

The marvelous unfolding story of microRNAs



Greetings from Worcester Massachusetts!

The marvelous unfolding story of microRNAs

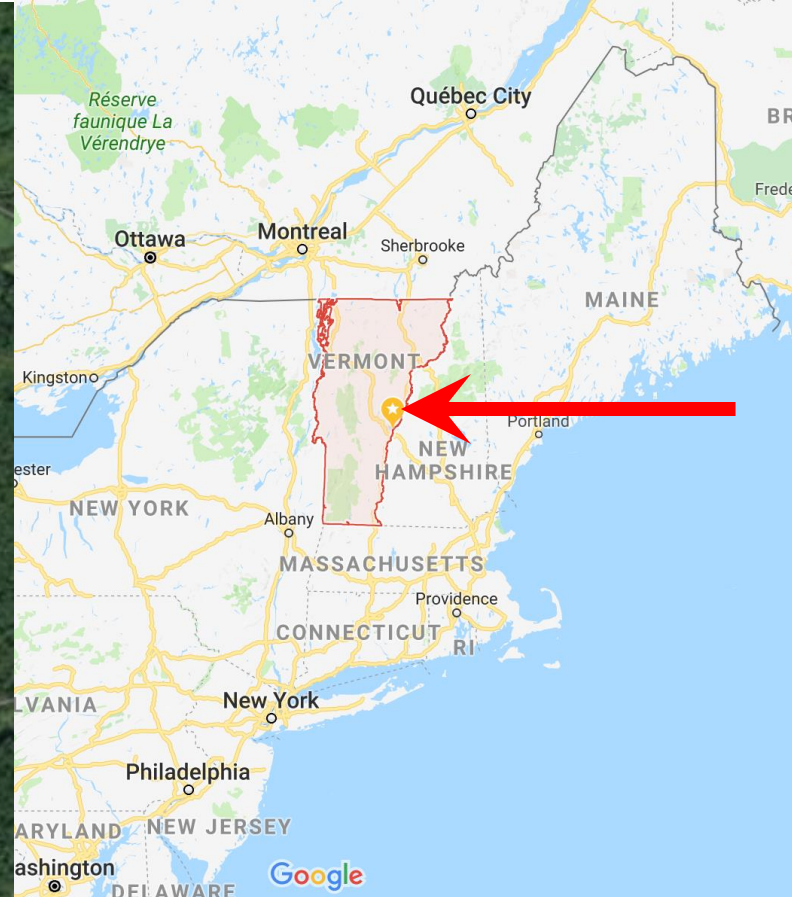
More than 30 years ago

Rosalind Lee, Rhonda Feinbaum and V. Ambros (1993) The *C. elegans* heterochronic gene *lin-4* encodes small RNAs with antisense complementarity to *lin-14* Cell 75

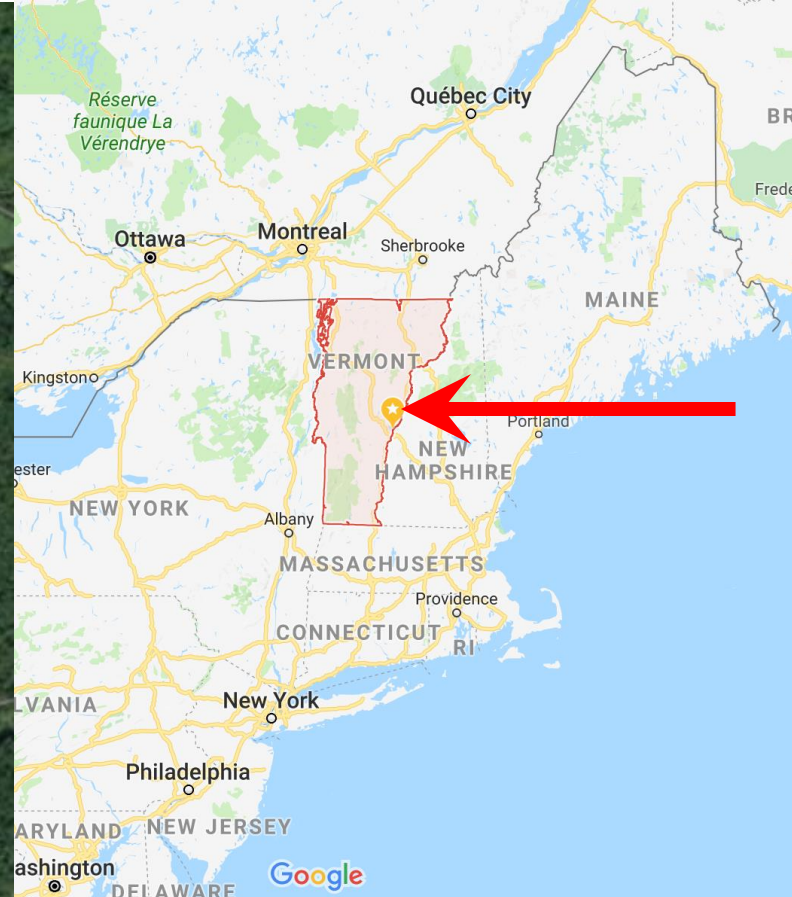


Rosalind Lee and Rhonda Feinbaum

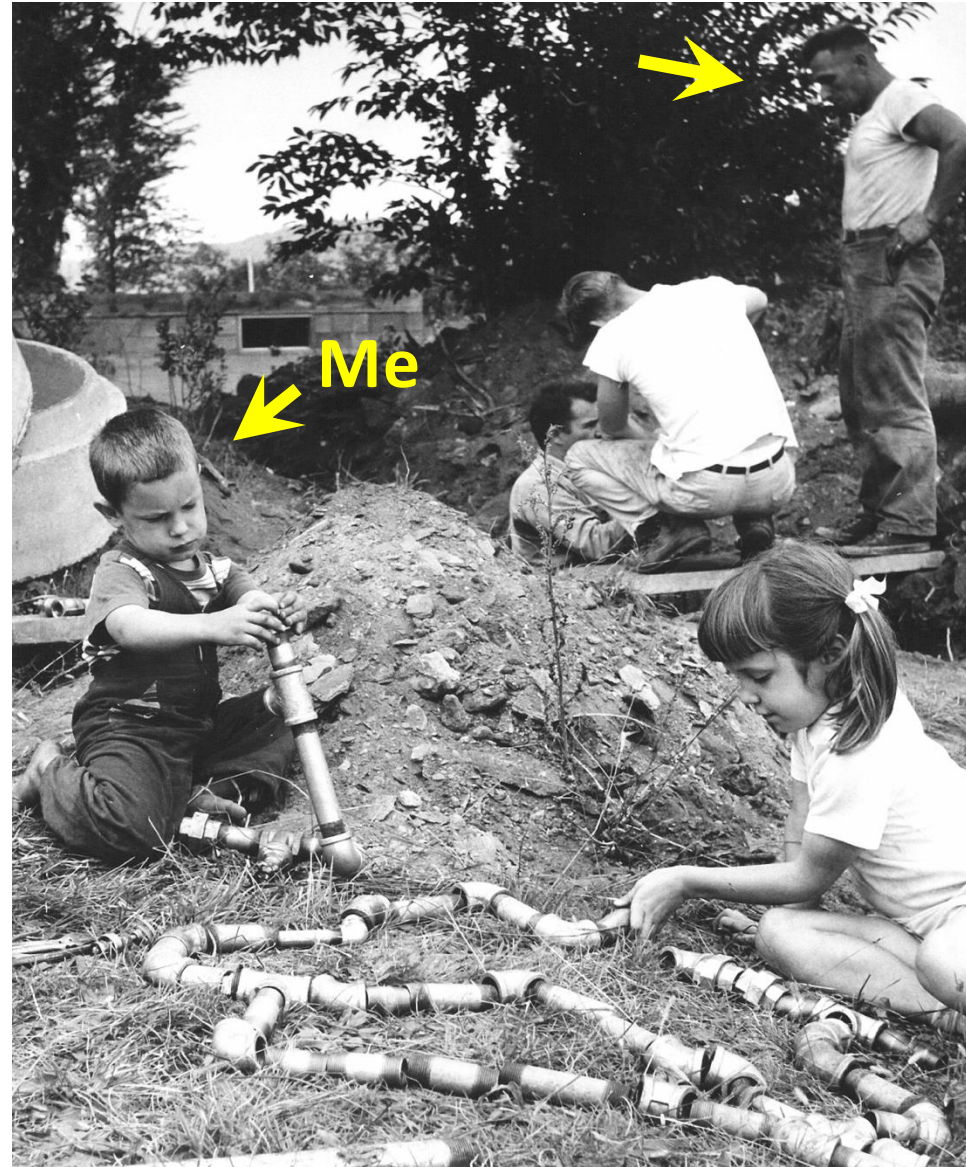
How did I get here?



I grew up on a farm in Vermont (USA)



I started out as a scientist, learning to figure things out



**Encouraged by my
dad, Longin Ambros**

The young scientist goes to school

Pupil Progress Report

HARTLAND PUBLIC SCHOOLS
Grades 3 - 8

Report of Victor Ambras

Grade Six Hartland Four Corners School

1964 1965

TO PARENTS:

Children vary greatly in their growth and ability. This card is an attempt to record for you the progress your child is making in attaining maximum growth. It is not intended to be used as a comparison of one child's accomplishment with that of another, but to point out to you the specific strong and weak points of your child's work.

We invite your cooperation and hope you will take time to come in and talk with us about the progress and development of your child.

David W. Eaton
Superintendent of Schools

ATTENDANCE


Report Periods	1st	2nd	3rd	4th	Total
Days Present	41	43	43	40	
Days Absent	0	2	0	0	
Times Tardy					

EXPLANATION OF RATING

A - Excellent
B - Very Good
C - Good
D - Passing
F - Unsatisfactory

Academic Progress	1	2	3	4	Avg.
Arithmetic	A'	B	B	B	B
Reading	A'	A'	A'	A'	
Language	A	A	A+	A+	
Social Studies	A	A	A-	A	
Science & Health	A	A	B+	B+	

Teacher's Comment:



PARENT'S COMMENTS:

PARENT'S SIGNATURE

Victor Ambras

1st Period

2nd Period *Longin B Ambras*

3rd Period *Longin B Ambras*

4th Period

PROMOTION INFORMATION

Promoted to Grade 7

Wallace Vaine

I was an amateur astronomer

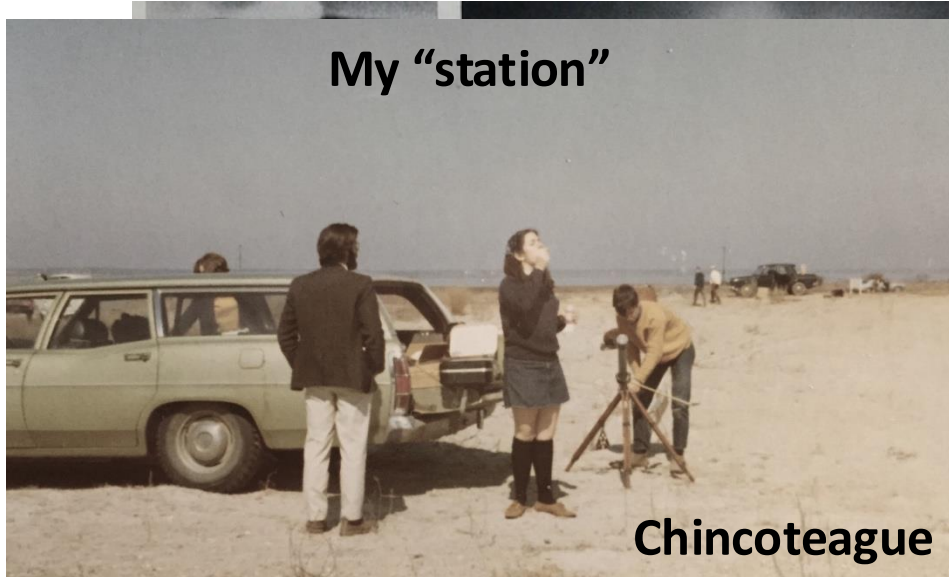
**Astrophoto of
Comet Bennett
I took from my
backyard**

May 15, 1970



My first published scientific result!

Sky and Telescope
May 1970



My "station"

Chincoteague
Virginia

My Dad (expedition sponsor)



observ-
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York.
from
line,
sondi

and 12 in-
at 20 to 30 f-
to northeast
moon's sha-
h the sha-
longer, acc-
ing to some observers. Thus, Victor A-
mbros found the bands visible for over f-
minutes before totality and for almost
three minutes afterward. His station was
one mile south of Chincoteague, Virginia,
and 35 miles from the central line.

Supporting testimony is offered by Jan
Finkelstein, who with his father watched
at Greenville, North Carolina, exactly on
the central line. He saw shadow bands
three minutes before second contact, ini-
tially spaced three or four inches apart
and moving at four feet per second. Dur-
ing the last minute before totality, the
bands were closer-spaced and faster (20
feet per second).

Edward S. Candidus, at Virginia Beach,
speaks of the bands as seen a full minute
up to the start of totality. On the white
screen he used, they were uniform and
evenly spaced.

BIOLOGICAL EFFECTS

The effects of total eclipses on the be-
havior of men and animals attract peren-
nial interest. Less than a century ago, a
warship of the Imperial Chinese Navy
ceremonially fired its Krupp guns to chase
away the dragon that was swallowing the
sun! At the eclipse this March, some

May, 1970, SKY AND TELESCOPE 287

four or five inches wide and 12 inches
apart. They were moving at 20 to 30 feet
per second from southwest to northeast, in
the general direction the moon's shadow
was traveling.

The time during which the shadow
bands persisted was much longer, accord-
ing to some observers. Thus, Victor Am-
bros found the bands visible for over four
minutes before totality and for almost
three minutes afterward. His station was
one mile south of Chincoteague, Virginia,
and 35 miles from the central line.

