Target complementarity in cnidarians supports a common origin for animal and plant microRNAs

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Abstract

microRNAs (miRNAs) are important post-transcriptional regulators that activate silencing mechanisms by annealing to mRNA transcripts. While plant miRNAs match their targets with nearly-full complementarity leading to mRNA cleavage, miRNAs in most animals require only a short sequence called 'seed' to inhibit target translation. Recent findings showed that miRNAs in cnidarians, early branching metazoans, act similarly to plant miRNAs, by exhibiting full complementarity and target cleavage; however, it remained unknown if seed-based regulation was possible in cnidarians. Here, we investigate the miRNA-target complementarity requirements for miRNA activity in the cnidarian *Nematostella vectensis*. We show that bilaterian-like complementarity of seed match or seed and supplementary 3' matches are insufficient for miRNA-mediated knockdown. Furthermore, mismatches in the cleavage site, positions 10-11 of the miRNA, decrease knockdown efficiency. Finally, we assayed miRNA silencing of a target with three seed binding sites in the 3' untranslated region to mimic typical miRNA targeting and observed no repression. Altogether, these results unravel striking similarities between plant and cnidarian miRNAs consolidating the evidence for common evolutionary origin of miRNAs in plants and animals.

Introduction

miRNAs are endogenous post-transcriptional regulators that are abundant in diverse eukaryotic lineages (Ameres & Zamore, 2013; Bartel, 2004, 2018; Moran *et al*, 2017). They have important roles in various biological processes and are essential for proper development of animals and plants (Bartel, 2018; Jones-Rhoades *et al*, 2006; Voinnet, 2009; Dexheimer & Cochella, 2020). miRNAs are transcribed by RNA polymerase II into long primary transcripts that are processed into hairpin-structured precursor-miRNAs (pre-miRNAs), which are later cleaved into short 20-22 nucleotides long duplexes. The duplexes are loaded into Argonaute (AGO) proteins that are a part of the RNA-Induced Silencing Complex (RISC), where only one strand is selected to remain loaded and the other is discarded (Kim *et al*, 2009). The loaded strand leads the RISC complex to a matching target and mediates its repression by inducing cleavage, translation inhibition or degradation by deadenylation of the mRNA (Jones-Rhoades *et al*, 2006; Jonas & Izaurralde, 2015).

The miRNA system is present in both plant and animal kingdoms, although a few major differences exist between them in the miRNA biogenesis pathway, mode of action and target recognition (Axtell *et al*, 2011; Moran *et al*, 2017). The biogenesis pathway in animals starts within the nucleus with the processing of the primary miRNA (pri-miRNA) by the microprocessor complex composed of RNase type III Drosha and its partner protein Pasha (known as DGCR8 in vertebrates) (Han *et al*, 2004a). The resulting pre-miRNA is transported by Exportin 5 into the cytoplasm where it gets cleaved into the mature miRNA by the RNase type III Dicer with the help of partner double-stranded RNA binding proteins such as Loqs and TRBP (Förstemann *et al*, 2005; Jouravleva *et al*, 2022; Fareh *et al*, 2016; Redfern *et al*, 2013; Wilson *et al*, 2015). In plants, both pri-miRNA and pre-miRNA are processed within the nucleus by DICER-LIKE1 (DCL1) assisted by its partner protein Hyponastic Leaves1 (HYL1) (Voinnet, 2009; Han *et al*, 2004b). Another difference between plant and animal miRNAs resides in their target recognition mode. In bilaterian animals, which include most known animal groups such as arthropods, nematodes, and vertebrates, miRNAs bind their targets with a short 5' sequence called the ‘seed’ that includes only seven nucleotides, at positions 2-8 of the miRNA (Brennecke *et al*, 2005). Supplemental complementarity at the 3' end, mostly of positions 13-16, occurs in some cases, but it is not as frequent and considered less crucial for target recognition (Bartel, 2009; Grimson *et al*, 2007). The contribution of the supplemental complementarity to target binding seems to change considerably between cases (Becker *et al*, 2019; Bertolet *et al*, 2019). Target recognition restricted to seed or mediated via a seed match and supplemental complementarity with mismatches at positions 10 and 11 often leads to translational inhibition and deadenylation of the mRNA, mitigated by the metazoan-specific GW182 protein family (called TNRC6 in vertebrates) (Hutvagner & Simard, 2008; Bartel, 2009; Iwakawa & Tomari, 2015). Contrastingly, plant miRNA target recognition and activity require nearly-full complementarity that frequently results in AGO-mediated target cleavage between positions 10-11 of the miRNA, known as the

cleavage site. Translational inhibition can also occur, but it still requires nearly-full complementarity (Iwakawa & Tomari, 2013).

The above-mentioned differences led to the notion that the miRNA system evolved independently in plants and animals; however, recent studies have shown that the miRNA system in the model sea anemone *Nematostella* vectensis, as well as other cnidarian species, is more similar to plants than previously thought (Moran *et al*, 2014; Modepalli *et al*, 2018; Tripathi *et al*, 2022; Baumgarten *et al*, 2018; Li & Hui). Cnidaria, the sister group to Bilateria, diverged over 600 million years ago from the vast majority of animal clades, and is composed of sea anemones, corals, jellyfish, and hydroids (Erwin *et al*, 2011; Kayal *et al*, 2018). Cnidarians possess a miRNA system (Grimson *et al*, 2008), and share some highly conserved miRNAs, some of them are known to be crucial for cnidarian development (Praher *et al*, 2021; Modepalli *et al*, 2018; Fridrich *et al*, 2020). Interestingly, cnidarian miRNAs operate by binding their targets with nearly-full complementarity that leads to mRNA cleavage, in a similar manner to plant miRNAs (Moran *et al*, 2014). Furthermore, miRNAs in *Nematostella* and plants are methylated at the 3' end, which is essential to prevent miRNA degradation (Modepalli *et al*, 2018). Importantly, it was shown recently that *Nematostella* Hyl1-Like a, a homolog to plant-specific HYL1, also takes part in miRNA biogenesis, which suggests that it likely took part in miRNA biogenesis before the separation of plants and animals (Tripathi *et al*, 2022). Yet, despite these striking similarities to the miRNA pathway of plants, the cnidarian miRNA system also exhibit clear metazoan-specific features such as Drosha and Pasha homologs and a GW182 homolog (Mauri *et al*, 2017; Moran *et al*, 2013). The similarities to the bilaterian miRNA pathway raise the question whether cnidarian miRNAs might be able to target mRNAs via more restricted interactions focused on the seed region like their bilaterian counterparts.

