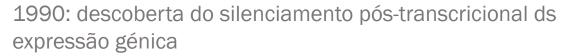
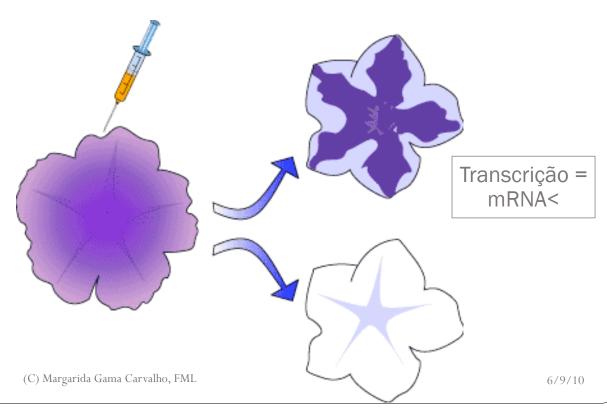
Parte III: Manipulação da informação

RNAi e microRNAs

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"for their discovery of RNA interference - gene silencing by double-stranded RNA"





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Potent and specific genetic interference by double-stranded RNA in Caenorhabditis elegans

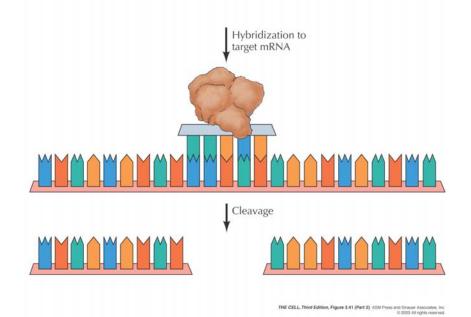
Andrew Fire*, SiQun Xu*, Mary K. Montgomery* Steven A. Kostas*†, Samuel E. Driver‡ & Craig C. Mello‡

* Carnegie Institution of Washington, Department of Embryology, 115 West University Parkway, Baltimore, Maryland 21210, USA † Biology Graduate Program, Johns Hopkins University, 3400 North Charles Street, Baltimore, Maryland 21218, USA ‡ Program in Molecular Medicine, Department of Cell Biology, University of Massachusetts Cancer Center, Two Biotech Suite 213, 373 Plantation Street, Worcester, Massachusetts 01605, USA

Experimental introduction of RNA into cells can be used in certain biological systems to interfere with the function of an endogenous gene^{1,2}. Such effects have been proposed to result from a simple antisense mechanism that depends on hybridization between the injected RNA and endogenous messenger RNA transcripts. RNA interference has been used in the nematode Caenorhabditis elegans to manipulate gene expression34. Here we investigate the requirements for structure and delivery of the interfering RNA. To our surprise, we found that double-stranded RNA was substantially more effective at producing interference than was either strand individually. After injection into adult animals, purified single strands had at most a modest effect, whereas double-stranded mixtures caused potent and specific interference. The effects of this interference were evident in both the injected animals and their progeny. Only a few molecules of injected double-stranded RNA were required per affected cell, arguing against stochiometric interference with endogenous



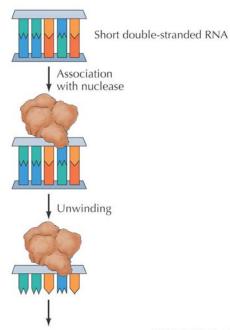
Interferência de RNA



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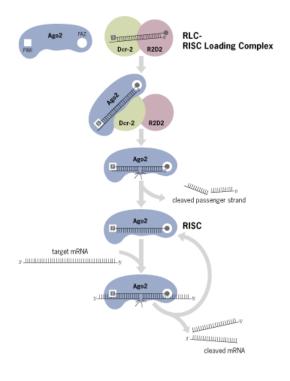
Interferência de RNA



THE CELL, Third Edition, Figure 3.41 (Part 1) ASM Press and Sinauer Associates, Inc. © 2003 All rights reserved.