Supporting testimony is offered by Jan
Finkelstein, who with his father watched
at Greenville, North Carolina, exactly on
the central line. He saw shadow bands
three minutes before second contact, ini-

March 7, 1970
Total Solar Eclipse

Observations of
Shadow Bands

My scientific career path

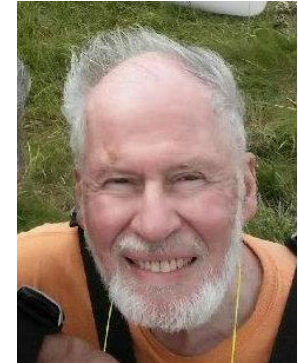


1971 MIT

Inspiration from other students
Kevin Struhl, Gary Struhl

Research
experience

Encouragement
from mentors

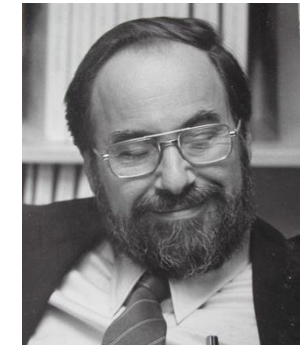


Ed Gruberg

BS 1975

MIT grad school

Ph.D. 1979



David Baltimore

@Umassmed
2008

@Dartmouth
1992

Faculty
@Harvard
1985

Postdoctoral
research



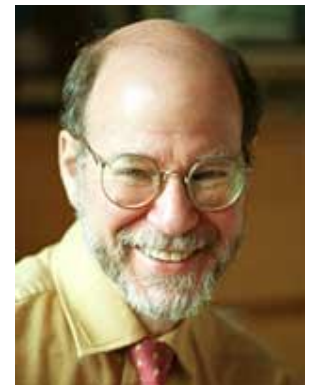
Craig Mello



My
PhD student
Craig Mello



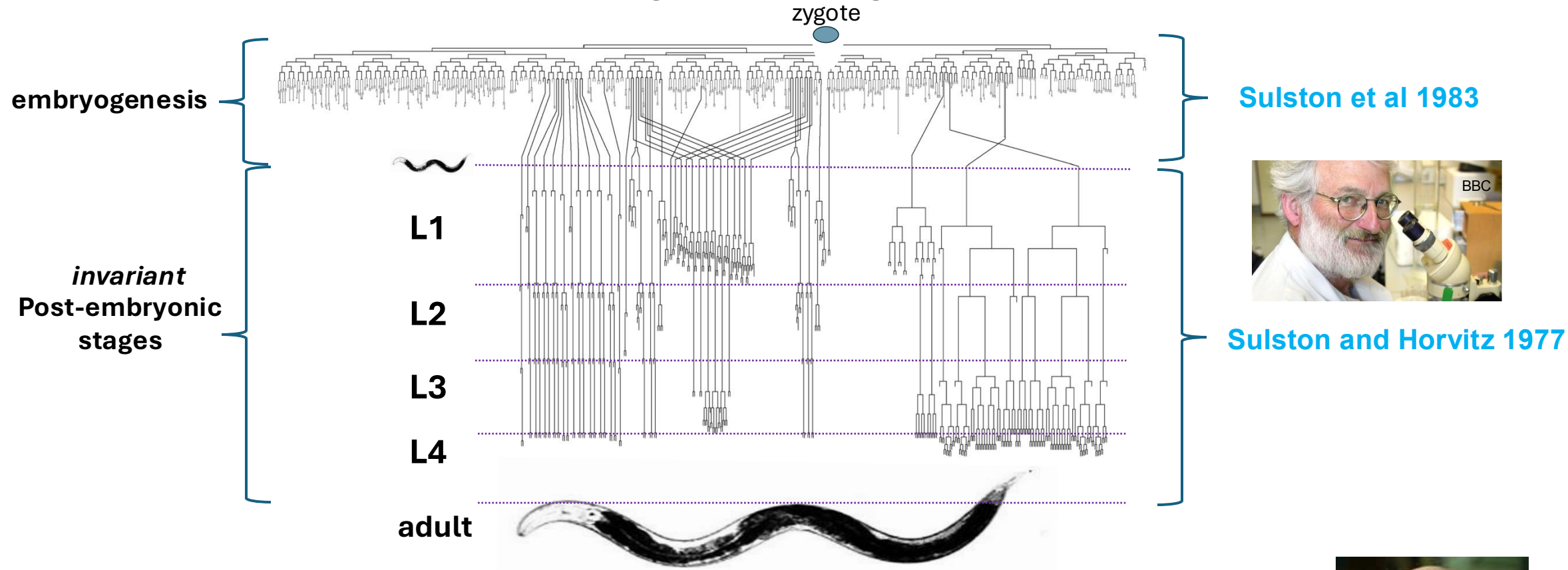
This Improbable Life!



Bob Horvitz

In the beginning - circa 1980 - Bob Horvitz's lab @ MIT

C. elegans cell lineages



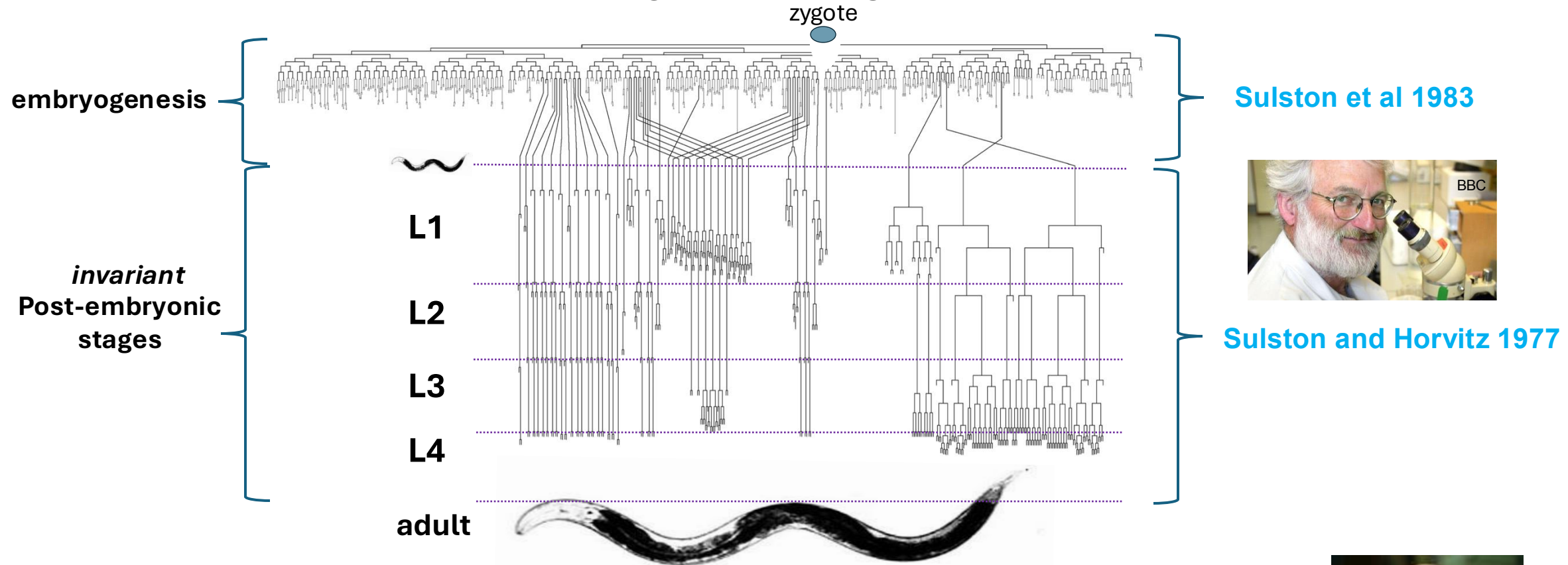
How is the development of an animal encoded in its genome?

Genetic Approach: Identify mutants with developmental defects. Find out what they can teach you.



Model Organism Developmental Genetics

C. elegans cell lineages



How is the development of an animal encoded in its genome?

Genetic Approach: Identify mutants with developmental defects. Find out what they can teach you.

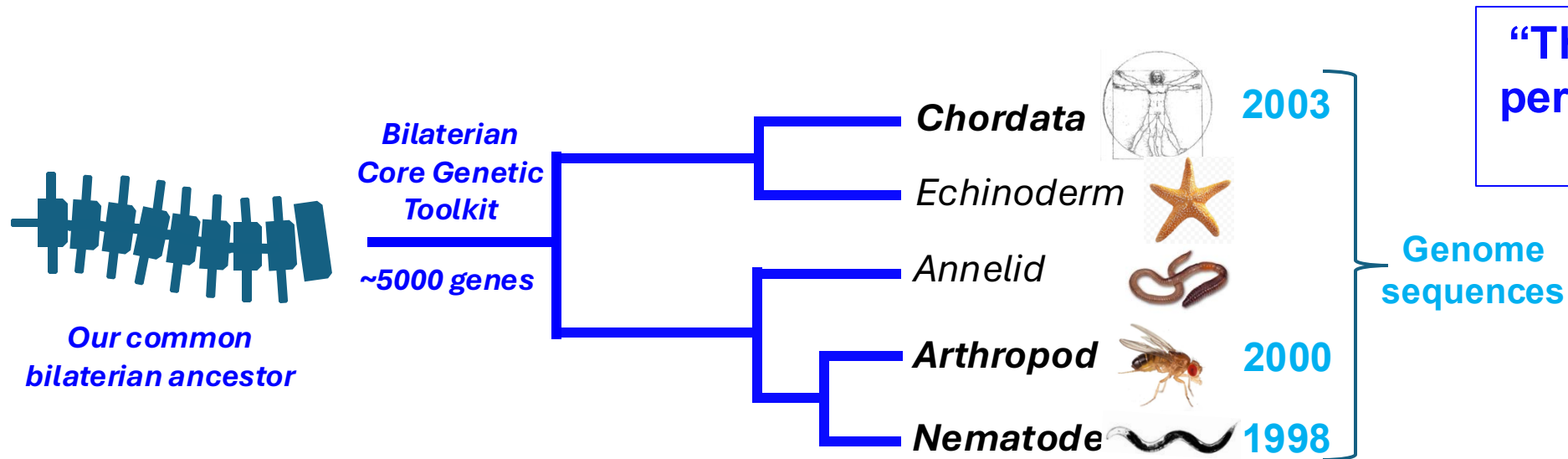


Model Organism Developmental Genetics

The Model Organism Premise

Developmental mechanisms in one animal → Can apply to distant animals

Evolutionary adaptation of the 'Core Genetic Toolkit' → animal complexity and diversity

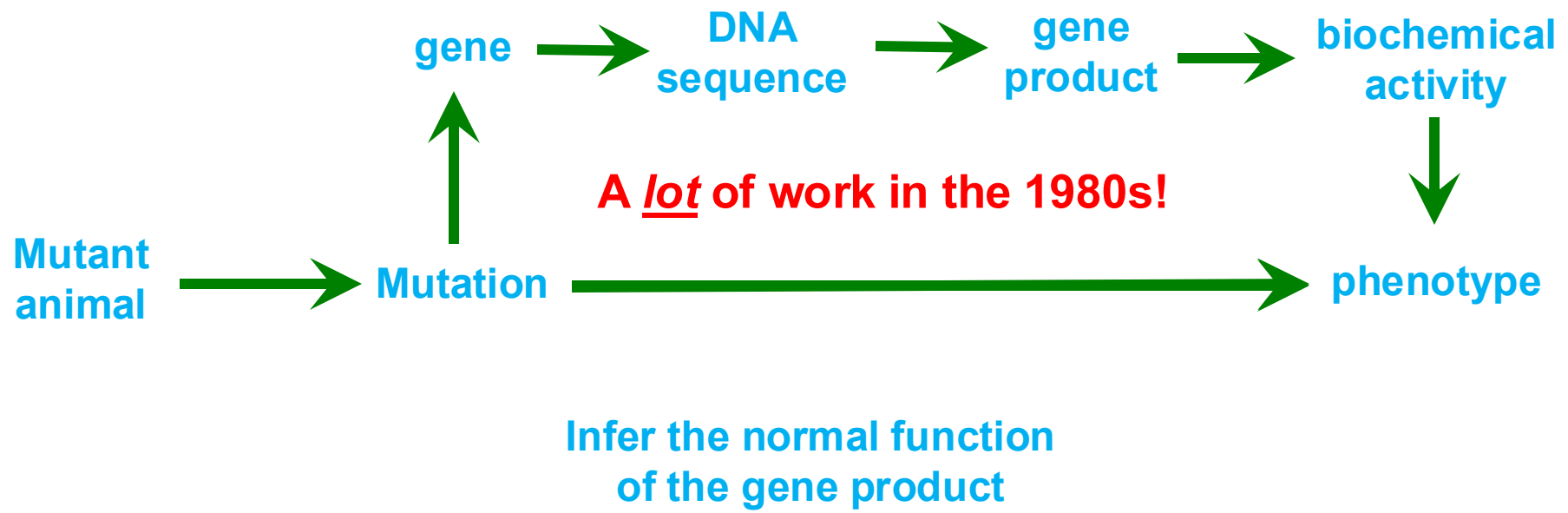


How is the development of an animal encoded in its genome?

Genetic Approach: Identify mutants with developmental defects. Find out what they can teach you.

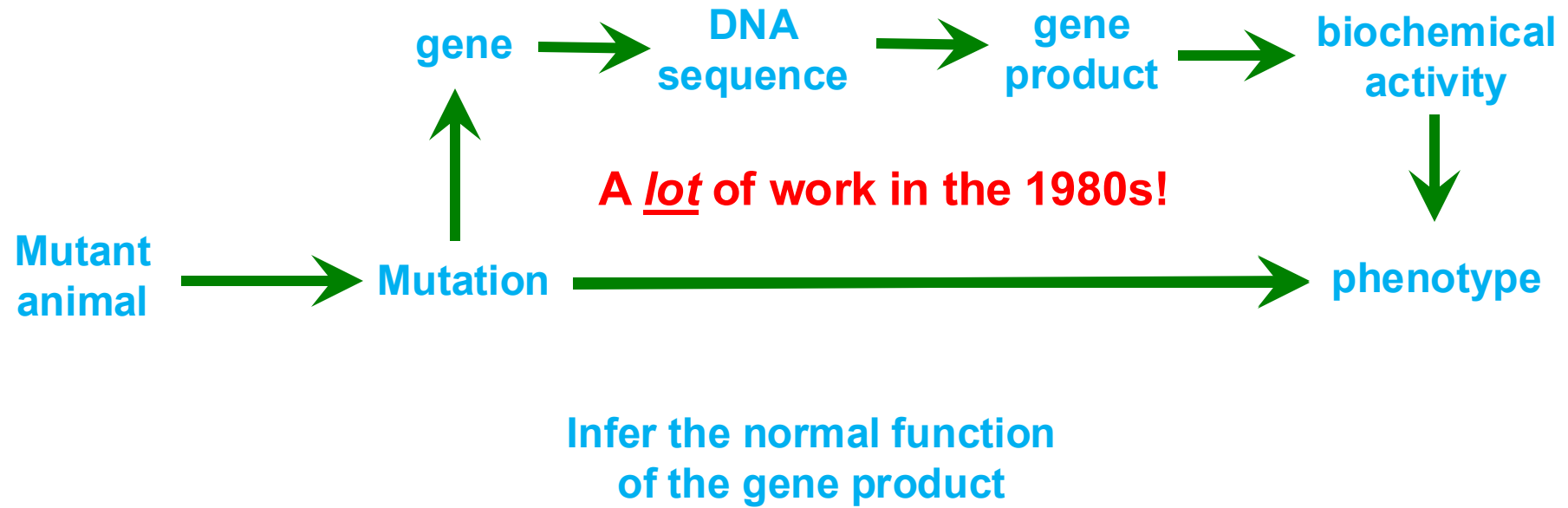


Model Organism Developmental Genetics



Genetic Approach: Identify mutants with developmental defects; find out what they can teach you.

