MicroRNA functions in animal development and human disease

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Summary

Five years into the ‘small RNA revolution’ it is hard not to share in the excitement about the rapidly unravelling biology of microRNAs. Since the discovery of the first microRNA gene, lin-4, in the nematode Caenorhabditis elegans, many more of these short regulatory RNA genes have been identified in flowering plants, worms, flies, fish, frogs and mammals. Currently, about 2% of the known human genes encode microRNAs. MicroRNAs are essential for development and this review will summarise our current knowledge of animal microRNA function. We will also discuss the emerging links of microRNA biology to stem cell research and human disease, in particular cancer.

Introduction

MicroRNAs (miRNAs) are about 22-nucleotide, short, non-coding RNAs that are thought to regulate gene expression through sequence-specific base pairing with target mRNAs. Hundreds of microRNAs have been identified in worms, flies, fish, frogs, mammals and flowering plants using molecular cloning and bioinformatics prediction strategies (Lagos-Quintana et al., 2001; Lau et al., 2001; Lee and Ambros, 2001; Lim et al., 2003a; Llave et al., 2002; Reinhart et al., 2002; Watanabe et al., 2005). MicroRNAs are transcribed as long RNA precursors (pri-miRNAs) that contain a stem-loop structure of about 80 bases. Pri-miRNAs are processed in the nucleus by the RNase III enzyme Drosha and DGCR8/Pasha, which excises the stem-loop to form the pre-miRNA (Denli et al., 2004; Gregory et al., 2004; Han et al., 2004; Landthaler et al., 2004; Lee et al., 2003). Pre-miRNAs are exported from the nucleus by Exportin-5 (Bohnsack et al., 2004; Lund et al., 2003; Yi et al., 2003). In the cytoplasm, another RNase III enzyme, Dicer, cuts the pre-miRNA to generate the mature microRNA as part of a short RNA duplex. The RNA is subsequently unwound by a helicase activity and incorporated into a RNA-induced silencing complex (RISC). For more information on microRNA biogenesis and maturation, please see the accompanying article by Du and Zamore (Du and Zamore, 2005).

Most microRNAs in animals are thought to function through the inhibition of effective mRNA translation of target genes through imperfect base pairing with the 3’-untranslated region (3’UTR) of target mRNAs (Bartel, 2004). The underlying mechanism is still poorly understood, but it appears to involve the inhibition of translational initiation (Pillai et al., 2005). MicroRNA targets are largely unknown, but estimates range from one to hundreds of target genes for a given microRNA, based on target predictions using a variety of bioinformatics approaches (Brennecke et al., 2005; John et al., 2004; Kiriakidou et al., 2004; Lewis et al., 2005; Lewis et al., 2003; Rajewsky and Socci, 2004; Stark et al., 2003; Xie et al., 2005). In addition, at least one microRNA, miR-196, can cleave a target mRNA, HOXB8, in the same manner as a short interfering RNA (siRNA) does during the process of RNA interference (RNAi) (Mansfield et al., 2004; Yekta et al., 2004). This mechanism is the preferred one for plant microRNAs (Meins et al., 2005). MicroRNAs may also play a role in AU-rich element-mediated mRNA degradation (Jing et al., 2005). See Du and Zamore for a further discussion of this (Du and Zamore, 2005). Finally, the involvement of microRNAs in transcriptional gene silencing (TGS), which has been observed in plants, remains an intriguing possibility (Baulcombe, 2004).

This review focuses on the function of animal microRNAs only. For a recent review of our current understanding of the roles of microRNAs in plants, please see (Kidner and Martienssen, 2005), and for recent accounts of the history of this field, please see recent articles by the pioneers of the field themselves (Lee et al., 2004a; Ruvkun et al., 2004). Here, we describe how microRNAs contribute to different aspects of animal development and what we know of their involvement in human disease (see Table 1).

