### Title
Molecular evolution of microRNAs in bilaterian animals revealed by large-scale genomic analysis

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### Abstract
MicroRNAs (miRNAs) are small noncoding RNAs that regulate the expression of messenger RNAs (mRNAs). Although miRNAs may have strongly influenced the evolution of animals, the details of their evolution are yet to be resolved. Therefore, I have sought to clarify miRNA evolution by analyzing the conservation of miRNAs in both model and non-model species.

First, I predicted the fundamental regulatory relationships between miRNAs and their target genes that have been conserved throughout the evolution of the bilaterian animals. For this purpose, I designed a bioinformatics procedure to extract conserved miRNA/target-gene pairs, which predicted 31 evolutionarily conserved miRNA/target-gene pairs. The downregulation of six of these pairs was observed in HeLa cells, using a reporter-gene assay. I inferred that these pairs were present in the primitive gene regulatory network of the common bilaterian ancestor.

I also examined the "living fossil" Triops cancriformis, the tadpole shrimp. Because this non-model species has an interesting evolutionary history and morphology, I hypothesized that as-yet-undiscovered miRNA regulatory mechanisms and evolutionary trends would be revealed by comparing the miRNAs of this organism with those of model species. Deep-sequencing identified 180 miRNAs and six components of the RNAi machinery. The expression patterns of four of the conserved T. cancriformis miRNAs differed from those of Drosophila melanogaster. Most of the conserved T. cancriformis miRNAs share sequence similarities with those of the arthropods. However, the let-7 sequence and domains of DICER are more similar to those of the vertebrates, suggesting that the miRNA system of T. cancriformis evolved in a unique way.

In conclusion, even when the miRNA target genes are conserved among species, they may function differently depending on their expression patterns. I discuss the evolution of miRNAs in bilaterian animals with reference to the miRNA biology in model and non-model species.

### Notes
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Keywords: microRNA, evolution, development, genome informatics, comparative analysis