverlapping results and experimental assessment of their impact has been limited. Here, we compare two large sets of miRNA targets: targets identified using an improved Ago1 immunopurification method and targets identified among transcripts up-regulated after Ago1 depletion. We found surprisingly limited overlap between these sets. The two sets showed enrichment for target sites with different molecular, structural and functional properties. Intriguingly, we found a strong correlation between UTR length and other contextual features that distinguish the two groups. This finding was extended to all predicted microRNA targets. Distinct repression mechanisms could have evolved to regulate targets with different contextual features. This study reveals a complex relationship among different features in miRNA-target recognition and poses a new challenge for computational prediction.

Argonaute | gene regulation | RISC complex

Animal genomes contain hundreds of microRNA genes (miRBase 13.0). Recent estimates suggest that miRNAs comprise $\approx 1\%$ of genes in *Drosophila* and *Caenorhabditis elegans* and 2–3% of genes in mouse and human. To date, functional analysis in vivo has revealed biological roles for only a small fraction of these (1–3). One issue limiting progress in understanding the miRNA functions is identification of the target mRNAs that they regulate. Computational target identification is primarily based on sequence complementarity to the miRNA (reviewed in ref. 2), but many computational strategies also make use of sequence context to predict miRNA targets. Comparisons of different methods show limited overlap among the predicted targets, although those that place more emphasis on pairing to the seed sequence at the 5' end of the miRNA tend to produce similar results. Most of these methods identify many possible targets for each miRNA, often hundreds (e.g., refs. 4–9).

A growing body of experimental evidence shows that miRNAs can regulate many targets. Overexpression of miRNAs in heterologous cell types can affect the levels of hundreds of mRNAs with target sites (e.g., ref. 10). Conversely, depletion of miRNAs can lead to increased levels of a comparable number of target mRNAs (11, 12). Changes in target RNA stability can result from miRNA-induced deadenylation of the mRNA (13–15). mRNA up-regulation, combined with target prediction has helped to identify biologically relevant targets of specific

miRNAs (e.g., ref. 16). Whole proteome analyses have shown that miRNA induced changes in protein expression correlate with changes in mRNA level, in trend if not in magnitude (17, 18). Yet, there are well-documented instances of miRNA-mediated regulation at the protein level that do not involve changes in mRNA level (14, 17, 18). Therefore, methods to identify targets by miRNA-induced changes in expression profile can only tell part of the story. This highlights the need for alternative means to identify miRNA targets.

One such alternative involves identification of microRNA targets by virtue of their physical association with miRNA-containing ribonucleoprotein complexes (19–24). In ref. 19, we reported a method based on Ago1 immunopurification (IP) that proved to be effective. Eleven new targets were identified for miR-1, including some that had not been predicted. Although the specificity was high, with all new targets experimentally validated, the method had limited sensitivity, identifying $\approx 1/10$ th of the expected number of targets. Here, we present an improved Ago1 IP protocol, which permits identification of hundreds of potential miRNA targets, and compare the contextual features of targets identified by IP to the targets destabilized at the mRNA level upon Ago1 depletion.

Results

In an effort to improve the sensitivity of miRNA IP, with minimal loss of specificity, we tested a variety of antibody concentrations, incubation times and wash conditions (Fig. S1). Sensitivity was assessed by quantitative PCR to monitor miRNA levels (over a broad range of abundance: miR-184 comprises 17% of S2 cell miRNA; miR-305: 1.5%; miR-7: 0.1%; miR-92b: 0.01%; (25)). The 4 miRNAs were enriched >50 -fold in IP from cells expressing HA-tagged Ago1 compared with control cells not expressing the transgene (Fig. 1A, *, $P < 0.05$). The small nucleolar RNA (snoR227) showed no enrichment ($\log_2 = 0.18$). Thus, the IP protocol can recover miRNAs over a broad range of expression levels without enriching for unrelated small RNAs.

The association between miRNAs and targets must be stable for IP to be useful. To assess this association, we measured the recovery of *reaper* mRNA, a known target of miR-2a. The miR-2 family comprises $>13\%$ of S2 cell miRNAs. *reaper* mRNA was enriched ≈ 32 -fold by IP. A control lacking known miRNA binding sites was not enriched (Fig. 1B). This compares favorably with the 2- to 3-fold enrichment of *reaper* obtained in the study in ref. 19.