Developmental timing

Interest in the genes controlling developmental timing in C. elegans (Ambros and Horvitz, 1984; Chalfie et al., 1981; Horvitz and Sulston, 1980) led to the cloning of the first microRNA, lin-4 miRNA (Lee et al., 1993), and the identification of the first microRNA target, lin-14 mRNA (Wightman et al., 1993). The developmental-timing, or heterochronic, pathway regulates stage-specific processes during C. elegans larval development. For a recent, detailed review of this pathway, please see Rougvie (Rougvie, 2005). One focus of the study of the heterochronic pathway in C. elegans has been the developmental fate of several stem cells in the lateral hypodermis, collectively known as the seam cells. The seam cells undergo a cell division pattern that is synchronised with the four larval molts of the animal (Fig. 1A). Only at the adult stage will the seam cells exit mitosis and terminally differentiate. In lin-4 mutant animals, the seam cells repeat the cell division pattern that characterises the first larval stage (L1) and fail to differentiate. This mutant phenotype has been interpreted as a heterochronic change with the
developmental clock being stuck at the L1 stage, resulting in developmental ‘retardation’. Gain-of-function mutations in the lin-4 microRNA target lin-14 lead to an identical phenotype, whereas loss-of-function mutations in lin-14 result in an opposite, ‘precocious’ phenotype, where the seam cells skip the cell division of the first larval stage. The lin-4 and lin-14 gene products therefore act as a developmental switch that controls the L1 to L2 transition (Fig. 1A,B). Three microRNAs of the let-7 family, mir-48, mir-84 and mir-241 act redundantly to control the next developmental transition, from the L2 to the L3 stage (Fig. 1B) (Abbott et al., 2005; Lau et al., 2001; Lin et al., 2005; Reinhart et al., 2000). Loss-of-function mutations in these three microRNAs lead to the repetition of the cell division pattern of the second larval stage, whereas a gain-of-function mutation in mir-48 results in a precocious phenotype. A likely target of mir-48, mir-84 and mir-241 during this transition is the C. elegans hunchback orthologue hbl-1. The microRNA let-7, the second microRNA to be identified (Reinhart et al., 2000), controls the transition from the fourth larval stage to the adult stage, and two of its targets in the heterochronic pathway are the lin-41 and hbl-1 genes, both of which are also heterochronic genes (Abrahante et al., 2003; Lin et al., 2003; Slack et al., 2000). More recently, two additional let-7 target genes, the transcription factor genes daf-12 and pha-4, were identified using a combination of bioinformatics-based prediction and RNAi analyses (Grosshans et al., 2005). daf-12 is also a regulator of the heterochronic pathway controlling seam cell fate (Antebi et al., 1998). Finally, the two let-7 family microRNAs mir-48 and mir-84 also control cessation of the larval molting cycle at the adult stage, with mir-48; mir-84 double mutant animals undergoing a supernumerary molt at the adult stage (Fig. 1A,B) (Abbott et al., 2005).

It is striking that at least two microRNA families and at least four microRNAs are involved in the control of developmental timing in C. elegans. As the lin-4 and let-7 microRNA families are conserved, they might play similar roles in other organisms. This notion is supported by the temporal regulation of let-7 expression in several species (Pasquinelli et al., 2000). However, at least one potential role for let-7 family

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**Table 1. Function of animal microRNAs in vivo**

<table>
<thead>
<tr>
<th>Process</th>
<th>microRNA</th>
<th>Targets</th>
<th>Function</th>
<th>Evidence</th>
<th>Key citations</th>
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<tr>
<td><strong>C. elegans</strong></td>
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<tr>
<td>Developmental timing</td>
<td>lin-4</td>
<td>microRNA</td>
<td>lin-14, lin-28</td>
<td>LOF</td>
<td>Lee et al., 1993; Wightman et al., 1993</td>
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<tr>
<td>Developmental timing</td>
<td>let-7</td>
<td>microRNA</td>
<td>lin-41, hbl-1, daf-12, pha-4</td>
<td>LOF</td>
<td>Reinhart et al., 2000; Abrahante et al., 2003; Lin et al., 2003; Slack et al., 2000; Grosshans et al., 2005</td>
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<tr>
<td>Developmental timing</td>
<td>miR-48, miR-84, miR-241</td>
<td>hbl-1</td>
<td>Stem cell differentiation</td>
<td>LOF</td>
<td>Abbott et al., 2005; Lin et al., 2005</td>
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<tr>
<td>Organogenesis</td>
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<td>Cessation of molting</td>
<td>LOF</td>
<td>Abbott et al., 2005</td>
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<td>Differentiation</td>
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<td>microRNA</td>
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<tr>
<td>Differentiation</td>
<td>mir-273</td>
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<td>cog-1</td>
<td>GOF</td>
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<td><strong>D. melanogaster</strong></td>
<td>bantam</td>
<td>microRNA</td>
<td>hid</td>
<td>LOF</td>
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<tr>
<td>Growth control and programmed cell death</td>
<td>miR-14</td>
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<td>Proliferation/programmed cell death</td>
<td>LOF</td>
<td>Xu et al., 2003</td>
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<td>Programmed cell death</td>
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<td>GOF</td>
<td>Breenecke et al., 2005; Lai, 2002; Lai et al., 2005; Stark et al., 2003</td>
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<tr>
<td>Patterning and embryogenesis</td>
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<td>Neurogenesis</td>
<td>Dicer rescue</td>
<td>Leaman et al., 2005</td>
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<td>Embryogenesis and programmed cell death</td>
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<td><strong>D. rerio</strong></td>
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<td>Differentiation and organogenesis</td>
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<td>GOF</td>
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<td>Differentiation and organogenesis</td>
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<td>Unknown</td>
<td>Hematopoiesis</td>
<td>GOF</td>
<td>Chen et al., 2004</td>
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<td>Insulin secretion</td>
<td>miR-375</td>
<td>Myotrophin (Mtn)</td>
<td>Exocytosis</td>
<td>2-O-Me-RNA</td>
<td>Poy et al., 2004</td>
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<td>Human disease</td>
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<td>Unknown</td>
<td>Tumorigenesis</td>
<td>2-O-Me-RNA</td>
<td>He et al., 2005; O’Donnell et al., 2005</td>
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<tr>
<td>Human disease</td>
<td>miR-32</td>
<td>PFV-1</td>
<td>Viral defense</td>
<td>LNA</td>
<td>Lecellier et al., 2005</td>
</tr>
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</table>