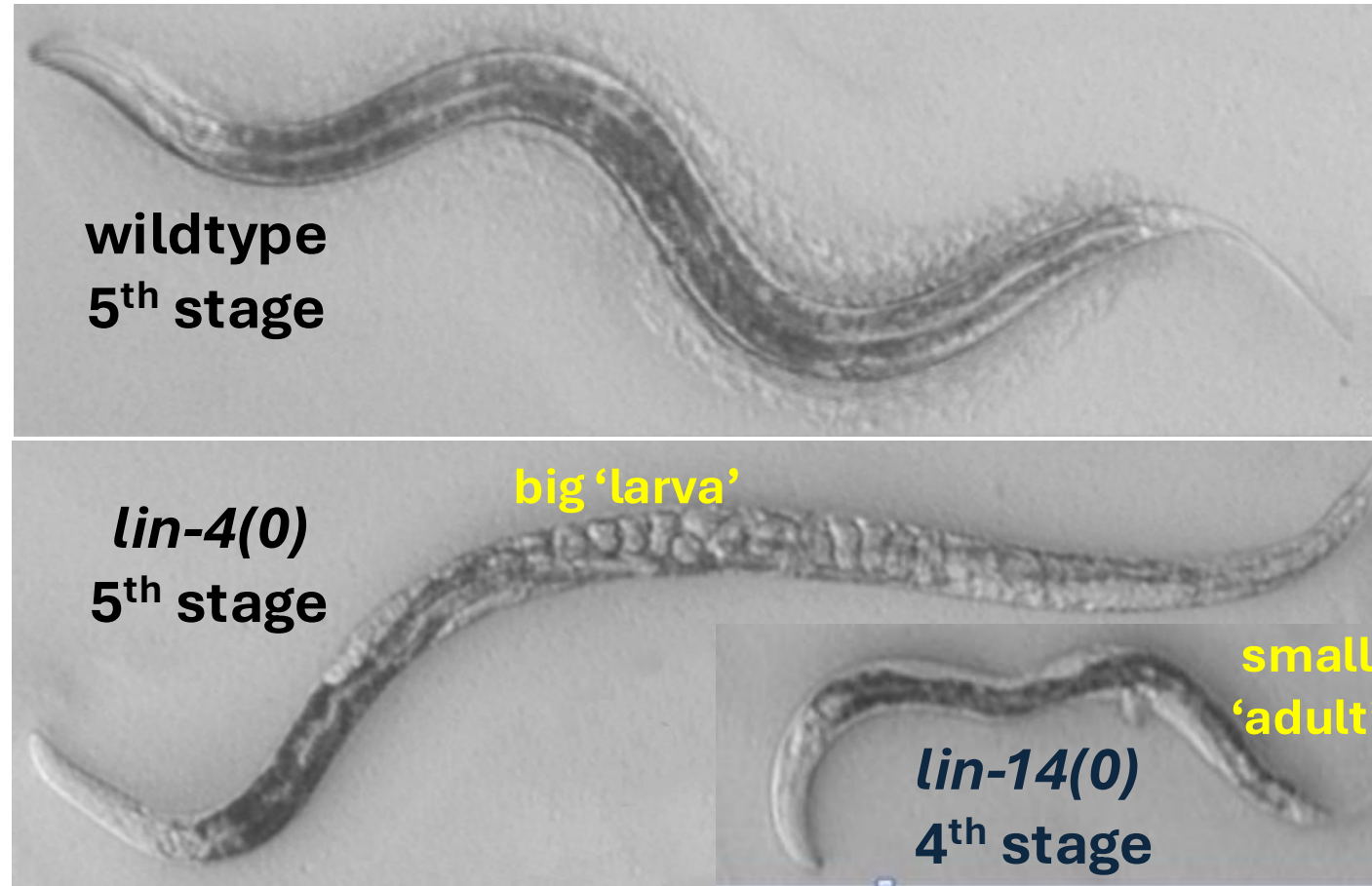
Choosing what mutants to follow



Genetic Approach: Identify mutants with developmental defects; find out what they can teach you.

Choosing what mutants to follow

Bob's genetic screens → *C. elegans* Developmental Timing Mutants



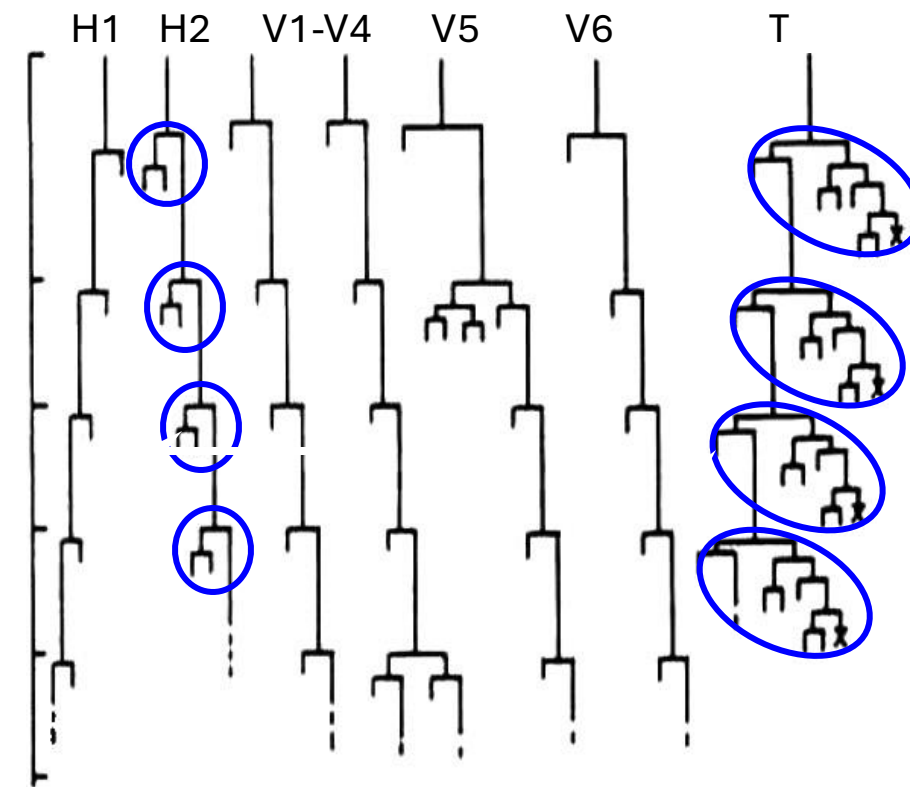
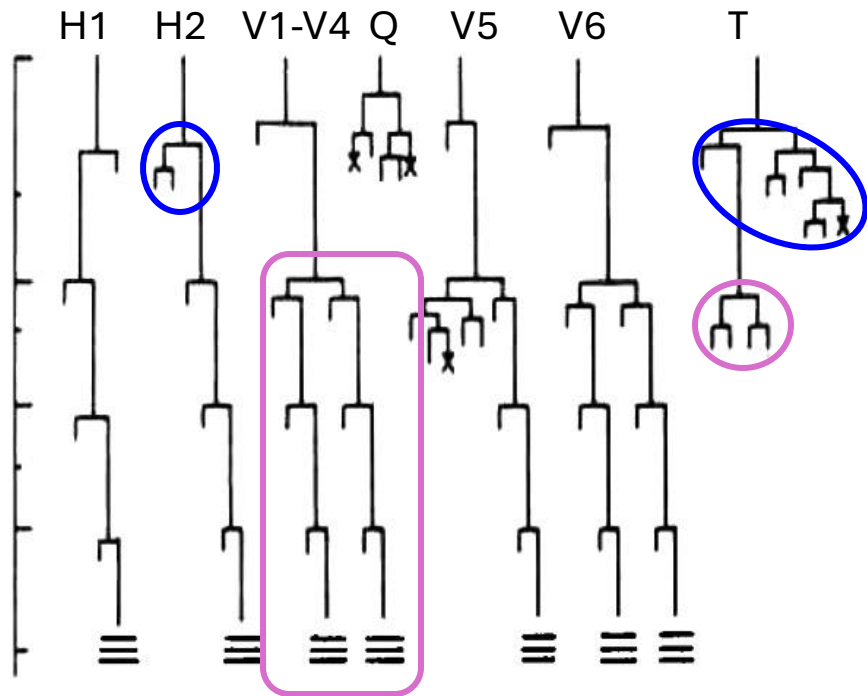
Chalfie, Horvitz & Sulston (1981)

C. elegans Developmental Timing Mutants

“Retarded” development
lin-4(0) mutant



Wild type



lin-4 → L1 fates
lin-4 → L2 fates

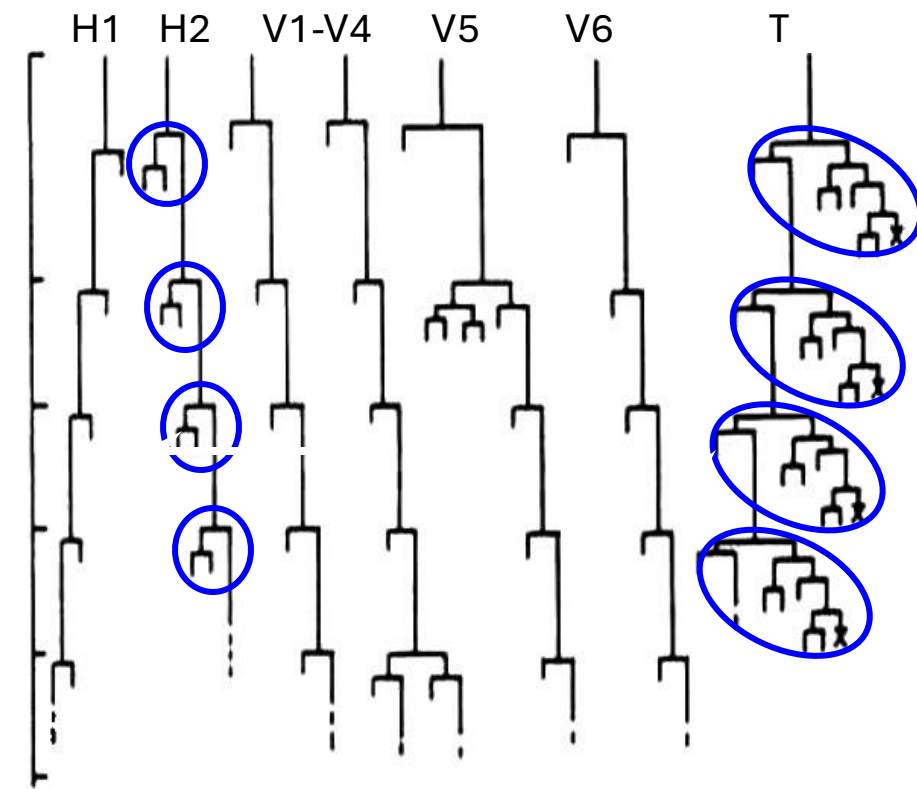
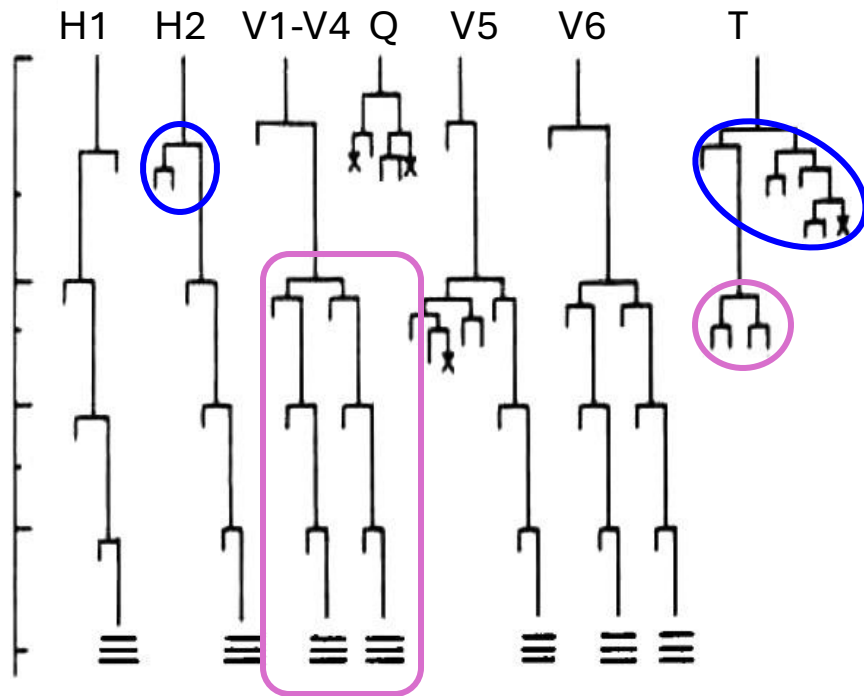
Chalfie, Horvitz & Sulston (1981)