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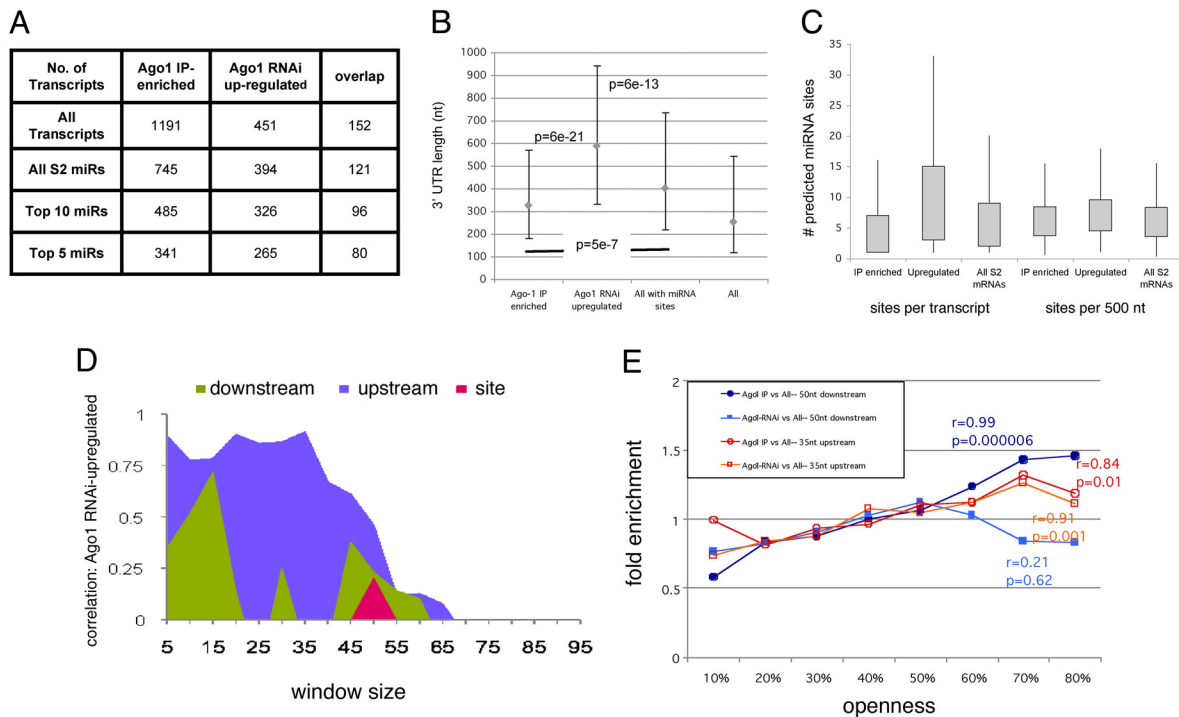


Fig. 4. A comparative analysis on Ago1 IP-enriched transcripts Vs Ago1 RNAi-up-regulated transcripts. (A) Numbers of mRNAs with target sites identified by IP or by Ago1 RNAi. IP-enriched used a cutoff >1.4 -fold and $P < 0.05$. Ago1 RNAi set from (12): up-regulated >1.5 -fold ($P < 0.05$). All: all S2 cell mRNAs; all S2 miRNA: those with sites for any S2 miRNA. (B) y axis: median UTR length (nt) represented by gray squares. The range between 1st and 3rd quartiles are indicated by bars. P values: Wilcoxon U test, Bonferroni corrected (4 tests per group). The median for the Ago1 RNAi set is 262 nt longer than the IP set ($P = 6e-21$) and 187 nt longer than for all RNAs with sites ($P = 6e-13$). The IP set was 75 nt shorter than all RNAs with sites ($P = 5 \times 10^{-7}$). (C) Site density profiles in IP-enriched vs. Ago1 RNAi-up-regulated targets and all S2 miRNAs. The up-regulated set has more sites/transcript than the IP set (median shift 4, $P = 2 \times 10^{-18}$) or than all RNAs with sites (median shift 3, $P = 1 \times 10^{-14}$). Median site density was 6.9/500 nt in the up-regulated set vs. 6.0 for the IP set and 5.6 for all RNAs. These differences were significant using a K-S test (two tail). (D) Assessment of site openness for the Ago1 RNAi up-regulated set vs. all RNAs with sites (as in Fig. 3B). (E) Fold enrichment for the optimal upstream and downstream windows in IP-enriched and Ago1 RNAi up-regulated sets. x axis: average nucleotide openness binned from 10% to 80%. y axis: fold enrichment as compared with all S2 transcripts with sites, which were used as the common control. Pearson's correlation coefficient, r values and associated P values are shown.