This table includes all microRNAs that have been analyzed in vivo using loss-of-function studies, and microRNAs for which a likely function has been demonstrated by using an indirect approach, e.g. mis-expression experiments. It table does not contain microRNAs for which a target mRNA has been predicted and validated using overexpression experiments, but for which no further functional characterization at the cellular or organismal level has been carried out.

PFV-1, primate foamy virus type 1; E(spl)/bHLH, Enhancer of Split/basic helix loop helix transcription factor cluster; LOF, microRNA has been studied using loss-of-function approaches only; 2-O-Me-RNA, microRNA has been studied by depletion using 2’-O-Methyl antisense oligoribonucleotides; LNA, microRNA has been studied by depletion using locked oligonucleotides (LNA); Dicer rescue, microRNA has been studied using rescue experiments in a Dicer mutant background.
microRNAs outside of the heterochronic pathway has been reported, as discussed below (Johnson et al., 2005).

**Patterning and embryogenesis**
In the absence of loss-of-function mutants for most microRNA genes, organisms with defective microRNA biogenesis are a useful tool for investigating the biological roles of microRNAs, particularly during embryogenesis and early development. This is because such organisms allow one to study the roles of the first set of microRNAs required during development. Dicer knockout mutants have been particularly useful in this regard, although RNAi, and other biological processes as well as microRNA function, might be de-regulated in these mutants. Dicer was first analyzed genetically in *C. elegans*, where it is called DCR-1, and it was found to be essential for germline development (Knight and Bass, 2001). A similar phenotype was observed for *C. elegans* mutants of the other RNase III enzyme required for microRNA biogenesis, Drosha (DRSH-1) (Denli et al., 2004). As *dcr-1* mutants are sterile, all homozygous animals had to be derived from heterozygous mothers. It is likely that maternal contribution of DCR-1 masks earlier abnormal phenotypes. This is supported by the occurrence of additional abnormal phenotypes when *dcr-1* mRNA is inactivated by RNAi (Grishok et al., 2001). RNAi of *dcr-1* mRNA results in a mixed phenotype that includes embryonic lethality and developmental timing defects that are reminiscent of the *lin-4* and *let-7* mutants (Grishok et al., 2001). These observations suggest that microRNAs have essential roles in *C. elegans* embryogenesis. This hypothesis was further supported by RNAi knockdown of the mRNA
Box 1. miRNA knockdown

To study loss-of-function phenotypes of miRNAs in the absence of knockout strains, miRNA knockdown approaches are being developed. Two strategies are based on artificial oligonucleotides, 2′ O-Methyl RNA and locked nucleotide RNA (LNA). The principle for both reagents is the same: an excess of modified RNA complimentary to a miRNA is injected or transfected so that it can compete for the miRNA interaction with its target miRNAs. 2′ O-Methyl RNA offers an increased in vivo half-life over RNA and was initially used in human cells and in C. elegans (Hutvagner et al., 2004; Meister et al., 2004; Poy et al., 2004) for the sequence-specific inhibition of small RNAs for a limited time-span, but it suffers from some pleiotropic effects (Leaman et al., 2005). LNA is a modified ribonucleic acid in which the ribose ring is constrained by a methylene bridge between the 2′ O and the 4′ C atoms. This modification leads to a higher thermal stability and discriminative power due to a greater difference in the melting temperature of a Watson-Crick base pair versus a mismatch (Petersen and Wengel, 2003).

transcripts for the two C. elegans argonaute genes required for miRNA biogenesis, ALG-1 and ALG-2 (Grishok et al., 2001). RNAi-treated worms showed a mixed phenotype that included embryonic and larval lethality and heterochronic defects.

