

miRNA annotation

- **A uniform system for microRNA annotation**
- VICTOR AMBROS, BONNIE BARTEL, DAVID P. BARTEL, CHRISTOPHER B. BURGE, JAMES C. CARRINGTON, XUEMEI CHEN, GIDEON DREYFUSS, SEAN R. EDDY, SAM GRIFFITHS-JONES, MHAIRI MARSHALL, MARJORI MATZKE, GARY RUVKUN, and THOMAS TUSCHL *RNA* 2003 9: 277-279

Expression criteria

- A. Detection of a distinct ~ 22 -nt RNA transcript by hybridization to a size-fractionated RNA sample (ordinarily by the Northern blotting method).
- B. Identification of the ~ 22 -nt sequence in a library of cDNAs made from size-fractionated RNA. Such sequences must precisely match the genomic sequence of the organism from which they were cloned

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Biogenesis criteria

- C. Prediction of a potential fold-back precursor structure that contains the ~ 22 -nt miRNA sequence within one arm of the hairpin.
 - the hairpin must be the folding alternative with the lowest free energy,
 - The hairpin must include at least 16 bp involving the first 22 nt of the miRNA and the other arm of the hairpin.

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- The hairpin should not contain large internal loops or bulges,
 - Animal: these fold-back precursors 60-80 nt
 - Plant: more variable, upto a few hundred nt

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- D. Phylogenetic conservation of the \sim 22-nt miRNA sequence and its predicted fold-back precursor secondary structure.
 - Minimal pairing requirement
- E. Detection of increased precursor accumulation in organisms with reduced Dicer function.

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- $A+D+E$ but $A+D$ is sufficient in the absence of processing data
- $A > B$
- $D > C$

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- miRNA: single molecule fold-back structure
- siRNA: RNA that are processed by Dicer from a hybrid between two antiparallel transcripts

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- miR prefix + unique identifying number
 - miR-1, miR-2
- The genes that encode the miRNA:
 - Three letter prefix
 - Some cases, hyphen
 - Capitalization
 - Italic
 - *MIR156, mir-1*

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- The identifying numbers: sequentially
 - with identical miRNAs having the same number, regardless of organism.
 - Nearly identical ortholog?
- Identical or very similar miRNA sequences within a species can also be given the same number, with their genes distinguished by letter and/or numeral suffixes
 - *mir-13a mir-13b*

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