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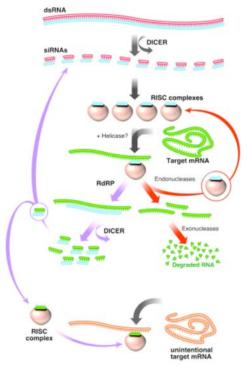
O Complexo RISC



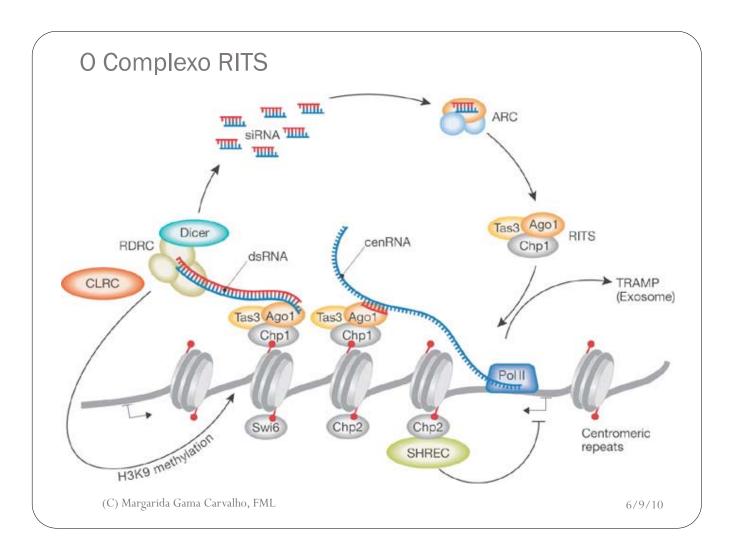
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Amplificação da interferência de RNA



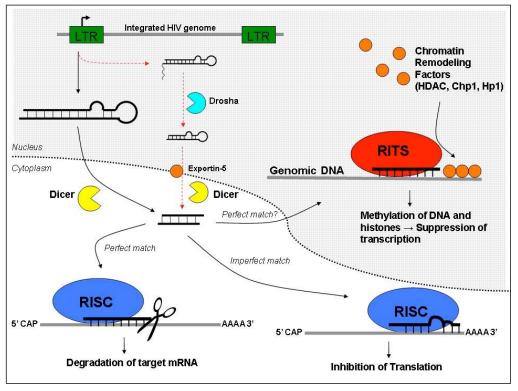
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Para que é que isto serve?

- Defesa contra transposões e genomas virais!
- Mas como sempre os vírus evoluíram armas de contra-ataque e aproveitamento dos mecanismos celulares:

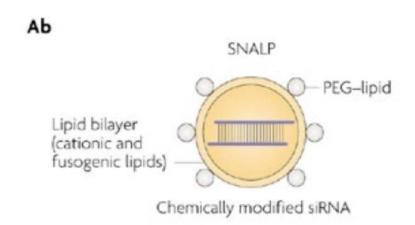
O HIV aproveita a via do complexo RITS para induzir a latência dos genomas integrados



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siRNAs no silenciamento de genes – uma nova arma na investigação e terapêutica



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A descoberta dos microRNAs

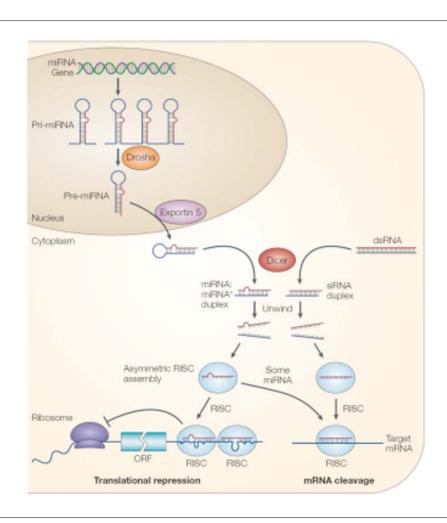
Cell, Vol. 75, 843-854, December 3, 1993, Copyright © 1993 by Cell Press