The fruitfly Drosophila melanogaster has two Dicer genes, Dicer-1 and Dicer-2, and genetic analysis suggests that Dicer-1 is the major Dicer gene required for microRNA biogenesis (Lee et al., 2004b). Although the phenotype of Dicer-1 mutant D. melanogaster has not been fully reported, it appears that Dicer-1 is required for wild-type development of both somatic tissues and the germline (Hattfield et al., 2005; Lee et al., 2004b) (for details see below).

In the zebrafish Danio rerio, a likely null allele of Dicer leads to a developmental arrest at 7 to 10 days post-fertilization (Wienholds et al., 2003). This late terminal phenotype is again likely to be due to maternal provision of Dicer and/or of microRNAs. Indeed, removal of the maternal Dicer contribution through the generation of germline clones leads to a more severe defect (Giraldez et al., 2005). In maternal-zygotic Dicer mutants, axis formation and early differentiation are normal, but many embryos have morphogenesis defects affecting gastrulation, brain formation, somitogenesis and heart development.

In the mouse, Mus musculus, Dicer1 mutants die around 7.5 days of gestation (Bernstein et al., 2003). A maternal contribution of Dicer is likely to have a much smaller effect in M. musculus due to the much smaller size of the egg. Homozygous Dicer1 null mutants from heterozygous mothers die around 7.5 days of gestation (Bernstein et al., 2003). Mutant embryos have defects in axis formation and gastrulation, and are depleted of Oct4-positive stem cells (Bernstein et al., 2003). In all cases where only Dicer1 mutants have been analysed, one cannot easily distinguish between defects that are due to a loss of microRNA processing and those that are due to a loss of endogenous RNAi or other pathways regulated by Dicer. For example, Dicer appears to have important roles in heterochromatin formation and chromosome segregation in the fission yeast Schizosaccharomyces pombe, in the ciliated protozoan Tetrahymena and in vertebrate cells (Fukagawa et al., 2004; Mochizuki and Gorovsky, 2005; Provost et al., 2002). As S. pombe does not encode any known microRNAs, these defects are unlikely to be caused by their loss.

A more direct approach to investigating the role of microRNAs during embryogenesis has been taken in D. melanogaster, where 2′ O-Methyl antisense oligoribonucleotides were used in microRNA depletion studies (see Box 1) (Leaman et al., 2005). A single injection of 2′ O-Methyl antisense oligoribonucleotides complementary to the 46 microRNAs known to be expressed in the D. melanogaster embryo resulted in a total of twenty-five different, abnormal phenotypes. These phenotypes included defects in blastoderm cellularization and patterning, morphogenesis and cell survival. Increased programmed cell death was observed in embryos injected with 2′ O-Methyl antisense oligoribonucleotides that targeted the D. melanogaster miR-2 family, and miR-6, miR-11 and miR-308.

Clearly, our current understanding of microRNA function during embryogenesis is only rudimentary. However, it is noteworthy that the only evidence for a role of miRNAs in tissue patterning during embryogenesis to date comes from depletion studies of miR-31 in D. melanogaster (Leaman et al., 2005). Could pattern formation be largely independent of regulation by microRNAs? With this question in mind, it will be exciting to see functional studies of mammalian miR-196, a microRNA that is located in a HOX cluster and can cleave HOXB8 mRNA (Mansfield et al., 2004; Yekta et al., 2004).

Differentiation and organogenesis

The heterochronic phenotypes of the lin-4 microRNA and the let-7 family of microRNAs in C. elegans are clear examples of cell differentiation defects. However, an example of a microRNA regulating differentiation that is uncoupled from cell division was first uncovered through the study of left-right asymmetry in C. elegans (Johnston and Hobert, 2003). In the worm, two bilateral taste receptor neurons, ASE left (ASEL) and ASE right (ASER), display a left/right asymmetrical expression pattern of the normally gcy-5, gcy-6 and gcy-7, three putative chemoreceptor genes (Chang et al., 2003; Hobert et al., 2002) (Fig. 2). In a genetic screen for mutants in which the normally ASE-specific expression of gcy-7 is disrupted, the microRNA gene lsy-6 was isolated (Chang et al., 2003). In lsy-6 mutants, ASEL neurons do not express gcy-7, but instead express the ASER-specific gcy-5 gene. Genetic interaction and GFP reporter studies showed that lsy-6 is a negative regulator of the NKX-type homeobox gene cog-1, which was identified in the same genetic screen. Interestingly, a second microRNA, miR-273, might act upstream in the same pathway as a regulator of die-1, which encodes a C2H2 zinc finger transcription factor (Chang et al., 2004). The transcription factor die-1 shows ASEL-specific expression and acts upstream of lsy-6.