To answer this question here we characterized the complementarity requirements between miRNAs and their targets in *Nematostella*. We tested the efficiency of different complementarity patterns in promoting gene knockdown, such as the bilaterian-like seed match and a cleavage site mutated sequence. We utilized *TBP::mCherry* transgenic sea anemones that ubiquitously express mCherry fluorescent protein (Admoni *et al*, 2020) and injected to their zygotes different miRNA mimics to compare their effect on the expression of the fluorescent reporter.

Results and Discussion

Bilaterian-like matches fail to repress gene expression

It was previously shown that injection of short hairpin RNAs (shRNAs) to *Nematostella* zygotes leads to efficient knockdown of chosen targets (Karabulut *et al*, 2019). For our study, we designed a miRNA mimic (mimiR) based on an endogenous miRNA template to resemble native *Nematostella* miRNA precursors and better predict their processing by Dicer and the strand selection by AGOs. We used the pre-miRNA sequence of Nve-miR-2022, a highly conserved miRNA among cnidarians (Moran *et al*, 2014; Praher *et al*, 2021), and changed the

mature miRNA sequence to nearly fully match the mCherry transcript. The target site is located in the 3' UTR, since the majority of canonical miRNA sites are found in this region (Bartel, 2018). To be able to test the effect of different complementarity patterns on knockdown efficiency, we first generated mimiR with nearly-full complementarity to mCherry transcript (except for position 19, see materials and methods), that was later altered to resemble bilaterian miRNA binding sites that are based on seed match or mismatched in the cleavage site (**Figure 1A**).

To test the impact of bilaterian-like miRNA-target complementarity pattern on transcript and protein levels, only the seed region at positions 2-8 of the miRNA was left matching the mCherry-encoding transcript while the rest of the sequence was changed. In addition, we generated a mimiR with supplemental matches to the seed at positions 13-16 (**Figure 1A**). The mimiRs were injected to *TBP::mCherry* zygotes that were observed after three days and mCherry transcript and protein levels were measured.

Interestingly, we observed that bilaterian-like mimiRs with 'canonical site, i.e., matching their target only via the seed region, which is the most common class of miRNA in Bilateria (Bartel, 2018), cause no measurable knockdown of mCherry. The fluorescence of the embryos was similar to the negative control group injected with short hairpin RNA (shRNA) with no matches to *Nematostella* transcripts and mCherry mRNA and protein levels showed no difference compared to the negative control; and were significantly higher than in the positive control groups (**Figure 1B, G and H, and Table 1**). Adding supplementary binding bases at the 3'-end of the miRNA, to resemble another type of common bilaterian targets, resulted in similar measurements, with both transcript and protein levels of mCherry remaining unaffected by the presence of the mimiR when compared to the control group (**Figure 1C, G and H, and Table 1**).

These results implicate that the previously described nearly-perfect plant-like matches between cnidarian miRNAs and their targets (Moran *et al*, 2014) are the major mode of interaction and bilaterian-like matches between miRNAs and targets are probably not functional in Cnidaria. In fact it was shown that bilaterian-like matches have very weak effect or none at all in plants (Iwakawa & Tomari, 2013; Liu *et al*, 2014). Our experimental validation supports the evolutionary scenario that miRNA targeting based on seed match is a bilaterian innovation, suggested to contribute to the expansion of regulatory networks by allowing a single miRNA to bind hundreds of targets (Moran *et al*, 2017). It is noteworthy that in plants despite having full complementarity to the targets, the seed region is still crucial for target recognition and mismatches in positions 1-8 lead to decrease in silencing efficiency (Liu *et al*, 2014), which could potentially also be the case for *Nematostella* miRNAs.

Cleavage site mismatches interfere with miRNA activity

Next, we assessed the necessity of miRNA binding in the site of target cleavage. We mismatched positions 10-11 of the mimiR and compared mCherry levels to nearly-full

complementarity control mimiR injection. Similarly to seed-restricted mimiRs, inhibition of cleavage site binding resulted in impaired miRNA activity, as mCherry fluorescence as well as transcript and protein levels showed no difference from the negative control (**Figure 1D, G, and H, and Table 1**).

These results are in accordance with plant miRNAs that also fail to induce target cleavage when central mismatches are introduced (Iwakawa & Tomari, 2013). Moreover, this experiment further validate the notion that *Nematostella* miRNAs promote target cleavage as the main mode of action (Moran *et al*, 2014). Cleavage is known to be the main mechanism for miRNA activity in plants as well, suggesting that it is the ancestral miRNA mode of action. This has been discussed in relation to the ancient RNA interference (RNAi) system for defense against invasive nucleic acids, such as transposons and viruses, that operates by binding of short interfering RNAs (siRNAs) to foreign RNA targets and eliminating their expression by cleaving them. It is a probable evolutionary scenario that the miRNA system evolved from the RNAi defense system (Cerutti & Casas-Mollano, 2006).