C. elegans 'Heterochronic' Mutants

"Retarded" development
lin-4(0) mutant



Wild type



lin-4 → L1 fates
lin-4 → L2 fates

Retention of ancestral juvenile characteristics

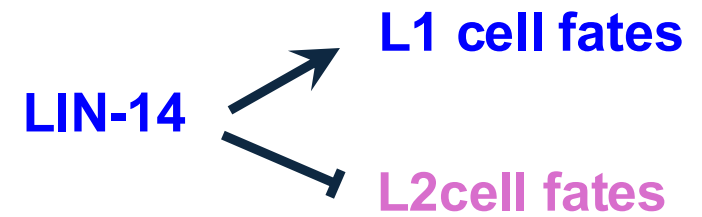
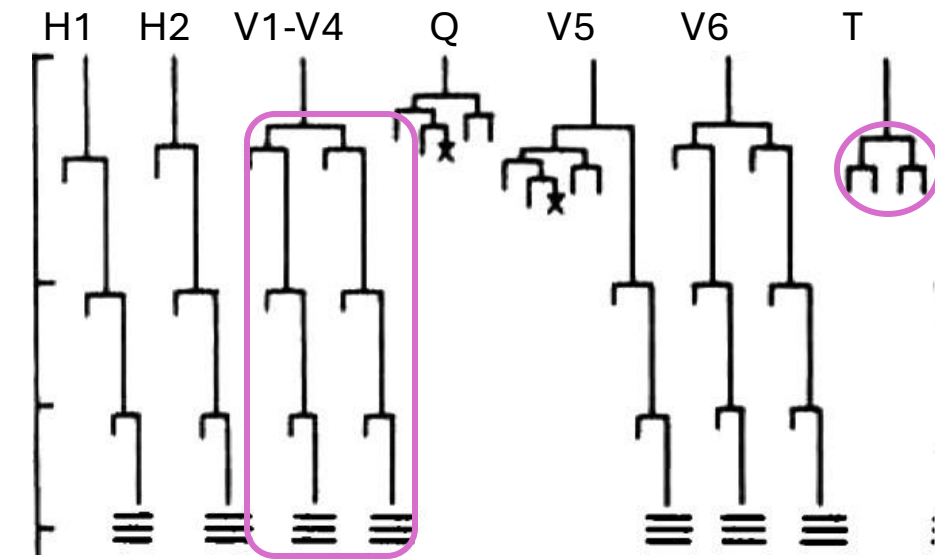
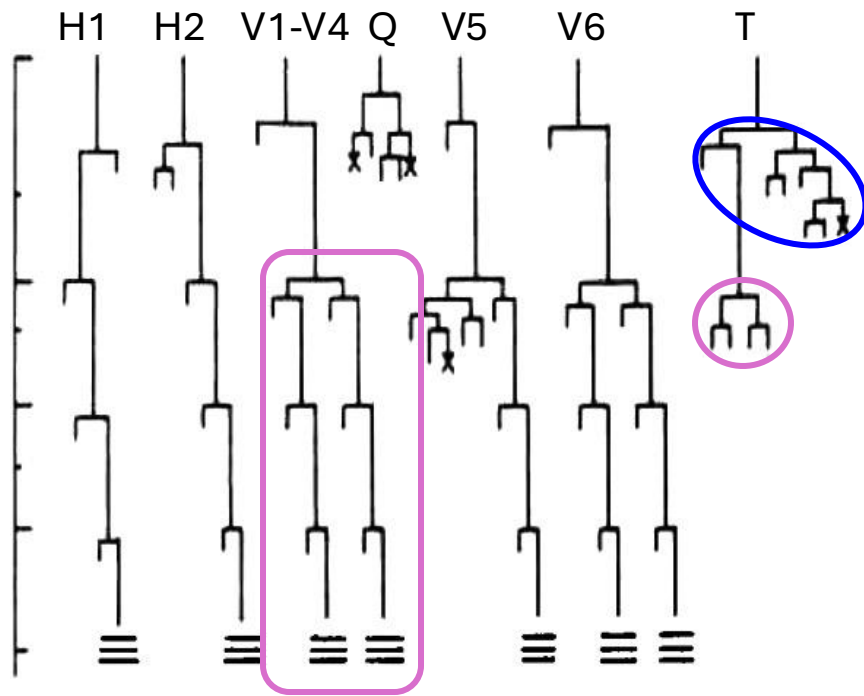
Chalfie, Horvitz & Sulston (1981)

An opposite class of Heterochronic mutant phenotype

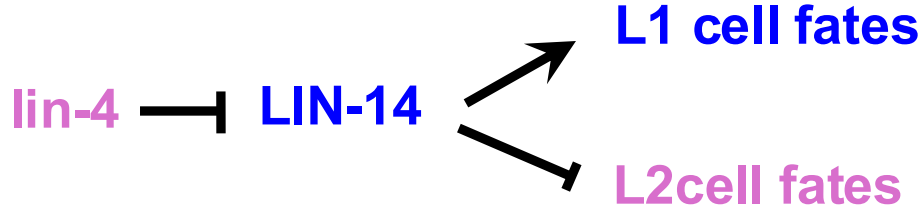
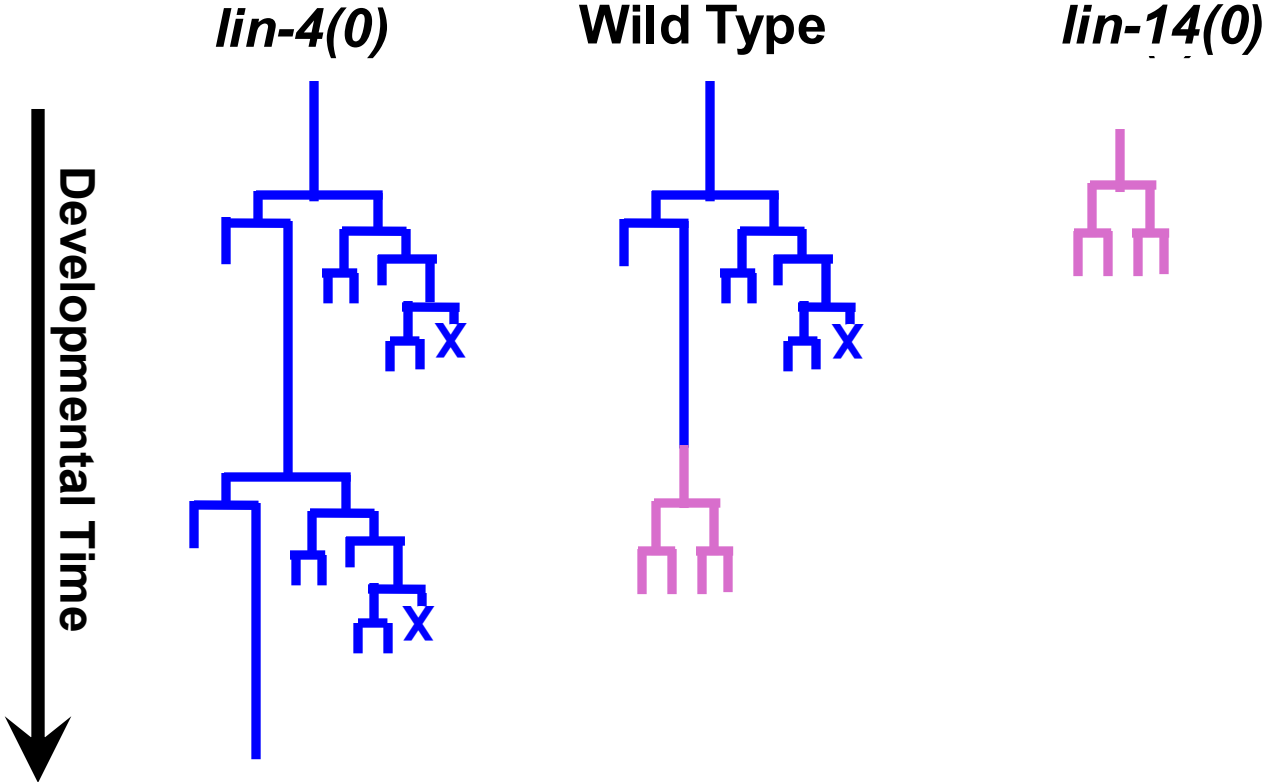


Wild type

“Precocious” development
lin-14(0) mutant

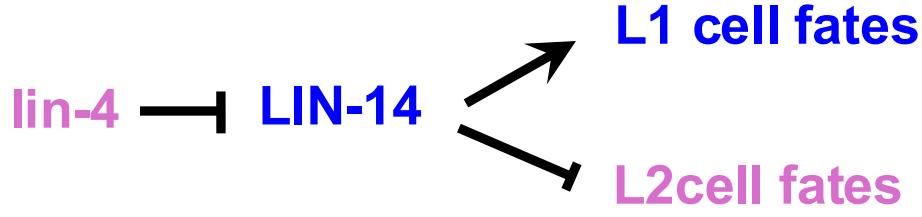
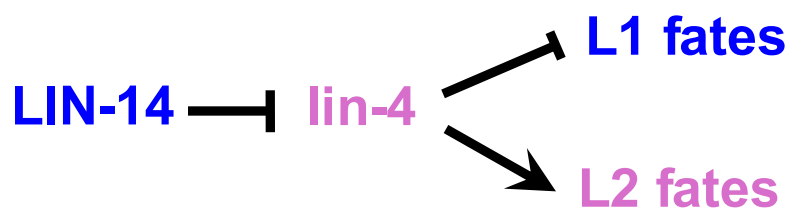
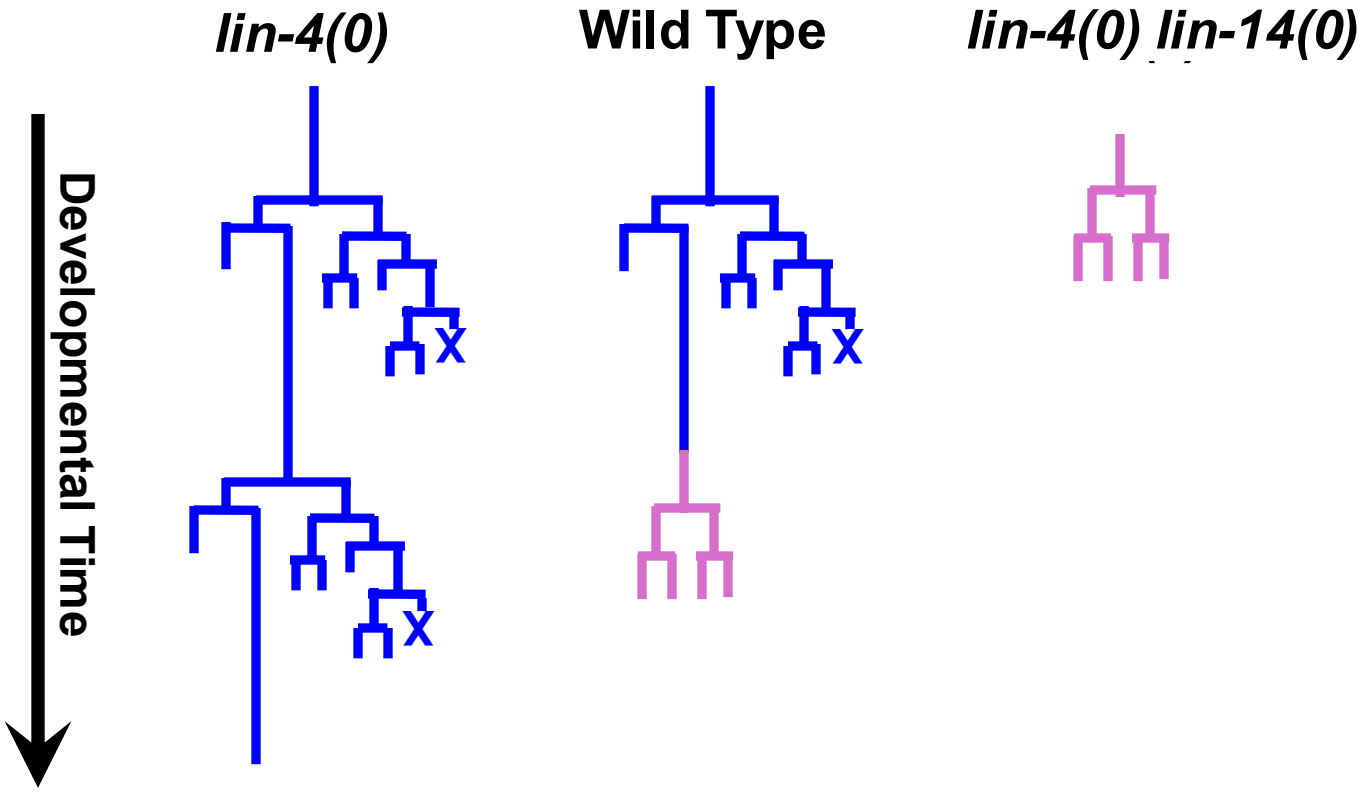


lin-4(0) and *lin-14(0)* mutants have opposite heterochronic phenotypes



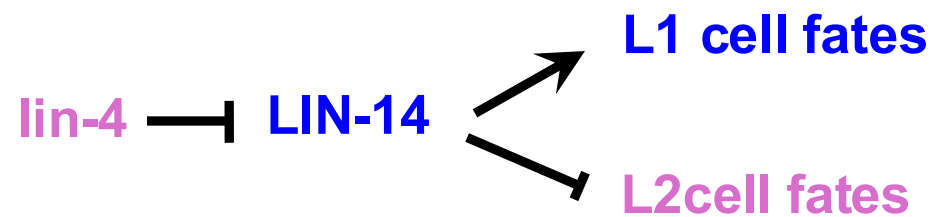
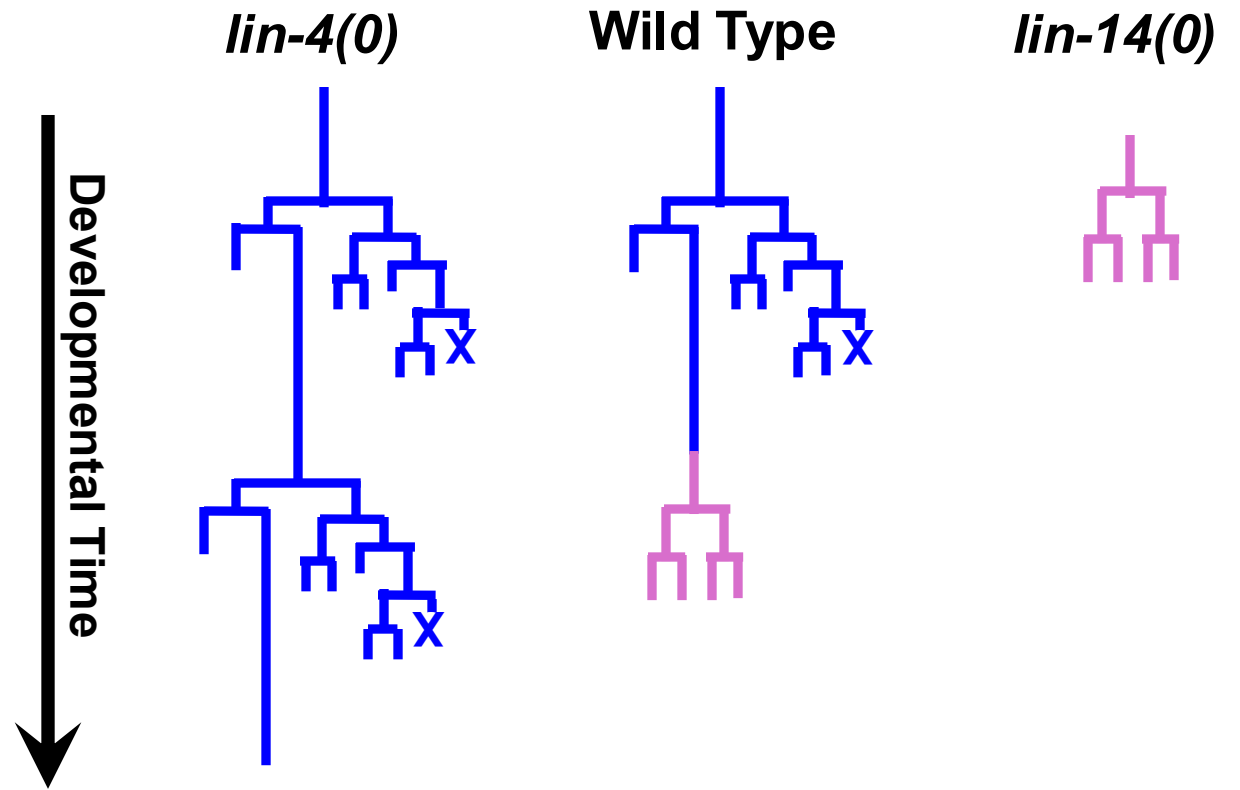
Which Model is Correct?