Evidence for a role of microRNAs in organogenesis has come from studies of vulval development in C. elegans. The C. elegans vulva is a ring-like structure that forms the connection between the hermaphrodite gonadal arms and the exterior, and is essential for egg-laying and sperm entry. It derives from a group of cells in the ventral hypodermis that are induced to undergo a series of cell divisions and differentiation by a signal from the gonadal anchor cell (Sulston and Horvitz, 1977). Vulval induction requires RAS/LET-60 signalling
(Beitel et al., 1990). Let-7 loss-of-function mutants die by bursting at the vulva (Reinhart et al., 2000; Slack et al., 2000), and this bursting is suppressed by RNAi against the C. elegans RAS orthologue LET-60 (Johnson et al., 2005). Furthermore, overexpression of the let-7 family microRNA miR-84 suppresses the let-60 gain-of-function phenotype. 3’UTR reporter experiments suggest that RAS/LET-60 expression levels are regulated post-transcriptionally and may be directly regulated by the let-7 family of microRNAs (Johnson et al., 2005).

In D. melanogaster, the discovery of an important role for post-transcriptional control of the Notch signalling pathway predates the discovery of the first microRNA in D. melanogaster by over a decade. The Notch signalling pathway is an evolutionary conserved signal transduction cascade that is required for patterning and normal development (Lai, 2004). Two clusters of Notch signalling target genes exist in D. melanogaster: the Enhancer of split-Complex and the Bearded-Complex, which encode transcription factors of the basic helix-loop-helix repressor and the Bearded families, respectively (Knust et al., 1992; Lai et al., 2000a; Lai et al., 2000b; Wurmbach et al., 1999). Gain-of-function alleles in members of these gene families were found to be due to short deletions in conserved regions of their 3’UTRs (Knust, 1997; Leviten et al., 1997). These 6- to 7-nucleotide motifs were named the GY-box, the Brd-box and the K-box. Some of these motifs have been shown to post-transcriptionally control the Enhancer of split-Complex and the Bearded-Complex genes (Lai et al., 1998; Lai and Posakony, 1997). More recently, it has been noted that GY-, Brd- and K-box sequences are complimentary to the newly identified D. melanogaster microRNAs (Lagos-Quintana et al., 2001; Lai, 2002). Candidate microRNAs regulating these motifs include three microRNA families and the following microRNAs: miR-2, miR-4, miR-5, miR-6, miR-7, miR-11 and miR-79 (Brennecke et al., 2005; Lai, 2002; Lai et al., 2005; Stark et al., 2003). Although no loss-of-function analyses of any of these microRNAs have been carried out, overexpression of some of them causes defects reminiscent of Notch loss-of-function mutants. These include notched wings and wing vein abnormalities, an increased number of micro- and macrochaetes (small and large bristles) in the adult notum, tufted sternopleural bristles and an increase in sensory organ precursor cells in imaginal discs (Lai et al., 2005). Interestingly, the list of microRNAs that might regulate Notch overlaps considerably with the microRNAs that were found to play important roles during embryogenesis in the 2’ O-Methyl antisense oligonucleotides microRNA depletion studies previously discussed (Leaman et al., 2005).

As outlined above, the analysis of Dicer mutant animals suggests that microRNAs have important roles to play during differentiation and organogenesis in D. rerio. In particular, neurogenesis, somitogenesis, and ear, eye and heart development were found to be disrupted in maternal-zygotic Dicer mutants (Giraldez et al., 2005). It is as yet unclear whether all of these defects are due to the lack of microRNAs or other Dicer-dependent processes. No microRNA knockout zebrafish strains are currently available; however, rescue experiments in maternal-zygotic Dicer mutant animals suggest an important role for the miR-430 family of microRNAs in neurogenesis (Giraldez et al., 2005). Maternal-zygotic Dicer mutant embryos have severe neurulation defects. Formation of the neurocoel and neural tube is impaired in these mutants, as is the formation of the brain ventricles and the midbrain-hindbrain boundary. Surprisingly, the injection of a single microRNA, miR-430, a member of a large family of microRNAs that is related to the miR-302 and miR-17 families (see below), rescued some aspects of this mutant phenotype. Injection of miR-430, but not of an unrelated microRNA, resulted in normal brain ventricles and a rescue of the midbrain-hindbrain boundary. In addition, miR-430 injection led to a partial rescue of gastrulation, retinal development and somatogenesis, but not of heart or ear development. Together, these findings clearly demonstrate that at least a subset of the abnormal phenotypes of maternal-zygotic Dicer mutant animals are due to the loss of microRNAs. In the absence of microRNA knockout strains, the maternal-zygotic Dicer knockout provides a unique system in which to study the function of other microRNAs in the zebrafish. The recent description of microRNA expression patterns in developing D. rerio using in situ hybridization provides a potential resource for candidate microRNA selection (Wienholds et al., 2005).