In addition to target cleavage, translational inhibition, which is the common miRNA mechanism in bilaterians, was also exhibited in plants (Liu *et al*, 2014; Li *et al*, 2013; Brodersen *et al*, 2008). It was shown in *Arabidopsis thaliana* that central mismatches abolish target cleavage, although still allow translational inhibition when the target site is in the 5' UTR (Iwakawa & Tomari, 2013). The extent to which translational inhibition is occurring in *Nematostella* is still unknown, although it was shown that *Nematostella* GW182 homolog can promote mRNA decay and translational repression when expressed in human cells (Mauri *et al*, 2017). Based on our experiments, it seems that translational inhibition or mRNA decay did not occur when central mismatches prevented target cleavage; however, we cannot exclude the scenario that this mechanism is active in *Nematostella* due to the conservation of GW182, but requires different complementarity pattern or different number of sites.

Partial mismatch in the cleavage site results in weaker repression

After testing positions 10-11, we wished to test how a single mismatch in the cleavage site affects the knockdown efficiency. For this we mismatched either position 10 or 11 separately and injected both variants to transgenic zygotes. Both mimiRs resulted in visibly lower mCherry fluorescence. On the molecular level, mCherry transcript levels were significantly lower than the negative control, hence knockdown still occured, but it was significantly weaker than the positive control inflicted repression (**Figure 1E-F and G, and Table 1**). On the protein level, despite a noticeable trend of higher protein levels compared to the positive control both in the ELISA measurement and the fluorescence of the transgenic animals, there was no statistically significant difference between protein concentration between a nearly-full match and a single position mismatch (**Figure 1E-F and H, and Table 1**). This raises the intriguing possibility that

translational inhibition contributes to the silencing effect beyond the effect at the RNA level. Yet, such a claim requires further biochemical proof.

Reduced knockdown efficiency due to mismatch of one nucleotide at the cleavage site could be due to different conformation of AGO-miRNA that changes the cleavage efficiency (Sheu-Gruttadauria & MacRae, 2017). Some *Nematostella* miRNAs naturally exhibit a mismatch to their target in position 10 or 11: position 10 was found mismatched in 67 miRNA-target pairs, while position 11 was mismatched in 41 pairs among degradome-verified targets (Moran *et al*, 2014). It is possible that the natural mismatches are selected for weaker knockdown of their targets, as weaker repression might be beneficial for some regulatory roles.

Multiple seed match sites in the 3' UTR are inefficient for miRNA activity

Single miRNA binding sites in bilaterians are capable of modulating protein target levels in a significant manner as demonstrated experimentally in *Drosophila* and zebrafish (Brennecke *et al*, 2005; Choi *et al*, 2007). However, many bilaterian miRNAs exhibit more than one site for each target they regulate (Grimson *et al*, 2007). Since multiple binding sites on the same target transcript can provide together synergic rather than additive repression effects (Briskin *et al*, 2020), we designed an mCherry-encoding mRNA that harbors three seed match sites in its 3' UTR (**Figure 2A**). The mRNA was injected to wild-type *Nematostella* zygotes along with the previously used seed match mimiR. A new nearly fully matching positive control mimiR was designed since the original sequence could potentially partially bind the three seed sites. After 24 hours from injection, mCherry fluorescence was weaker in the positive control group compared to the seed match group (**Figure 2B**). In accordance, protein concentrations were similar between seed match mimiR and negative control, both significantly higher than the positive control (**Figure 2C Table 1**). This result shows that increasing the number of target sites in the 3' UTR does not improve the efficiency of seed-match miRNAs and further validates that bilaterian-like matches are ineffective in *Nematostella*. Further, together with our previous results it suggests that bilaterian miRNAs seed-restricted matches between miRNAs and their targets is a bilaterian innovation (**Figure 3**).

In this study, we show through *in-vivo* assays that *Nematostella* miRNAs act similarly to those of plants in terms of the complementarity requirements to their targets to induce efficient gene repression. We show that bilaterian matches that rely either solely on seed matches or seed matches with supplementary 3' matches fail to perform measurable gene repression in *Nematostella*. In addition, a cleavage site is crucial for miRNA activity in Cnidaria, and a single mismatch in the cleavage site reduces repression efficiency on the qualitative level.

Overall, the results of this study reveal important similarities between plants and cnidarians in the complementarity requirements between miRNAs and their targets and together with

previous findings provide multiple lines of evidence for common origin of miRNA regulation before the separation of plants and animals (**Figure 3**).

Materials and Methods

Nematostella cultures and microinjection

Nematostella polyps culturing, spawning and fertilization were conducted as previously described (Genikhovich & Technau, 2009) with minor modifications. Cultured anemones and were maintained at 18 °C under dark conditions and fed with freshly hatched *Artemia salina* nauplii three times a week. Anemones were induced to release gametes in 25 °C for 8 hours followed by fertilization of WT eggs with heterozygote *TBP::mCherry* sperm. The gelatinous sack surrounding the eggs was removed by incubation in 3% L-Cysteine (Merck Millipore, USA) while rotated by hand for 15 minutes. Microinjection to zygotes was performed with Eclipse Ti-S Inverted Research Microscopes (Nikon, Japan) connected to an Intensilight fiber fluorescent illumination system (Nikon) for visualization of the fluorescent injected mixture. The system is mounted with a NT88-V3 Micromanipulator Systems (Narishige, Japan). Every replicate included injection of three groups of 400-700 zygotes each: negative control shRNA group, positive control mimiR and altered mimiR. The shRNA/mimiRs were injected at 500 ng/µl with dextran Alexa Fluor (Thermo Fisher Scientific, USA) for tracing of injection mix. The injected animals were kept in an incubator at 22 °C, counted and transferred to fresh *Nematostella* medium (16 ‰ artificial sea water made from dry Red Sea salt) every day. The animals were visualized before flash-frozen in liquid nitrogen with ~150 animals in each sample. The frozen samples were kept in -80 °C until either RNA or protein extraction.