lin-4(0) and *lin-14(0)* mutants have opposite heterochronic phenotypes

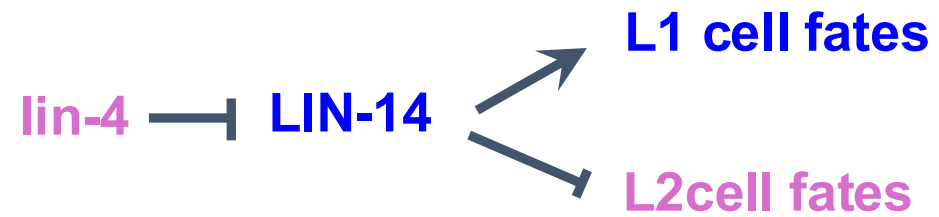
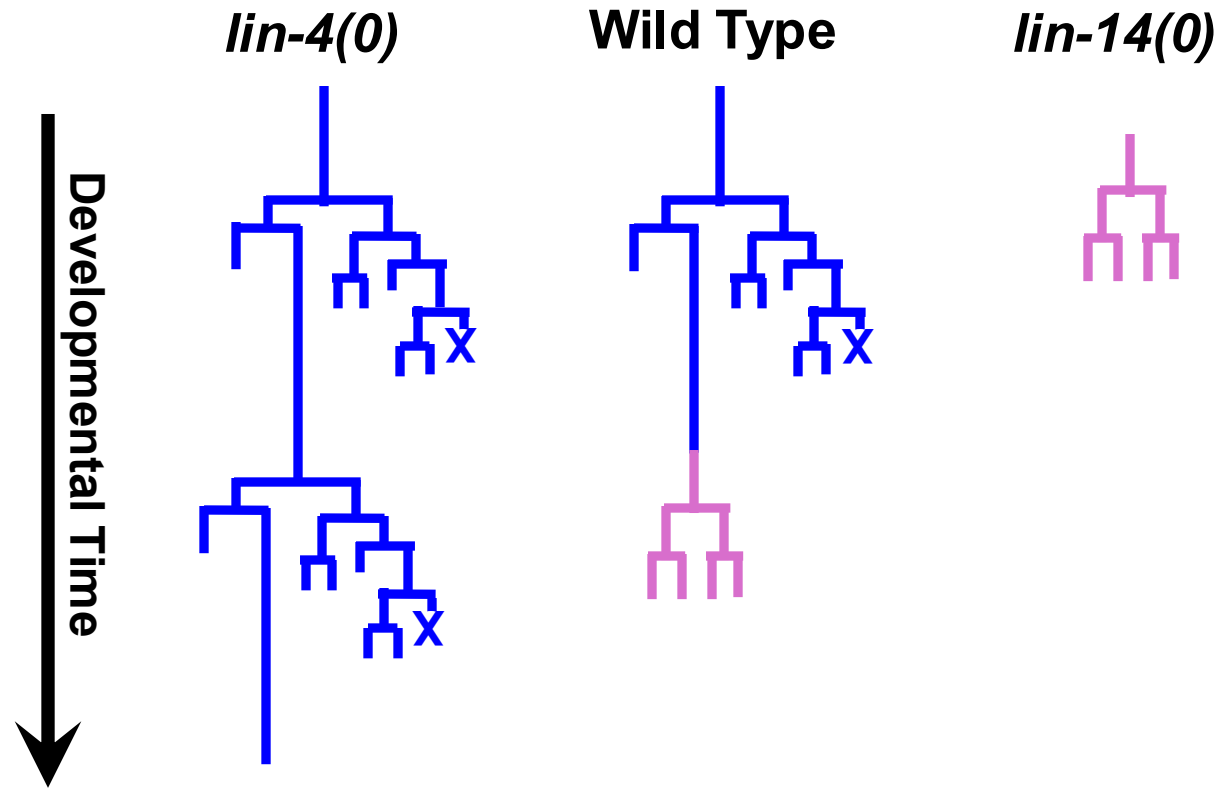


Which Model is Correct? This one!

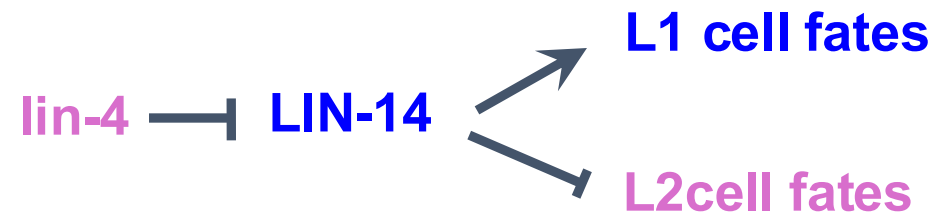
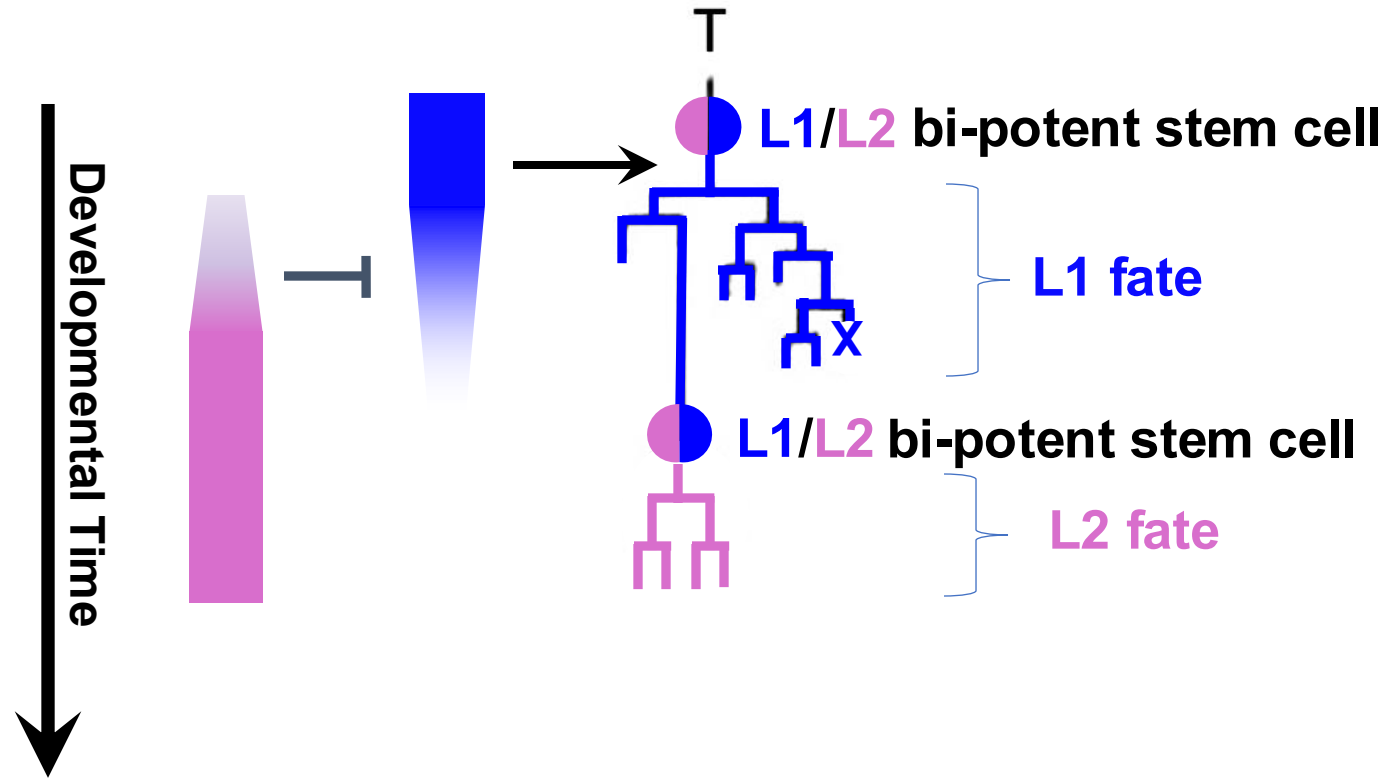
Opposite temporal transformations in cell fate in *lin-4(0)* and *lin-14(0)* mutants



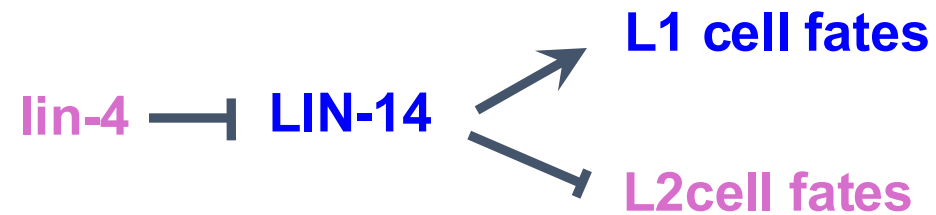
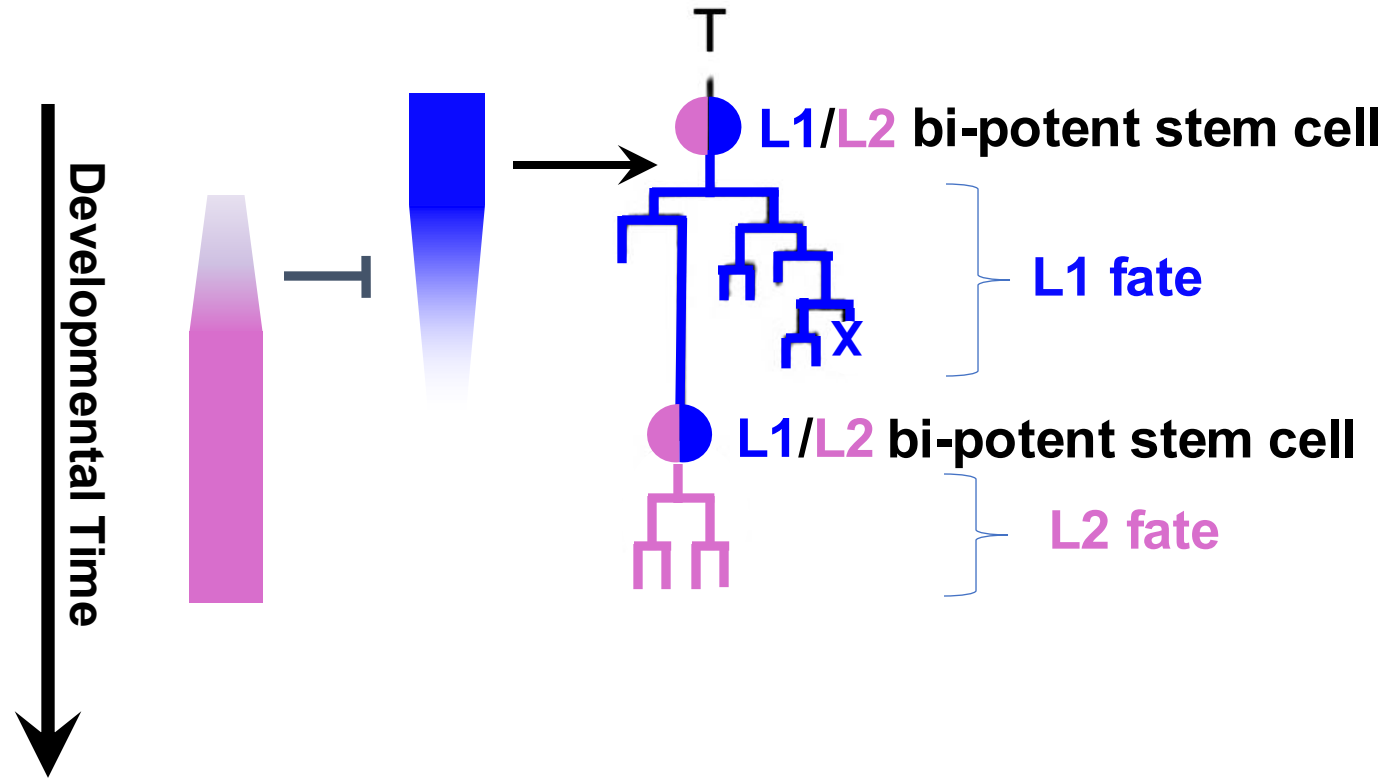
Lineally-related stem cells with multiple potential temporal cell fates



Lineally-related stem cells with multiple potential temporal cell fates



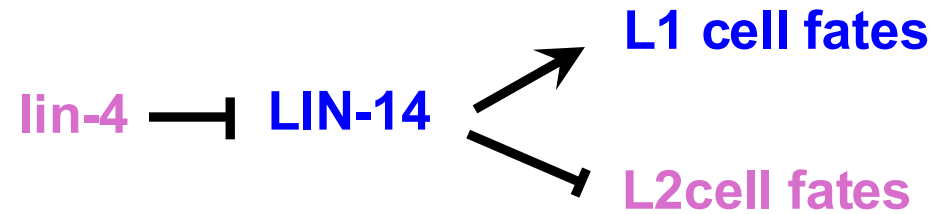
The *lin-4* and *lin-14* genes and their developmental context was super-interesting