The C. elegans Heterochronic Gene *lin-4* Encodes Small RNAs with Antisense Complementarity to *lin-14*

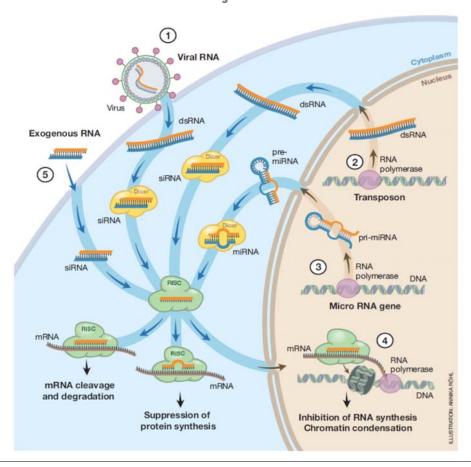
Rosalind C. Lee,*† Rhonda L. Feinbaum,*‡
and Victor Ambros†
Harvard University
Department of Cellular and Developmental Biology
Cambridge, Massachusetts 02138

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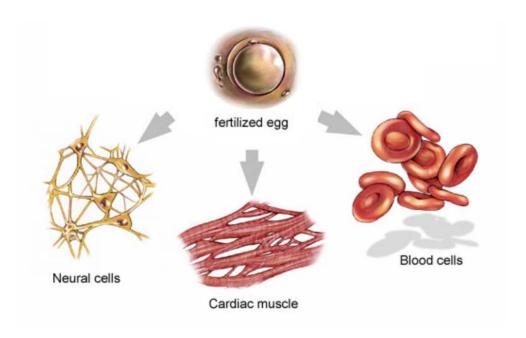
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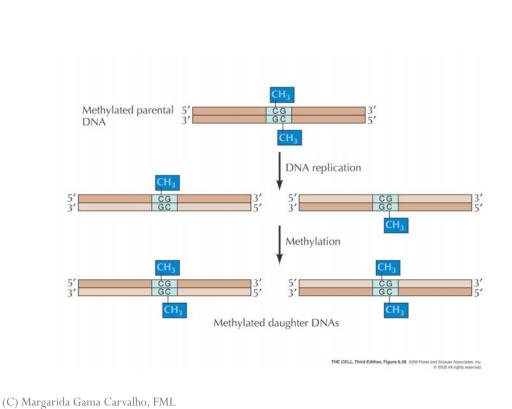


Sumário: mecanismo de acção de siRNAs e miRNAs



RNAs não codificantes e diferenciação celular





Metilação dependente de RNA nas plantas

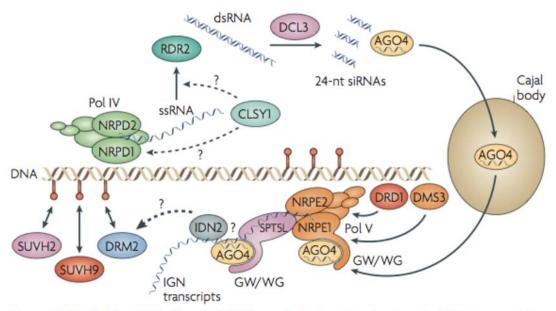


Figure 2 | Model for RNA-directed DNA methylation. Single-stranded RNA transcripts

