

## Ancient animal microRNAs and the evolution of tissue identity

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Top of page

### Abstract

**The spectacular escalation in complexity in early bilaterian evolution correlates with a strong increase in the number of microRNAs<sup>1,2</sup>. To explore the link between the birth of ancient microRNAs and body plan evolution, we set out to determine the ancient sites of activity of conserved bilaterian microRNA families in a comparative approach. We reason that any specific localization shared between protostomes and deuterostomes (the two major superphyla of bilaterian animals) should probably reflect an ancient specificity of that microRNA in their last common ancestor. Here, we investigate the expression of conserved bilaterian microRNAs in *Platynereis dumerilii*, a protostome retaining ancestral bilaterian features<sup>3,4</sup>, in *Capitella*, another marine annelid, in the sea urchin *Strongylocentrotus*, a deuterostome, and in sea anemone *Nematostella*, representing an outgroup to the bilaterians. Our comparative data indicate that the oldest known animal microRNA, miR-100, and the related miR-125 and let-7 were initially active in neurosecretory cells located around the mouth. Other sets of ancient microRNAs were first present in locomotor ciliated cells, specific brain centres, or, more broadly, one of four major organ systems: central nervous system, sensory tissue, musculature and gut. These findings reveal that microRNA evolution and the establishment of tissue identities were closely coupled in bilaterian evolution. Also, they outline a minimum set of cell types and tissues that existed in the protostome–deuterostome ancestor.**

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