RNA extraction

Total RNA was extracted from ~150 injected animals (3 days old planulae) with the aid of Tri-Reagent® (Merck Millipore) according to the manufacturer's protocol, with a few minor changes. At the RNA isolation phase, samples were centrifuged at 21,130 × *g*. Removal of residual genomic DNA from the extracted RNA was conducted by treatment with Turbo DNase twice for 30 minutes at 37 °C (Thermo Fisher Scientific) and repeating the RNA purification procedure for a second time. Final RNA pellets were re-suspended in 23-25 µl of RNase-free water (Biological Industries, Israel). Final concentration was measured by Qubit™ RNA BR Assay Kit (Thermo Fisher Scientific. RNA integrity was assessed by gel electrophoresis with 1:1 formamide (Merck Millipore) and 1 µl of loading dye on 1.5% agarose gel. RNA samples were stored at -80 °C until used.

shRNA /mimiR design

shRNA sequence to serve as negative control with no matches in *Nematostella* genome was taken from an existing protocol (Karabulut *et al*, 2019). mimiRs to target mCherry transcript

were designed based on *Nematostella* miR-2022, an endogenous miRNA stem-loop that was used as template to allow better prediction of cleaving sites by Dicer and to ensure selection of the desired strand and loading onto AGO1 (Fridrich *et al*, 2020; Moran *et al*, 2014). The targeted sequence was selected have U as a 5' terminal nucleotide, according to *Nematostella* guide strand characteristics, and mismatches were introduced to the predicted star strand in positions 1, 8, 9 and 17 (Fridrich *et al*, 2020). mimiRs were designed to the 3' UTR region of the mCherry transcript. The base in position 19 was always cytosine, due to in-vitro transcription requirements. mimiR sequence alterations included mismatches in positions 10-11, position 10 or 11, only positions 1-8 base-pairing with the mCherry sequence (seed-match), and positions 1-8 and 13-16 matching (seed + supplemental matches).

In-vitro transcription

The shRNA and mimiRs were transcribed according to the manufacturer's instructions using the AmpliScribe™ T7-Flash™ Transcription kit protocol (Lucigen, USA) with a few changes. The shRNA/mimiR DNA templates were ordered from Integrated DNA Technologies, Inc (Integrated DNA Technologies, USA) as reverse complements to the sequence of T7 promoter followed by shRNA/mimiR precursor. Templates were annealed with a T7 promoter primer prior to the in-vitro transcription reaction, which was carried out for 15 hours, followed by addition of 1 µl of DNase, incubation at 37 °C for 15 min, and product clean up with Quick-RNA MiniPrep Kit (Zymo Research, USA). Concentration of transcripts was measured by Epoch Microplate Spectrophotometer (BioTek Instruments, Cole-Parmer, USA) and product integrity was validated with gel electrophoresis. The ready to use hairpins were kept at -80 °C until used.

cDNA synthesis

cDNA synthesis was conducted with iScriptTM (Bio-Rad, USA) according to manufacturer's protocol. 100 ng of RNA (extracted from ~150 treated 3 days old planulae) per sample were used as template, resulting in final concentration of 5 ng/µl. cDNA was stored at -20°C.

Reverse transcription-quantitative PCR

Primers to amplify mCherry transcript for RT-qPCR were designed via Primer3 version 0.4.0 (Untergasser *et al*, 2012) and calibrated at concentrations of 25, 5, 1, 0.2 and 0.04 ng/µl to generate standard curves with StepOnePlus Real-Time PCR System v2.2 (ABI, Thermo Fisher Scientific). Primer quality was 125% efficiency, -2.83 slope and R2 >0.99. The specificity of the amplified products was determined by the presence of a single peak in the melting curve. RT-qPCR was performed using StepOnePlus Real-Time PCR System v2.2 (ABI, Thermo Fisher Scientific) and cDNA amplification was quantitatively assessed with using Fast SYBR Green Master Mix (Thermo Fisher Scientific). Each sample was quantified in triplicates for mCherry transcript and housekeeping gene 4 (HKG4) as an internal control (Columbus-Shenkar *et al*, 2018). 1 µl of cDNA template was used for all replicates. For negative control cDNA was replaced with RNase-free water. The Reaction thermal profile was

95 °C for 20 sec, then 40 amplification cycles of 95 °C for 3 sec and 60 °C for 30 sec, a dissociation cycle of 95 °C for 15 sec and 60 °C for 1 min and then brought back to 95 °C for 15 sec (+0.6 °C steps). mCherry fold change was analyzed using a comparative Ct method ($2^{-\Delta\Delta Ct}$) (Schmittgen & Livak, 2008). Thresholds for HKG and mCherry detection were equalized between individual experiments. Each experiment was composed of at least three biological replicates.

Protein extraction

Total protein extraction from ~150 three days old planulae was implemented by adding 200 µl of the following lysis buffer: 50 mM Tris-HCl (pH 7.4), 150 mM KCl, 10% glycerol, 0.5% NP-40, 5 mM EDTA (all chemicals purchased from Merck Millipore) and Halt™ Protease Inhibitor cocktail (Thermo Fisher Scientific). Then, samples were homogenized with pestle mixer (Argos Technologies, cat. No.A0001) and incubated at 4 °C for two hours in rotating mixer (Intelli Mixer™ RM-2, ELMI, function 1, 7 rpm). Samples were later centrifuged at 4 °C, 16,000 × *g* for 15 min and the aqueous phase was transferred to a new tube. Concentration of total protein was measured using Pierce™ BCA Protein Assay Kit (Thermo Fisher Scientific) on Epoch Microplate Spectrophotometer (BioTek Instruments). Samples were kept at -80 °C until used.