Similar to D. rerio, and with the same caveats, M. musculus Dicer1 mutant animals indicate that microRNAs have wide-ranging roles in differentiation and development during mouse embryogenesis (Bernstein et al., 2003) (see above). In the
mouse, additional insights can be gained from studying conditional-knockout strains, which allow one to the study the requirement for Dicer and microRNAs in different tissues at different developmental time points. In vitro, Dicer mutant embryonic stem (ES) cells, derived from conditional gene targeting, have severe differentiation defects (Kanellopoulou et al., 2005). One study that analyzed the effects of genetically inactivating Dicer1 early during T-cell development found evidence for the functioning of microRNAs in αβ cells, but not in CD4/CD8, lineage commitment (Cobb et al., 2005). Another study found that knocking out Dicer1 during T-cell development blocked peripheral CD8+ T-cell development, whereas CD4+ T cells, although reduced in numbers, were viable; however, upon stimulation, these CD4+ T cells proliferated poorly and underwent increased programmed cell death (Muljo et al., 2005).

The particular caveat with these conditional-knockout studies in mice is that it is often unclear how efficiently Dicer and any existing microRNA pools are depleted upon the somatic deletion of Dicer1. Indeed, microRNAs seem to persist for some time (Cobb et al., 2005). One specific microRNA that has been directly implicated in B-cell development is miR-181 (Chen et al., 2004). This microRNA is highly expressed in B-lymphoid cells of mouse bone marrow. When overexpressed in hematopoietic progenitor cells, it leads to an increase in the fraction of B-lineage cells in in vitro differentiation experiments and in vivo in adult mice. Conditionally inactivating Dicer1 in discrete areas of the limb mesoderm in mice led to severe growth defects in the limbs of mutant embryos, but no defect in basic limb patterning or in tissue-specific differentiation was observed (Harfe et al., 2005). This is a striking finding that is somewhat reminiscent of the Dicer1 knockout in D. reio. However, it remains unknown whether residual Dicer activity or microRNA pools could have disguised earlier roles of microRNAs in limb development.

MicroRNA expression analysis has led to the discovery of a potential role for the microRNA mir-1 in mammalian heart development. The microRNA miR-1, which is the product of two genes, mir-1-1 and mir-1-2, is highly expressed in mouse heart and muscle (Lagos-Quintana et al., 2001; Lee and Ambros, 2001). An analysis of the upstream-regulatory sequence of these two genes has led to the identification of serum response factor (Srf), myocardin, Mef2 and Myod as transcriptional regulators of miR-1 expression in vitro (Zhao et al., 2005). Of these, Srf was found to be required for miR-1 expression in the developing mouse heart, using a conditional Srf-knockout strain (Zhao et al., 2005). Overexpression of miR-1 under the β-myosin heavy chain promoter resulted in developmental arrest at embryonic day 13.5, after heart failure. Transgenic embryos developed thin ventricle walls and ventricular cardiomyocyte proliferation defects. One candidate target for miR-1 in myocardial development is the transcription factor Hand2, which was found to be reduced in transgenic mice overexpressing miR-1 without an apparent change in Hand2 mRNA levels (Zhao et al., 2005).