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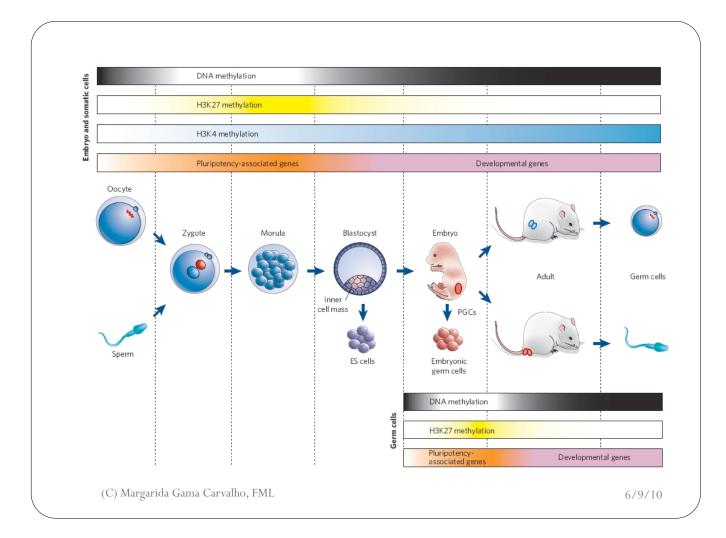
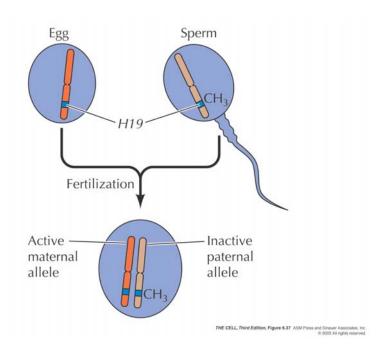


Figure 3: Epigenetic gene regulation during mammalian development.

This figure depicts key developmental events together with global epigenetic modifications and gene expression patterns. Very early in development, DNA methylation is erased. In addition, pluripotency-associated genes begin to be expressed, and developmental genes are repressed by the PcG protein system and H3K27 methylation. During the differentiation of pluripotent cells such as embryonic stem (ES) cells, pluripotency-associated genes are repressed, potentially permanently, as a result of DNA methylation. At the same time, developmental genes begin to be expressed, and there is an increase in H3K4 methylation. During the early development of primordial germ cells (PGCs), DNA methylation and repressive histone modifications (such as H3K9 methylation) are also erased. Pluripotency-associated genes are re-expressed during a time window that allows embryonic germ cells to be derived in culture. Imprinted genes are demethylated during this period, and developmental genes are expressed afterwards. Flexible histone marks such as H3K27 methylation enable developmental genes to be silenced for a short time in pluripotent cells. By contrast, DNA methylation enables the stable silencing of imprinted genes, transposons, and some pluripotency-associated genes.

Copyright 2007 Nature Publishing Group, Reik, W., Stability and flexibility of epigenetic gene regulation in mammalian development, Nature 447, 425-432

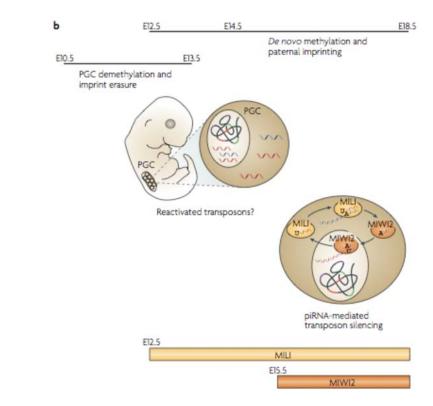
Imprinting de genes paternos e maternos



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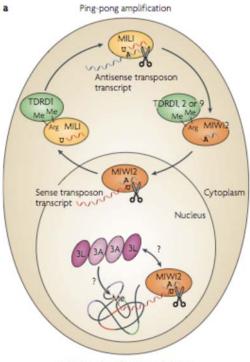
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PiRNAs e o silenciamento de transposões



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PiRNAs e o silenciamento de transposões



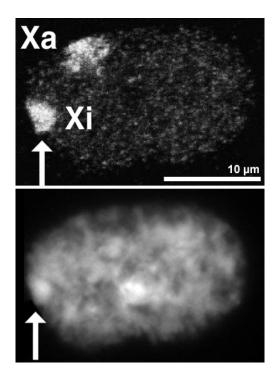
piRNA-mediated DNA methylation

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Inactivação do cromossoma X





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