Red Fluorescence Protein Enzyme-Linked Immunosorbent Assay (RFP ELISA)

mCherry protein levels were detected with the aid of RFP ELISA kit (Cell Biolabs, Inc., USA). All protein samples were diluted to equal concentration prior to loading on antibody plate, and the experiment was carried out according to protocol. Epoch Microplate Spectrophotometer (BioTek Instruments) was used for absorbance measuring. Fit for standard curve was found using CurveExpert Basic 2.2.3 (Hyams Development, USA).

Rapid Amplification of cDNA Ends (3' RACE)

In order to reveal the exact length of the 3' end of the transgenic *TBP::mCherry* transcript, SMARTer® RACE 5'/3' Kit was used (Takara Bio, Japan). Prior to the reaction, RNA was extracted from 3-months-old animals, with one round of Tri-Reagent® (Merck Millipore). cDNA synthesis was conducted according to manufacturer's protocol with 500 ng of RNA. Gene specific primers were designed for the PCR and Nested PCR reactions, which were carried out by Advantage® 2 Polymerase (Takara Bio). Final products were outsourced for Sanger sequencing (HyLabs, Israel).

mRNA generation and injection

mCherry mRNA template was ordered as gBlock gene fragment (Integrated DNA Technologies). The sequence included T7 promoter, EF1α kozak sequence `TGTTAAACCAACCAACCACC` and 3' UTR with three seed sites 21 bases apart (two were inserted in addition to the original one). In addition, the 3' UTR included one site for full match

mimiR and two nucleotides' changes to make gBlock synthesis efficient. The DNA fragment was dissolved in TE buffer to final 20 ng/µl and incubated at 50 °C for 20 min. The template was cloned to pGEM®-T Easy plasmid (Promega) and amplified with forward primer to add T7 promoter class II phi2.5. In-vitro transcription was conducted with HighYield T7 Cap 1 AG (3'-OMe) mRNA Synthesis Kit (m5CTP) (Jena Bioscience, Germany) using 800 ng of amplified template followed by Turbo DNase treatment (Thermo Fisher Scientific) by incubation with 1 µl of DNase for 30 minutes at 37 °C twice sequentially. In-vitro transcription product was cleaned using RNA clean & concentrator 25 (Zymo Research) and eluted with 33 µl RNase free water. Concentration was measured using Qubit ™ RNA Broad Range Assay Kit with the Qubit Fluorometer (Thermo Fisher Scientific). Poly-adenylation followed using *Escherichia coli* Poly(A) Polymerase (New England Biolabs) for 30 minutes at 37°C and products were further cleaned with RNA clean & concentrator 5 (Zymo Research) and eluted with 8 µl RNase free water. Single product was validated on 1.5% agarose gel after incubated at 95°C for two minutes in thermo cycler with hot lid then brought to 22 °C and mixed with formamide (Merck millipore) in 1:3 ratio. mCherry mRNA was stored in -80 °C until injected to *Nemaostella* zygotes in the concentration of 0.167 µM along with shRNA/mimiR in the concentration of 1 µM, ratio of 1:6.

Microscopy and Microinjection

Fluorescence of mCherry protein was detected by SMZ18 stereomicroscope (Nikon) connected to an Intensilight fiber illumination fluorescent system (Nikon). Images were captured by DS-Qi2 SLR camera (Nikon) and were analyzed and processed with NIS-Elements Imaging Software (Nikon).

Statistical analysis

Comparisons between groups of injected animals in transcript levels and protein concentration were tested with one-way ANOVA with Tukey's HSD post-hoc test. Normality of the data was validated beforehand. Statistical analysis for protein level comparison following mRNA injections was conducted with Welch's ANOVA without the assumption of homogeneity of variances. Pairwise comparison was done with Games-Howell post-hoc Test. For mCherry transcript level difference average ΔCt was compared between groups. All experiments included at least three biological replicates and three technical replicates for RT-qPCR and two for ELISA. The tests were performed in Rstudio 2021.09.0.

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Conflict of interest

The authors declare no conflict of interest.

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Figure legends

Figure1 – Silencing effects of different miRNA-target complementarity patterns in *Nematostella*

A. Schematic representation of complementarity between designed mimiRs and mRNA target

B-F. mCherry fluorescence captured in *TBP::mCherry* heterozygote embryos, three days after injection with mimiRs. Negative control groups (left) injected with shRNA with no match in *Nematostella* genome, displaying noticeable fluorescence. Positive control (middle) groups injected with nearly-full complementarity mimiR displaying no visible mCherry fluorescence. Groups injected with partial match mimiRs (right) displaying varying levels of fluorescence with (B) seed match (C) seed + supplemental matches and (D) mismatched positions 10-11 showing fluorescence similar to negative control and (E) mismatched position 10 and (F) mismatched position 11 showing intermediate fluorescence. Scale bars represent 500 µm.

G. mCherry transcript fold change three days after injection with different mimiRs. Significance is shown for pairwise comparisons (one-way ANOVA with Tukey's HSD post-hoc test, n=3 biological replicates for all groups but mismatched position 11 that has n=4 biological replicates).

H. mCherry protein concentration three days after injection with different mimiRs. Significance is shown for pairwise comparisons (one-way ANOVA with Tukey's HSD post-hoc test, n=3 biological replicates).

Figure2 – mRNA with multiple seed-match sites is not silenced by seed-match mimiR in *Nematostella*

A. Schematic representation of injected in-vitro transcribed mCherry mRNA, containing EF1α kozak sequence followed by mCherry-encoding transcript containing three seed-match sites in its 3' UTR.