energy of miRNA-target base pairing for transcripts enriched by IP with those not enriched (ΔG_{hybrid} as in ref. 9). The distribution of binding energies was significantly shifted toward more stable duplexes in IP-enriched transcripts ($P = 0.005$ using a two-sample Kolmogorov–Smirnov test). The correlation between binding energy ΔG_{hybrid} and degree of enrichment in the IP set was modest ($r = -0.60$), on the borderline of statistical significance ($P = 0.0503$). On this basis, IP does not appear to select strongly for more stable target site binding.

Local secondary structure in the UTR might affect function by making a miRNA site more or less accessible. Previous studies have developed ways to predict site “openness” and suggested that this could improve computational target prediction (7, 9, 33). We found a significant shift toward greater site openness (9) in IP-enriched targets compared with those not enriched (Kolmogorov–Smirnov two-sample, $P = 4 \times 10^{-6}$; Table S6). The degree of enrichment for openness correlated well with increasing site accessibility ($r = 0.865$, $P = 0.006$). A comparable correlation was found when all S2 mRNAs were used as the control set ($r = 0.868$, $P = 0.005$).

To examine the impact of nearby sequences, we tested windows from 5 to 95 nt in length upstream and downstream of the site (Table S7). Fig. 3B presents a surface plot showing the correlation coefficient between degree of openness and enrichment in the IP set compared with all S2 transcripts. Upstream of the site, the correlations were significant for windows of up to 50 nt. Downstream, the correlations were significant for windows from 10 to 70 nt with an optimum at 50 nt (Table S7 and Fig. 3B).

A previous analysis using a different miRNP protein in *C. elegans* (AIN-IP, GW182) found that a 25-nt upstream window had the best correlation with IP enrichment, but did not find evidence for downstream openness (9). These studies may have sampled different miRNP complexes, since antibodies to different RISC components were used, but species differences in UTR composition cannot be ruled out.

Comparison of Targets Identified by Ago1 IP and Ago1 Depletion. Expression profiling of cells depleted of miRNA function is gaining acceptance as a means of identifying potential targets (e.g., refs. 11, 12, 16, and 18). In this context, we asked whether similar target features are selected for by IP and Ago1 depletion. A priori we expect them to be similar, because both reflect activity of Ago1 complexes. To our surprise, we found $<1/3$ overlap in the RNAs identified by the two methods (Fig. 4A and Table S8 lists all transcript data). Recent reports using Ago-2 to pull down miRNA targets in mammalian cells over-expressing a miRNA also showed limited overlap with targets downregulated at the mRNA level (20, 23). To explore the basis for these differences we examined the two groups for distinct structural and molecular features, using all S2 mRNAs as a common control set.

There was little difference in seed types enriched by the two methods (Fig. S4A). However, sites with stronger binding energy were under-represented in the up-regulated transcript set ($P = 0.01$, cumulative distribution plot in Fig. S4B). There was a significant anti-correlation between more stable hybrids and

proaches that favor site context, overall binding energy or conservation are likely to favor one part of the UTR target spectrum over another. A systematic analysis of the interactions between contextual features, including synergistic regulation and structural openness, could improve the accuracy of prediction.

Materials and Methods

Immunopurification of *Ago1* from S2 cells is described in Fig. S1A and *SI Materials and Methods*. UTR luciferase reporter assays were performed as described in refs. 27 and 38 with modifications described in *SI Materials and Methods*. miRNA and mRNA quantitative PCR was performed as described in *SI Materials and Methods*. Expression profiling was performed by the EMBL

Gene Core using Affymetrix *Drosophila* 2.0 arrays (see *SI Materials and Methods*). miRNA target site prediction and statistical analysis is detailed in *SI Materials and Methods*. David bioinformatic tools were used for gene ontology. Functional annotation clustering was applied as described in ref. 39.

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