Setting out to clone the *lin-4* and *lin-14* genes

Ambros Lab
(Harvard Cambridge)
lin-4

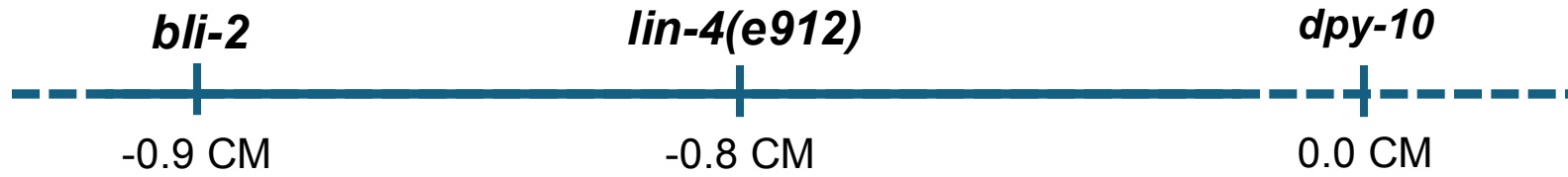
Ruvkun Lab
(Harvard Boston)
lin-14



lin-4(e912) mutant

lin-14(0) mutants
and
lin-14(gain of function) mutants

Getting started ~ 1988: Collecting cloned DNA in the *lin-4* region of LG II



Getting started ~ 1988: Collecting cloned DNA in the *lin-4* region of LG II

The MRC *C. elegans* Physical Mapping Project ~ 1988

Worm Breeder's Gazette 10(3) November 1988

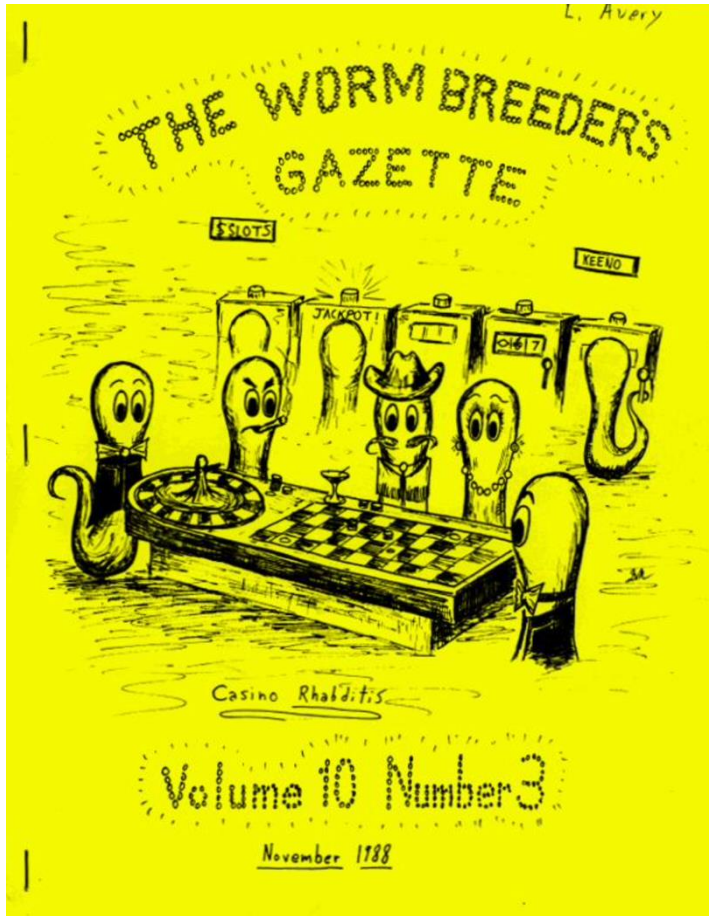
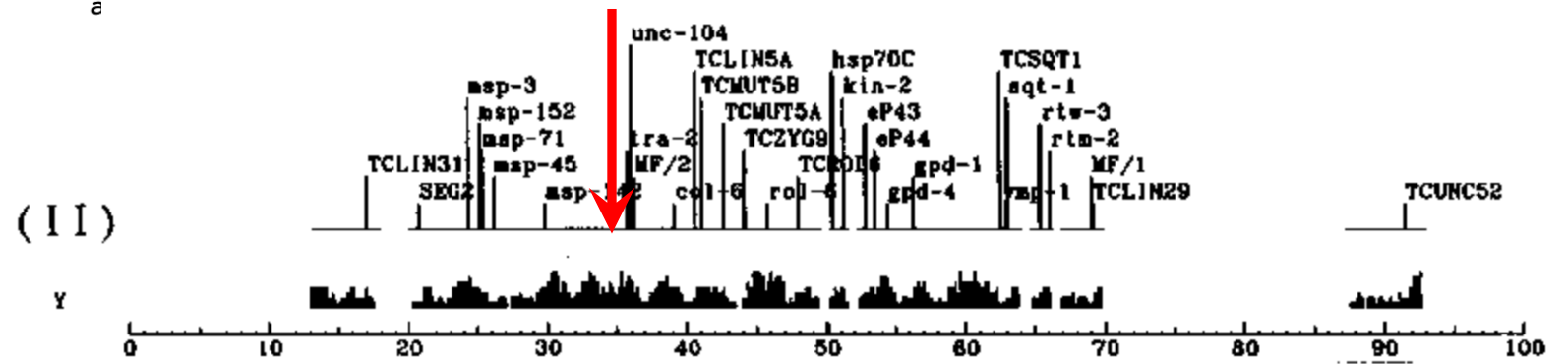
The Genome Map

Alan Coulson, John Sulston, Yiji Kohara, Donna Albertson, Rita Fishpool, Bob Waterston, Humaira Ameer

contigs=
251
mean contig size=
340kb

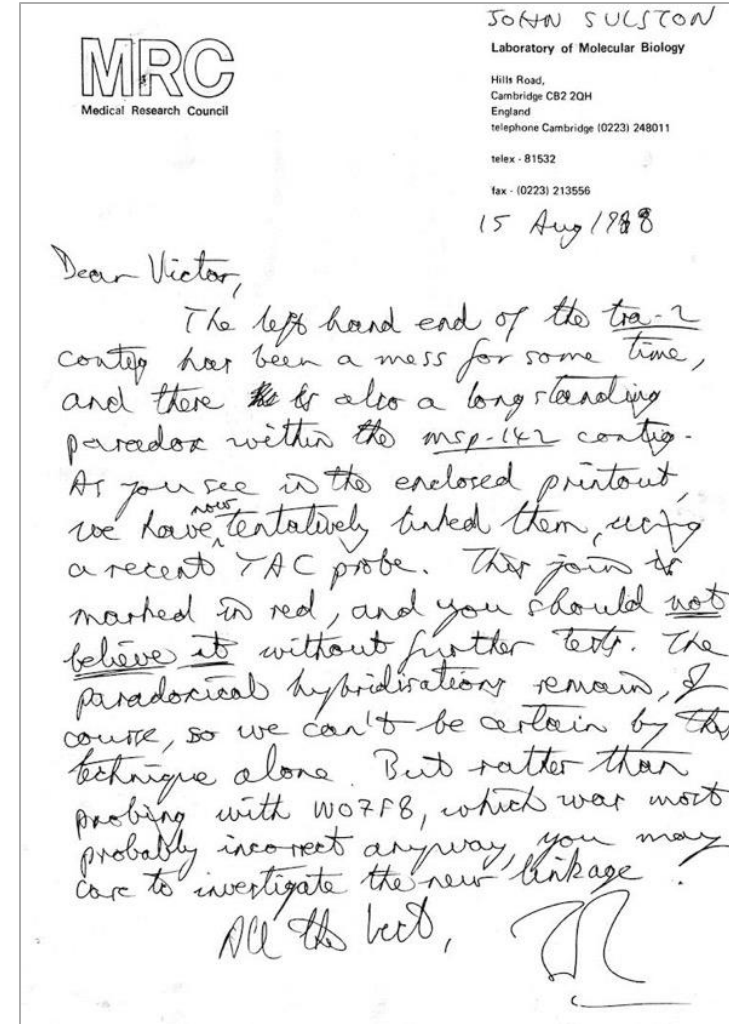
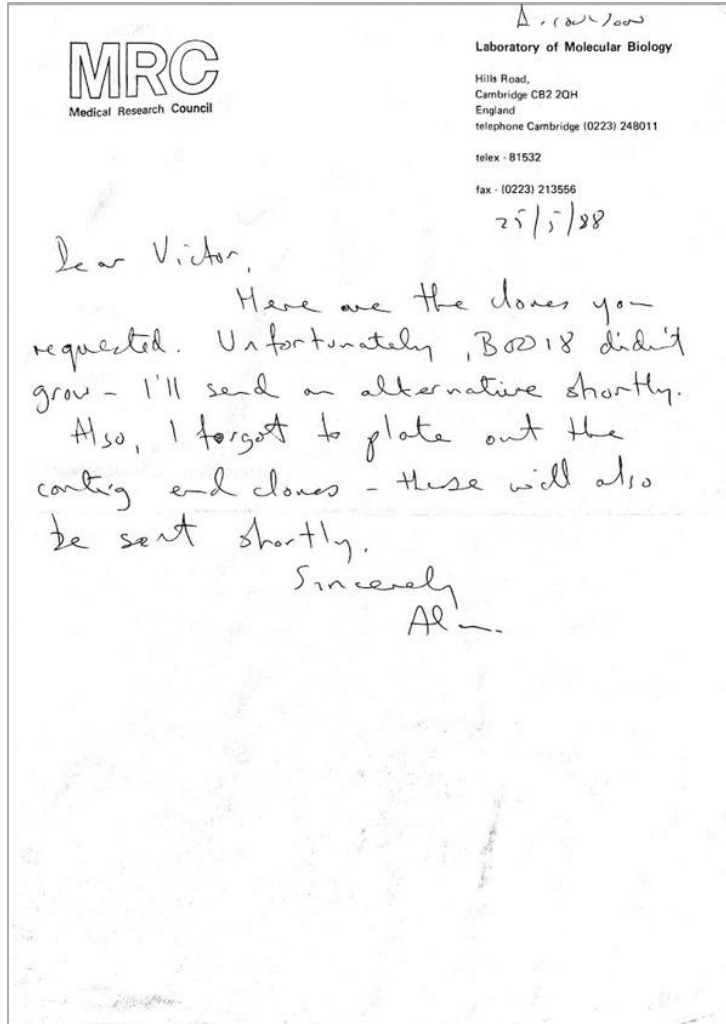
Since our previous report, 260 joins have been made. Mostly, we have been probing cosmid grids with YAC clones taken at random from a new bank of median insert size 250kb. The genetic cluster on each chromosome is now represented fairly completely by seven contigs on

.....
a
c
a



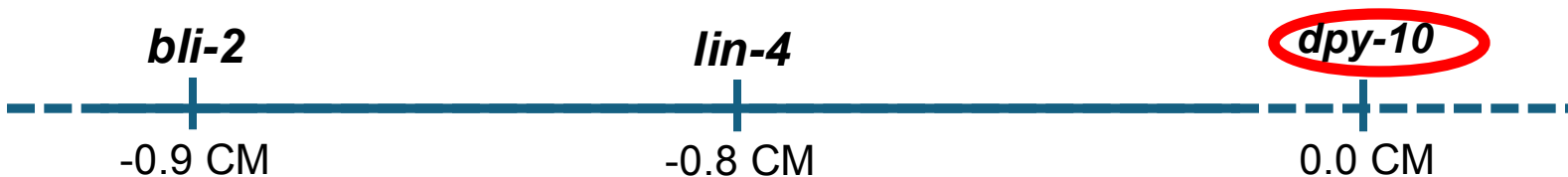
Getting started ~ 1988: Collecting cloned DNA in the *lin-4* region of LG II

Alan and John send clones and helpful hints

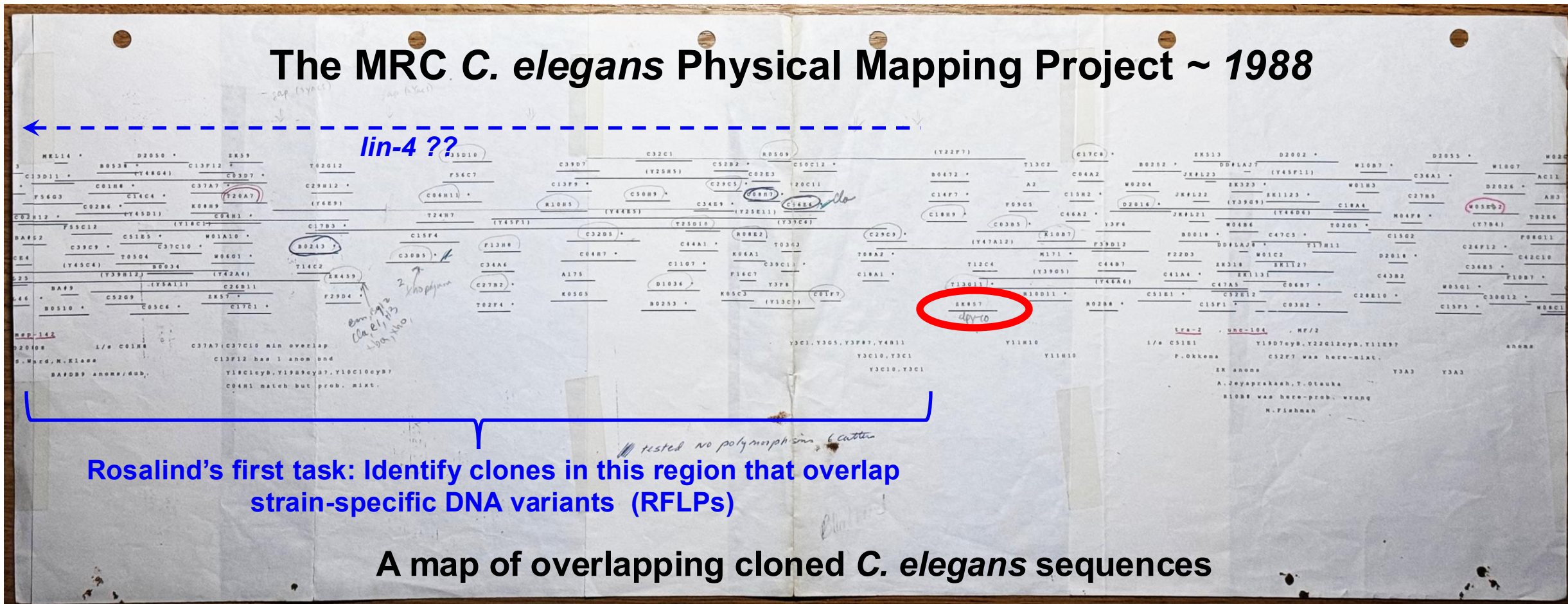


Pro Bono

Getting started ~ 1988: Collecting cloned DNA in the *lin-4* region of LG II

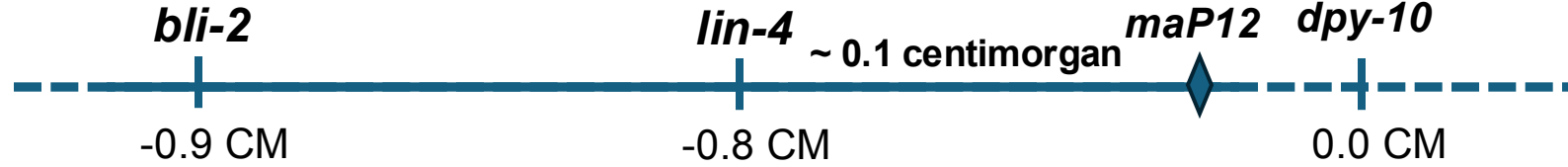


The MRC *C. elegans* Physical Mapping Project ~ 1988

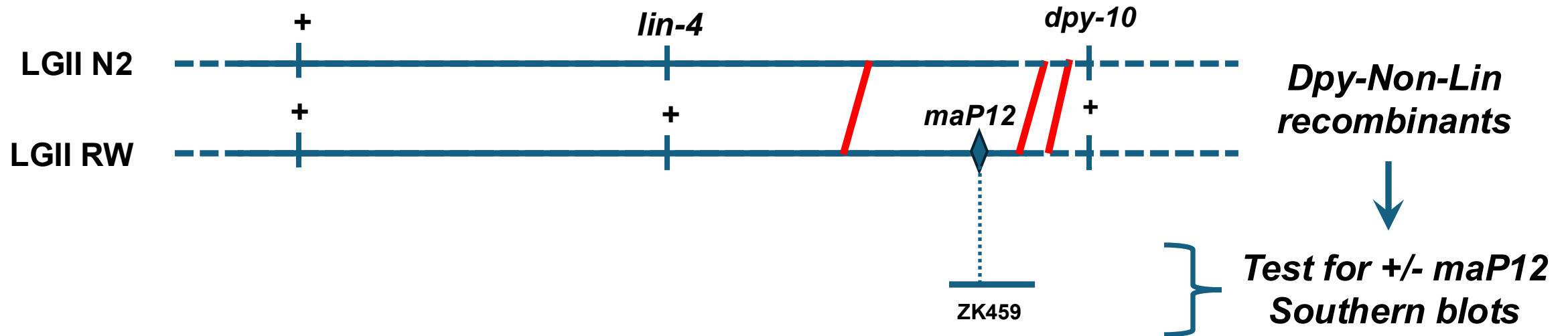


Rosalind Lee

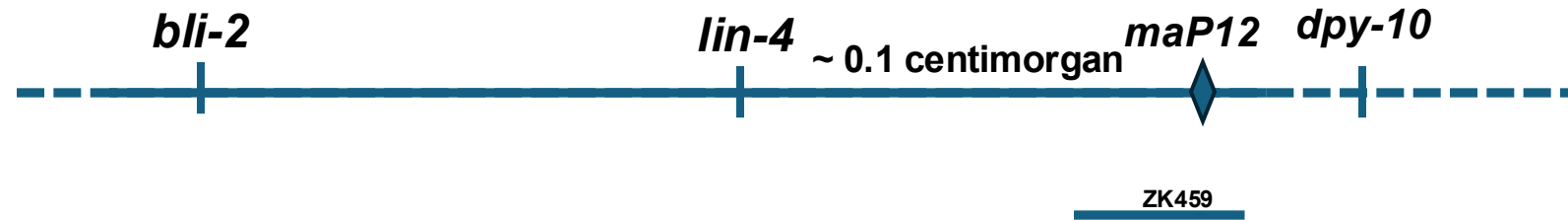
Getting started ~ 1988: Genetic/molecular mapping in the *lin-4* region of LGII