B. mCherry fluorescence observed in WT *Nematostella* embryos, 24 hours after injection with mCherry mRNA combined with a different mimiR in each panel. Negative control group (left) injected with shRNA with no match in *Nematostella* genome, displaying noticeable fluorescence. Positive control (middle) group injected with nearly-full complementarity mimiR displaying no visible mCherry fluorescence. Seed match group (right) injected with mimiR

matching the three seed sites in the 3' UTR showing fluorescence similar to negative control. Scale bars represent 500 µm.

C. mCherry protein concentration 24 hours after injection with mCherry mRNA combined with different mimiRs. Significance is shown for pairwise comparisons (Welch's ANOVA with Games-Howell post-hoc Test, n=4 biological replicates).

Figure3 – Evolution of the miRNA system in plants, Cnidaria and Bilateria

Results presented here and in previous publications (Moran *et al*, 2014, 2017; Tripathi *et al*, 2022; Mauri *et al*, 2017; Modepalli *et al*, 2018) suggest that miRNA post-transcriptional regulation evolved before the separation of plants and animals. HYL1 and HEN1 were present in the common ancestor of plans and animals where they had roles in miRNA biogenesis and methylation of miRNAs to protect from degradation, respectively. GW182 was mitigating target translational inhibition before the separation of Cnidaria and Bilateria over 600 million years ago. While plant and cnidarian miRNAs match their targets with nearly-full complementarity, bilaterian miRNAs evolved to depend on seed-match. In addition, bilaterians lost HYL1 that was replaced with other miRNA biogenesis proteins. Animal silhouettes are from http://phylopic.org/.