**Growth control and programmed cell death**

The D. melanogaster bantam gene was identified in a gain-of-function screen for regulators of cell growth (Hipfner et al., 2002). Overexpression of bantam causes the overgrowth of wing and eye tissue, whereas bantam loss-of-function mutant animals are smaller than wild-type animals and have reduced cell numbers. Bantam was found to interact with the growth regulatory gene expanded, but was epistatic to the CycD/Cdk4 pathway. Subsequent cloning of bantam identified it as a microRNA-encoding gene (Brennecke et al., 2003). The bantam microRNA regulates tissue growth cell autonomously. Overgrowth phenotypes due to overexpression of bantam do not result in increased levels of programmed cell death, and bantam overexpression rescued programmed cell death induced by overexpression of the transcription factor E2A element-binding factor (E2F) and its dimerisation partner (DP). Bantam overexpression also blocked programmed cell death induced by overexpression of the pro-apoptotic gene hid/Wrinkled (Fig. 3). Furthermore, Hid was shown to be the likely direct target of bantam mRNA (Brennecke et al., 2003). It is unclear whether the small body size of bantam mutant flies is due to the increased activity of Hid or the de-regulation of other target genes. A second D. melanogaster microRNA, miR-14, was also found to suppress programmed cell death (Xu et al., 2003). Whether this is a direct effect of the de-regulation of pro-apoptotic genes remains to be determined. Increased levels of programmed cell death were also found in depletion experiments using 2′O-Methyl antisense oligoribonucleotides targeting the D. melanogaster miR-2 family, miR-6, miR-11 and miR-308 (Leaman et al., 2005) (see previous discussion). Finally, the deletion of Dicer-1 in Drosophila results in a growth defect in germline stem cells (Hatfield et al., 2005) (see below). Together, these observations suggest an important role for microRNAs in growth control during D. melanogaster development.

Additional links between microRNAs, growth control and programmed cell death have also come from other species. The phenotype of mir-48; mir-84; mir-241 mutants in C. elegans is one of cellular overgrowth (Abbott et al., 2005). In D. reio, the zygotic removal of Dicer results in a larval growth arrest (Wienholds et al., 2003) (see above). And, finally, in M. musculus, removal of Dicer in the limb mesoderm leads to a dramatic programmed cell death in the developing limb (Harfe et al., 2005).

**Stem cells and the germline**

The first two microRNAs to be identified, the C. elegans microRNAs lin-4 and let-7, control cell divisions in the hypodermal blast lineage (Ambros and Horvitz, 1984; Chalfie et al., 1981; Horvitz et al., 1983). In the absence of either gene, this stem cell lineage fails to differentiate and continues its proliferative cycle. More recently, other let-7 family members have also been shown to be involved in the differentiation of this stem cell lineage (Abbott et al., 2005; Lin et al., 2005). In the mouse, Dicer is required for embryonic stem cell differentiation in vitro (Kanellopoulou et al., 2005) (see above). And in early Dicer1 mutant mouse embryos, the pool of pluripotent stem cells that is required for the proliferation of cells in the inner cell mass of the blastocyst is diminished, as assayed by in situ hybridization using probes against Oct4 mRNA (Bernstein et al., 2001). It is unclear whether the pool of Oct4 mRNA-positive cells fails to expand, differentiates or undergoes programmed cell death. The identities of any microRNAs that may be required for stem cell maintenance in the mouse are currently unknown. However, expression studies...
in ES cell lines and in mouse embryoid bodies have identified microRNAs (miR-302 family) that are specifically expressed in ES cells but not in adult mouse tissues (Houbaviy et al., 2003; Suh et al., 2004). These microRNAs may be candidates for stem cell renewal factors.

Suggestions for a role of microRNAs in the germline initially came from the analysis of Dicer loss-of-function mutants in C. elegans (Knight and Bass, 2002). However, it remained unclear whether microRNA-processing defects were the underlying cause of the sterility. Subsequently, Drosha was also shown to be required for fertility in C. elegans (Denli et al., 2004). No detailed analysis of either phenotype has been reported to date. However, such an analysis has been carried out in D. melanogaster Dicer-1 mutants. Dicer-1 is one of two Dicer genes in the fly and is the one that is largely required for microRNA biogenesis (Lee et al., 2004b), as previously discussed. It is unclear whether Dicer-1 is also required for other RNA-dependent processes. Dicer-1 mutant animals have somatic and germline defects (Lee et al., 2004b). The generation of germline mutant clones has revealed that defects exist in the maintenance of the germline stem cell pool (Hatfield et al., 2005). A Dicer-1 mutant germline had reduced germline cyst production. Based on cell-cycle marker analysis and epistasis experiments, germline stem cells appeared to be blocked in the G1/S transition phase. No microRNA required for germline stem cell proliferation has yet been identified.