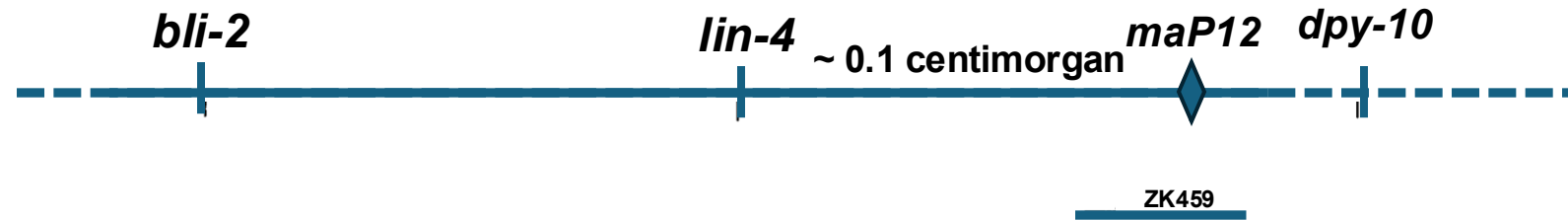
Mapping DNA polymorphisms (RFLPs) detected by Southern blots to genomic DNA



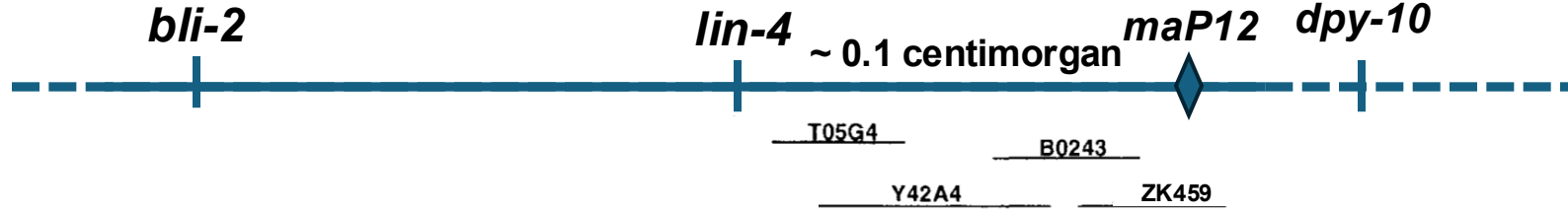
maP12* → toehold close and to the right of *lin-4* at *maP12



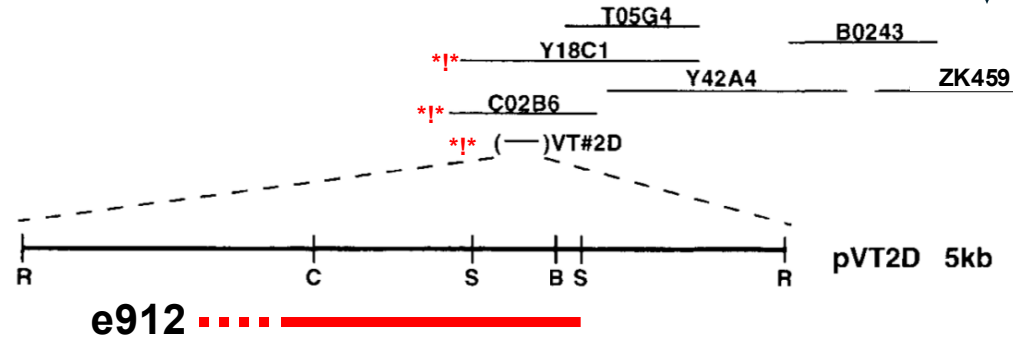
Chromosome walking from *maP12* to *lin-4* facilitated by the MRC



Chromosome walking from *maP12* to *lin-4* facilitated by the MRC

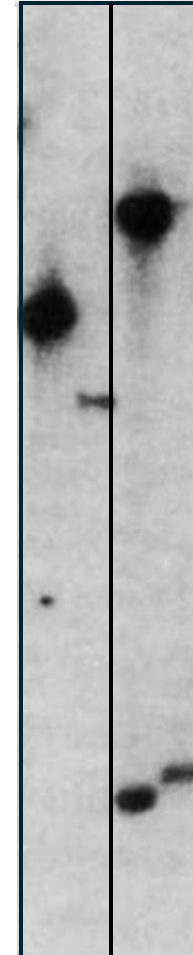


Finding the *lin-4(e912)* DNA lesion



Southern Blots with genomic DNA *lin-4(e912)* vs WT

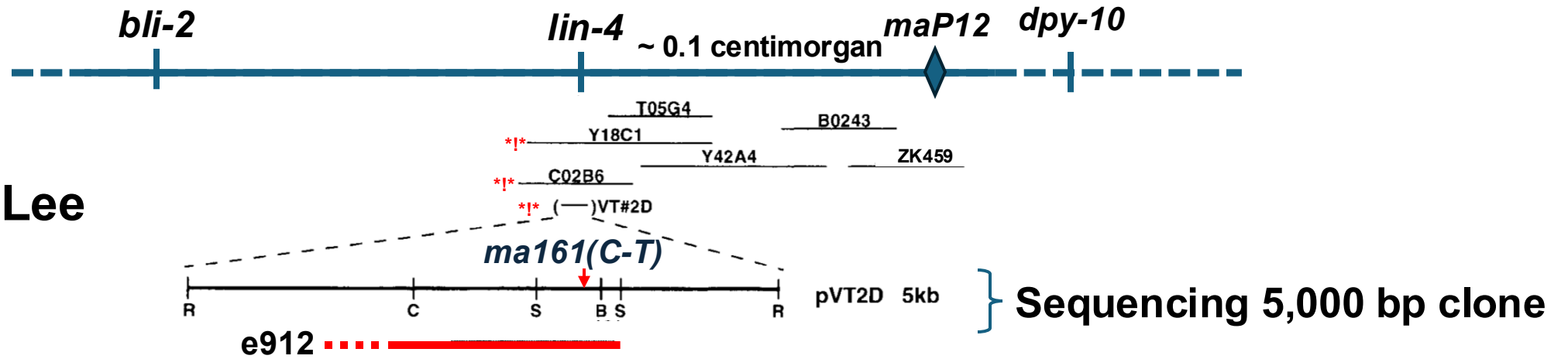
*bam*H1 *blg*II
wt *lin-4* wt *lin-4*



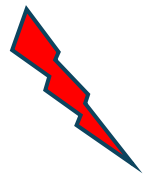
MJ Research
PPI 100
Pulse-field gel
electrophoresis

Finding the *lin-4(e912)* DNA lesion

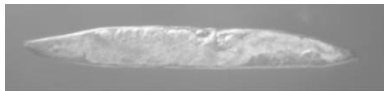
Rosalind Lee



Screening for new *lin-4* (ideally) *point* mutations



WT males X *lin-4(e912) dpy-10*



~20,000

lin-4(e912) dpy-10

+ +

normal

1

lin-4(e912) dpy-10

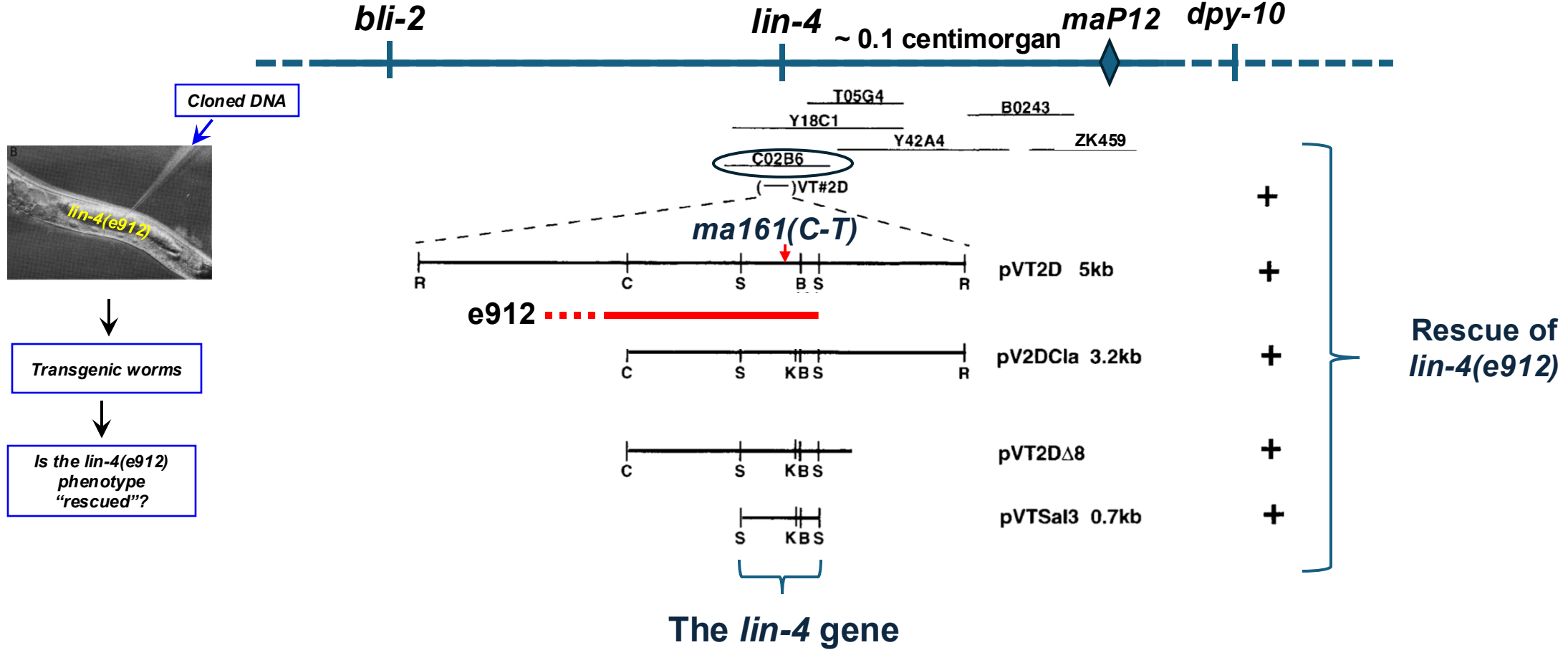
lin-4(new) +

“bag of eggs and larvae”