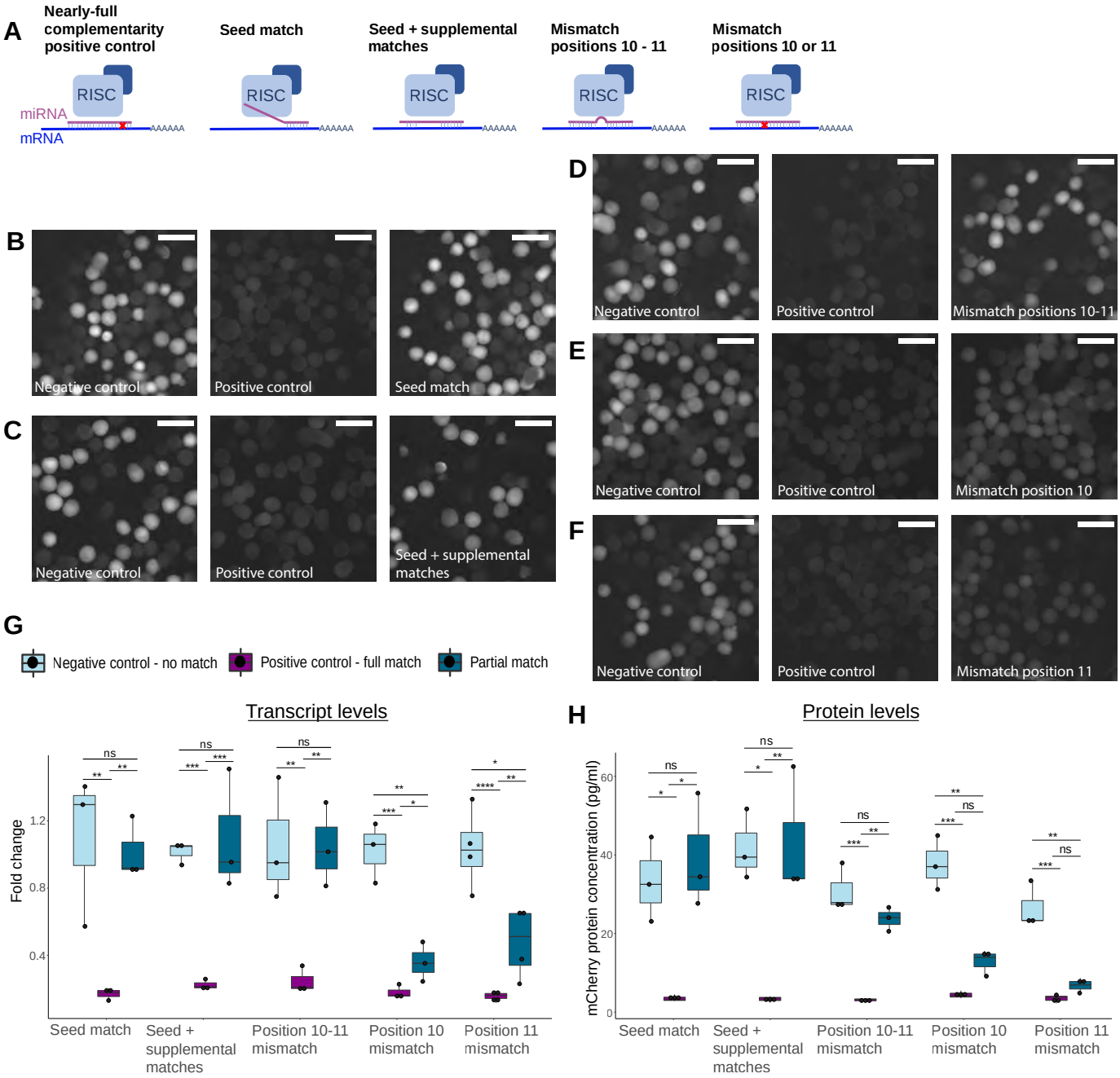
Tables and their legends

Transcript		Difference of means	95% CI	Adjusted p-value
	Full match – seed match	2.68132485	1.45547 , 3.907179	0.001295
	No match – seed match	-0.0096041	-1.23546 , 1.21625	0.999682
	No match – full match	-2.690929	-3.91678 , - 1.46508	0.001271
	Full match – seed + supplementary match	2.32389005	1.583794 , 3.063986	0.000176
	No match – seed + supplementary match	0.06702847	-0.67307 , 0.807124	0.958615
	No match – full match	-2.2568616	-2.99696 , 1.51677	0.000208
	Full match – position 10-11 mismatch	2.16048876	1.068762 , 3.252215	0.002196
	No match – position 10-11 mismatch	0.01938205	-1.07234 , 1.111108	0.998366
	No match – full match	-2.1411067	-3.23283 , 1.04938	0.002302
	Full match – position 10 mismatch	1.011219	0.056283 , 1.966155	0.040092
	No match – position 10 mismatch	-1.589497	-2.54443 , -0.63456	0.005294
	No match – full match	-2.600716	-3.55565 , -1.64578	0.000392
	Full match – position 11 mismatch	1.595208	0.589205 , 2.601211	0.004229
	No match – position 11 mismatch	-1.238501	-2.2445 , -0.2325	0.018366
	No match – full match	-2.833709	-3.83971 , -1.82771	6.74E-05
Protein	Full match – seed match	-35790.49	-62095.774 , -9485.21	0.013808
	No match – seed match	-5892.439	-32197.724 ,20412.85	0.779224

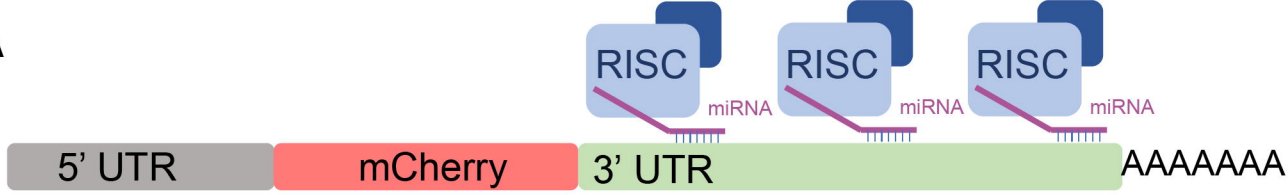
	No match – full match	29898.05	3592.766 , 56203.34	0.030149
	Full match – seed + supplementary match	-40122.849	-67276.71 , -12969	0.009418
	No match – seed + supplementary match	-1604.372	-28758.24 , 25549.49	0.982099
	No match – full match	38518.477	11364.61 , 65672.34	0.0114
	Full match – position 10-11 mismatch	-20684.861	-30598.14 , -10771.6	0.001664
	No match – position 10-11 mismatch	7165.728	-2747.55 , 17079	0.146316
	No match – full match	27850.588	17937.31 , 37763.87	0.00033
	Full match – position 10 mismatch	-8511.601	-19674.01 , 2650.81	0.125255
	No match – position 10 mismatch	24822.125	13659.71 , 35984.54	0.001186
	No match – full match	33333.726	22171.32 , 44496.14	0.000234
	Full match – position 11 mismatch	-3368.935	-12422.04 , 5684.172	0.525893
	No match – position 11 mismatch	19866.46	10813.35 , 28919.57	0.001273
	No match – full match	23235.395	14182.29 , 32288.5	0.000544
mRNA injections	Full match – seed match	25544.14	15900.65 , 35187.64	0.00291
	No match – seed match	1314.016	-7896.52 , 10524.55	0.897144
	No match – full match	-24230.127	-31337.1 , -17123.2	0.001204

Table1 - one-way ANOVA pairwise comparisons

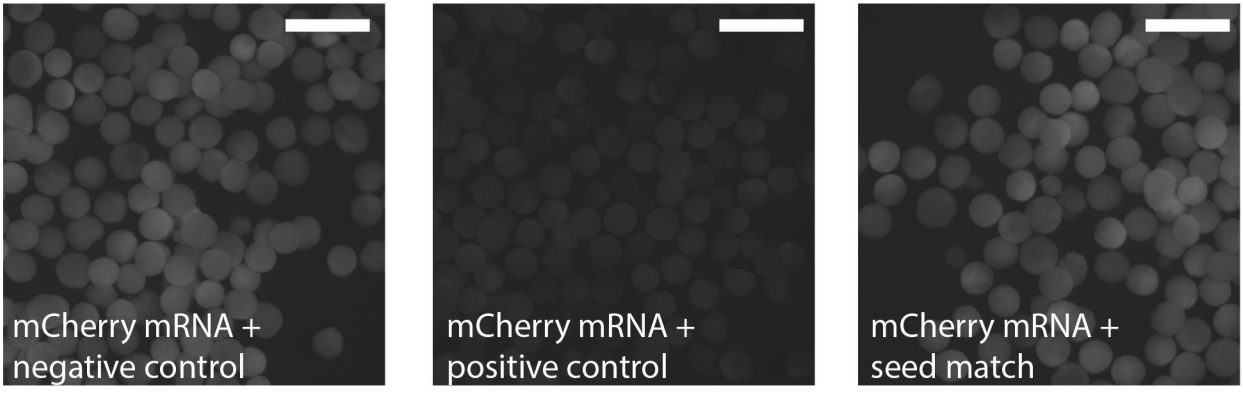
Post-hoc test results of pairwise comparisons between injected groups. Including difference of means for mCherry transcript (Δ Ct) or protein concentration, confidence interval and adjusted p-value for multiple comparisons. P-value was adjusted with Tukey's HSD for most experiments and with Games-Howell for mRNA injections. Full match refers to positive control group injected with nearly-full complementarity mimiR. No match refers to negative control group injected with shRNA with no match in *Nematostella* genome.