**Human disease**

Many of the functional roles of microRNAs discussed above hint at the potential involvement of microRNAs in human disease. For example, the lin-4 and let-7 mutant phenotypes observed in C. elegans can be interpreted as growth defects (Ambros and Horvitz, 1984; Chalfie et al., 1981; Horvitz et al., 1983). The let-7 family of microRNAs may also be regulators of the proto-oncogene RAS. In D. melanogaster, the bantam microRNA and miR-14 are required for growth control; for example, through the regulation of programmed cell death (Brennecke et al., 2003; Xu et al., 2003). If microRNAs are major regulators of growth and proliferation, is there also evidence for roles of microRNAs in human cancer? Many microRNAs are de-regulated in primary human tumours (Calin et al., 2002; Calin et al., 2004a; He et al., 2005; Lu et al., 2005). Moreover, many human microRNAs are located at genomic regions linked to cancer (Calin et al., 2004b; McManus, 2003). Of particular interest is the mir-17 microRNA cluster, which is in a region on human chromosome 13 that is frequently amplified in B-cell lymphomas (He et al., 2005). Overexpression of the mir-17 cluster was found to co-operate with Myc to accelerate tumour development in a mouse B-cell lymphoma model. Further evidence for such a link between Myc and the mir-17 cluster has come from microarray expression studies, which showed that mir-17 cluster gene expression was induced by the overexpression of Myc (O’Donnell et al., 2005). Predicted targets for the mir-17 cluster microRNAs include members of the E2F and retinoblastoma families (Lewis et al., 2003; mir-17 cluster microRNAs have been found to downregulate E2F1 expression (O’Donnell et al., 2005).

Another potential link between microRNAs and human disease comes from the identification of an essential co-factor for the microRNA biogenesis enzyme Drosha. This cofactor is encoded by DGCR8, which maps to chromosomal region 22q11.2, which is commonly deleted in DiGeorge syndrome (Denli et al., 2004; Gregory et al., 2004; Han et al., 2004; Landthaler et al., 2004; Lee et al., 2003; Lindsay, 2001; Shiohama et al., 2003). Haploinsufficiency of this region accounts for over 90% of individuals with DiGeorge syndrome, a disorder that affects 1 in 3,000 live births and results in heterogeneous defects including heart defects, immunodeficiency, schizophrenia and obsessive-compulsive disorder, among others. If indeed haploinsufficiency of DGCR8 contributes to DiGeorge syndrome, reduced levels of specific miRNAs may be to blame.

Potential roles of microRNAs in the development of the immune system have been discussed above; however, microRNAs might also be involved in immune defence. A cellular microRNA, miR-32, can regulate primate foamy virus type 1 (PFV-1) proliferation in cell culture (Lecellier et al., 2005). In addition, large DNA viruses of the herpesvirus family, including EBV (Pfeffer et al., 2005; Pfeffer et al., 2004) and SV40 (Sullivan et al., 2005), encode viral microRNA genes. These viral microRNAs have no apparent homologues in host genomes and their function is currently not understood.

**Evolution**

The labelling of C. elegans lin-4 and let-7 as heterochronic genes (Ambros and Horvitz, 1984) was highly provocative, suggesting potential roles for these genes during evolutionary change, but was well received by the evolutionary biology...
community (Gould, 2000). With the identification of lin-4 and let-7 as microRNAs, their small size added only to the attractiveness of an evolutionary role for these genes. But how quickly do microRNAs themselves evolve? One of the early, exciting findings in the field was the realization that the let-7 microRNA is 100% conserved between C. elegans and humans (Pasquinelli et al., 2003). Overall, about 40% of the C. elegans microRNA families are conserved in humans (Lim et al., 2003b) (Fig. 4). By contrast, many primate-specific microRNAs that have no counterparts in the mouse have been identified (Berezikov et al., 2005), and several microRNA-encoding genes occur in highly repetitive and fast-evolving regions of the genome, such as in LINE-2 transposable elements (Smalheiser and Torvik, 2005). For the mir-17 cluster and the microRNAs in the HOX gene cluster, an evolutionary analysis has been reported (Tanzer et al., 2005; Tanzer and Stadler, 2004). These initial studies suggest that microRNA families, rather than single microRNAs, are evolutionary conserved. One of the next questions to answer will be how the interactions between microRNAs and their targets evolve.

Conclusions

Research over the past five years has put microRNAs at centre stage. Early cloning experiments (Lagos-Quintana et al., 2001; Lau et al., 2001; Lee and Ambros, 2001) combined with expression studies (e.g. Wienholds et al., 2005), global approaches (such as Dicer knockouts) and selected functional studies have generated a tremendous amount of excitement about microRNAs in many areas of biology (see Table 1). In parallel, many new tools for the study of microRNAs have been developed (see Du and Zamore, 2005). We expect that soon we will appreciate what we have learned about microRNAs to date is just the tip of the iceberg.

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References


Fig. 4. MicroRNA family conservation. MicroRNAs can be grouped into families according to primary sequence similarity. As a cut-off, we used less than five conserved nucleotides out of the first eight. This Venn diagram shows the conservation of microRNA families between C. elegans, D. melanogaster and mammals. Primary sequence data was obtained from MiRBase version 7.0 (Griffiths-Jones, 2004).