A
Nearly-full complementarity positive control
Seed match
Seed + supplemental matches
Mismatch positions 10 - 11
Mismatch positions 10 or 11
RISC
miRNA
mRNA
AAAAAA
B
Negative control
Positive control
Seed match
C
Negative control
Positive control
Seed + supplemental matches
D
Negative control
Positive control
Mismatch positions 10-11
E
Negative control
Positive control
Mismatch position 10
F
Negative control
Positive control
Mismatch position 11
G
Negative control - no match
Positive control - full match
Partial match
Transcript levels
Fold change
Seed match
Seed + supplemental matches
Position 10-11 mismatch
Position 10 mismatch
Position 11 mismatch
H
Protein levels
mCherry protein concentration (pg/ml)
Seed match
Seed + supplemental matches
Position 10-11 mismatch
Position 10 mismatch
Position 11 mismatch

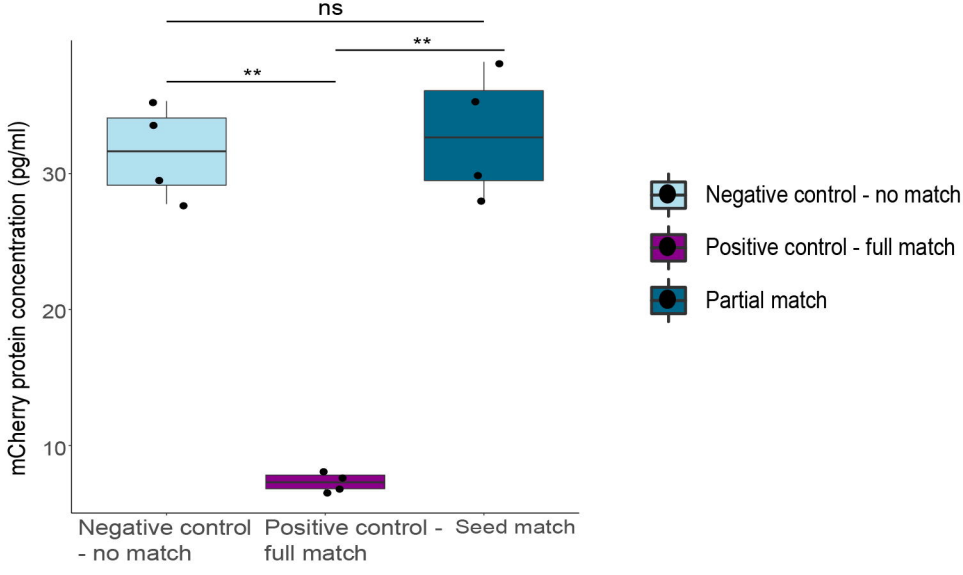
A

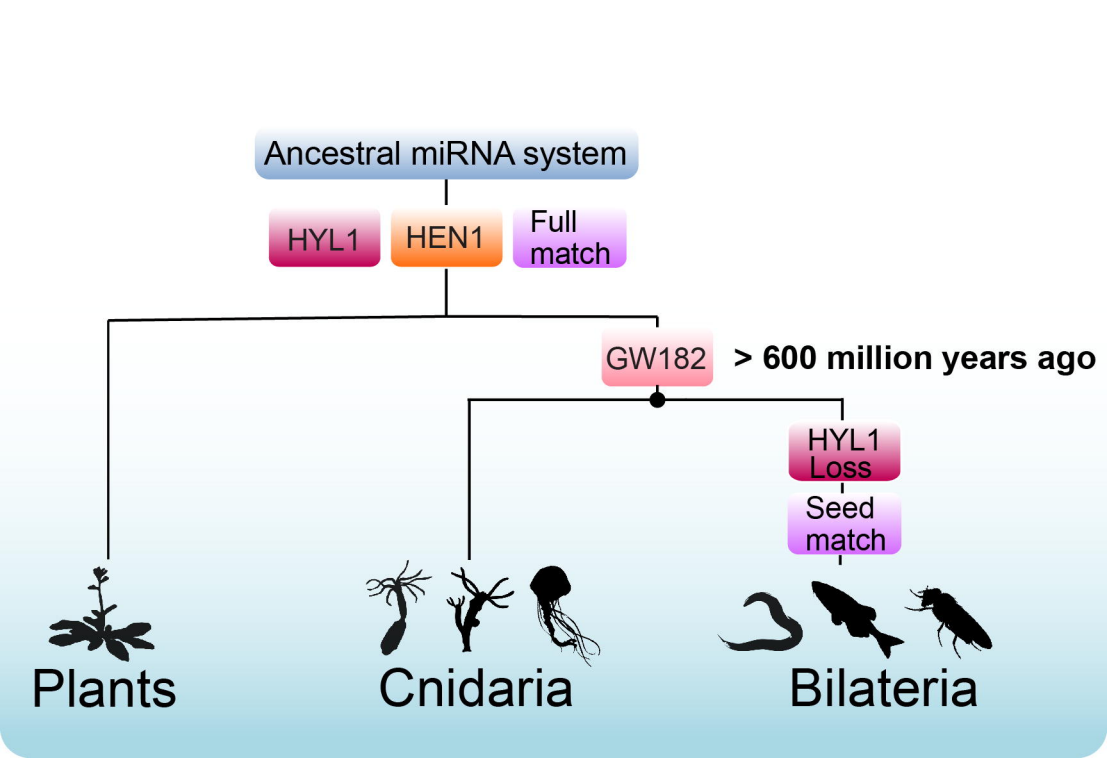

RISC
miRNA
RISC
miRNA
RISC
miRNA
5' UTR
mCherry
3' UTR
AAAAAAA

B


mCherry mRNA +
negative control
mCherry mRNA +
positive control
mCherry mRNA +
seed match

C


ns
**
**
mCherry protein concentration (pg/ml)
30
20
10
Negative control - no match
Positive control - full match
Seed match
Negative control - no match
Positive control - full match
Partial match


Ancestral miRNA system
HYL1
HEN1
Full match
GW182
> 600 million years ago
HYL1 Loss
Seed match
Plants
Cnidaria
Bilateria