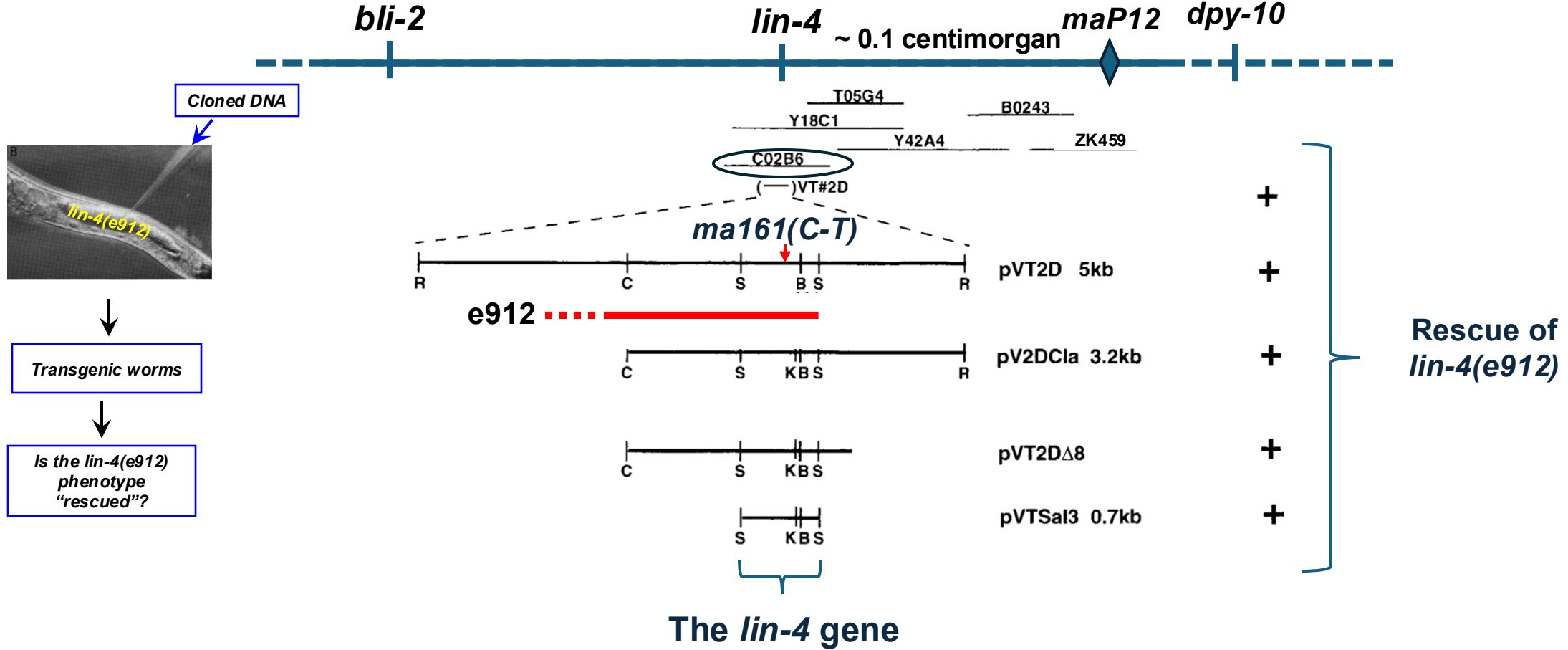


Rhonda Feinbaum

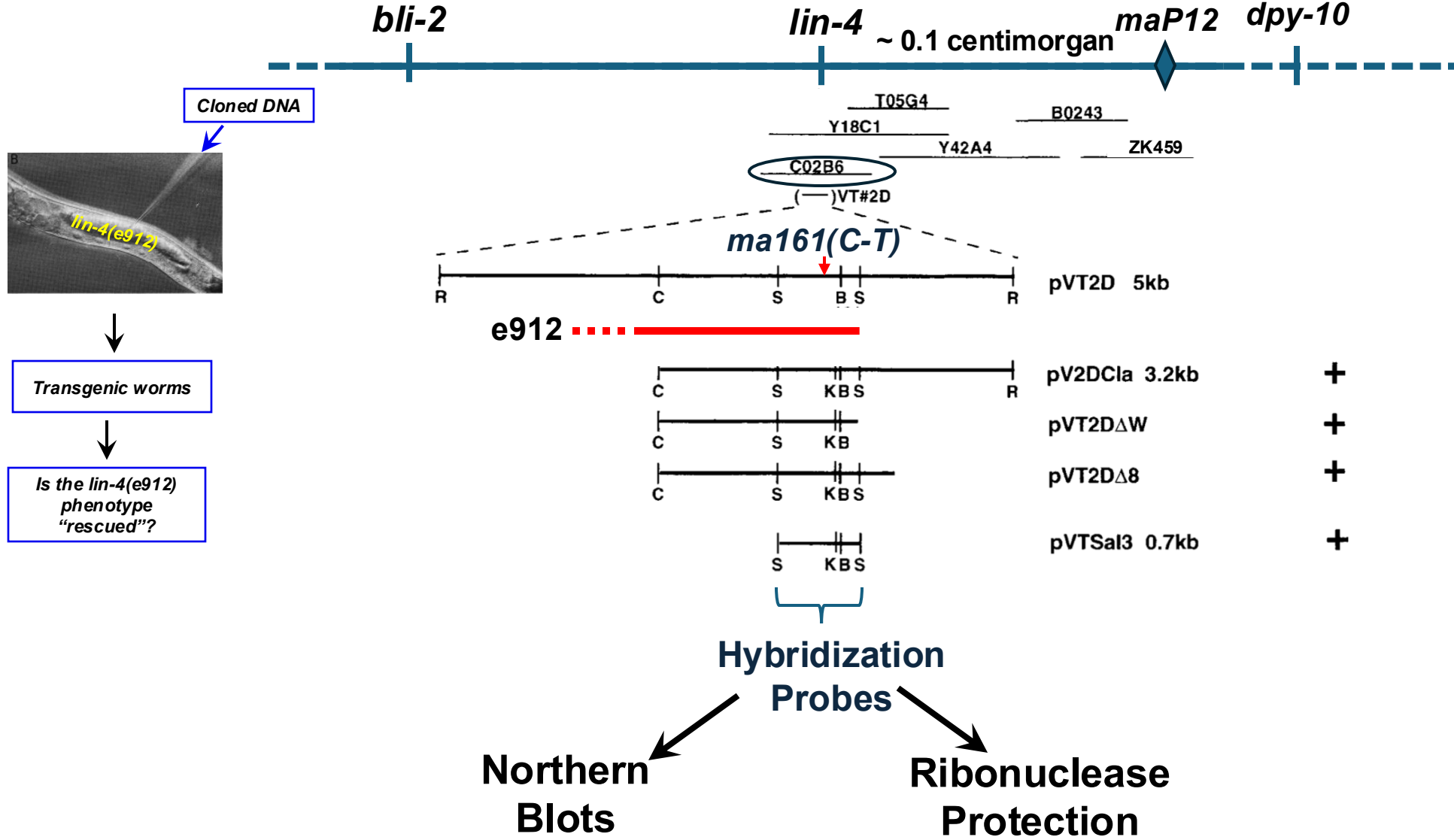
Mapping the boundaries of *lin-4* by transgenic rescue of *lin-4(e912)*



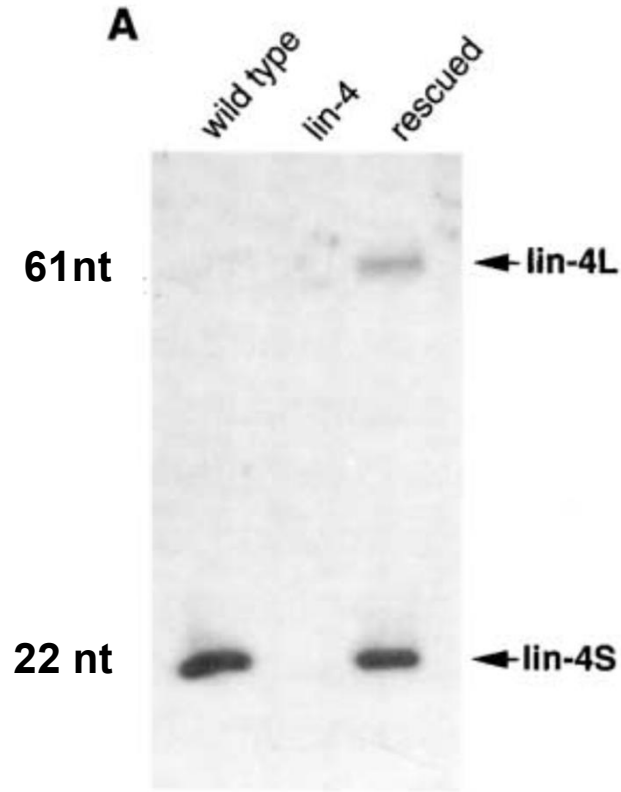
Mapping the boundaries of *lin-4* by transgenic rescue of *lin-4(e912)*



Detection and mapping of *lin-4* transcripts

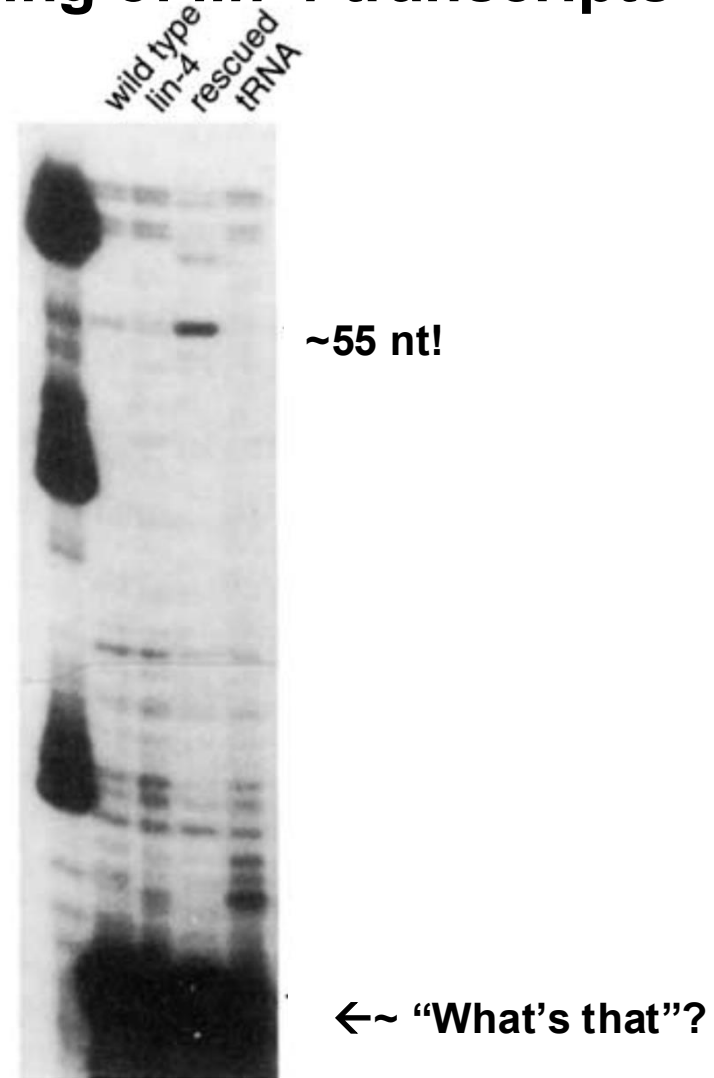


Detection and mapping of *lin-4* transcripts



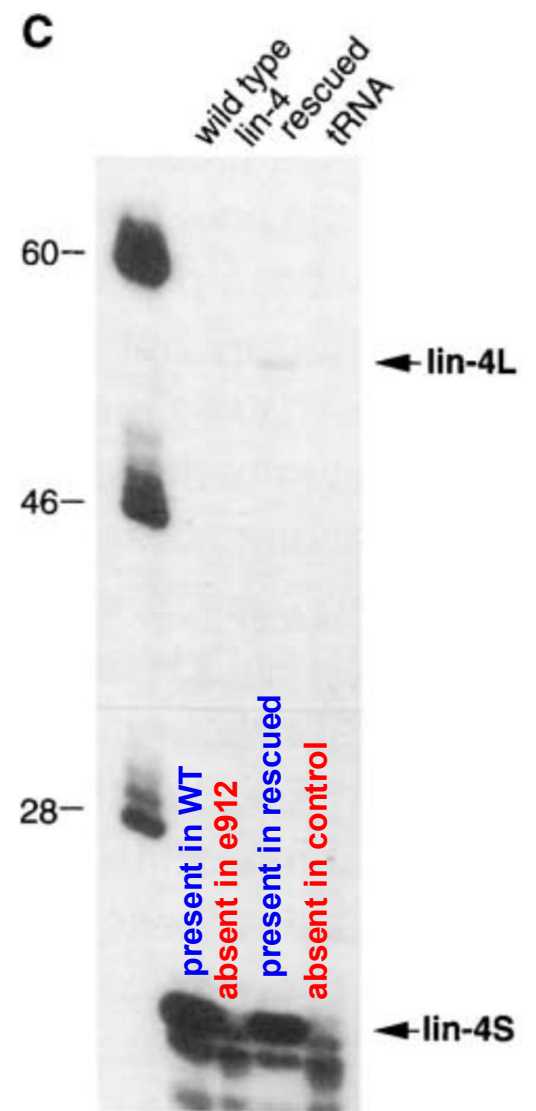
Northern
Blots

Rhonda Feinbaum

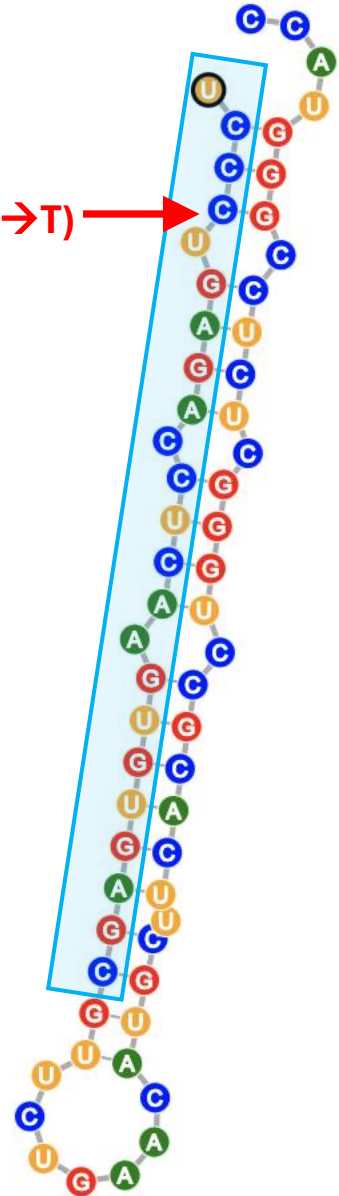


Ribonuclease
Protection

Victor Ambros



22 nucleotide and 61 nucleotide *lin-4* transcripts



Ruling out putative *lin-4* protein coding capacity

```
GCACCTAACACTATTTTCGGGGACCGCTCGGCCAAGCGGTTTGGTGCCAGCCTCACGGAAGGCTTGCGGGGCGCCGCTCGTGCCCTCCGCTCTCTCTCGGTGTGCTCCCTTCGCTTCCTCGTCTCG  
TCCTCTCTCTCAGTGGGCGGGGGACCGCGGCAAAAAGAATAACGACGAAGCGACCGAATGACCCAGTCTCTTCACTTCTCTACTTTTCGATCCCTCTCTCTCAGCTACTCTCTCCATGTCCATCCA  
TCCTCGCCCCATCACTCCAGAGACCTTTGGTCACTCTTTCCATTAGACTCTAACCACAATCGGTCGGACTCATCACACTTACCTTTCAATATCTAAACTATTCTGATTAATAAATCTTAT  
AGTTTTTAGATTCTTAGACAATTTCTTAGAGTTTGGTTGGTTTATGAGTTTATGCTTCCGGCCTGTTCCCTTGAGACCTCAGGTGTGAGTGTATATGATGCTTCACACCTGGGCTCTCCGGGTACCA
```



The diagram shows a DNA sequence with several start codons (ATG) highlighted in green and stop codons (TAA, TAG, TGA) highlighted in red. A blue arrow indicates a frameshift mutation, showing the sequence being shifted to the right.

There are some start codons

And numerous stop codons

We introduced frameshifts, and a stop → Still rescues *lin-4(e912)*

“Evolutionary mutagenesis” → clones from *C. briggsae*, *C. remanei*, and *C. vulgaris* rescue *lin-4(e912)*

Evolutionarily divergent *lin-4* sequences rescue *C. elegans lin-4(e912)*

```
elegans      GCACCTAACACTATTTTCGGGGACGCCTGCCAAGCGGTTGGTGGTGCAGCCTCACGGAAAGGCTTGC GGGG CGCCGCGCTCGTGTCCCTCCGTGCTCTGCTGCCTGTGGCC ---TTCCGCTTCTCCTCTCTCTCA
briggsae    CGAGCGCGCCCGCCGCAAGGACGCCTGCCAAGCGTGGTGGTGGTGCAGCCTCACGGAAAGGCTTGC GGGG CGCCGCGCTCGTGTCCCTCCGTGCTCTC-CTGCGTGTGCCGCTTCCGCTTCTCCTCTCTCCCA
remanei     GCAGAGC GCGCTTTCAGAGGGTGCCTGCCAAGCGTGGTGGTGGTGCAGCCTCACGGAAAGGCTTGC GGGG CGCCGCGCTCGTGTCCCTCCGTGCTCTC-CTGCGTGTGCCGCTTCCGCTTCTCCTCTCTCTCA
vulgaris    GACCATTATGTCTCGTAGGGACGCGTGCAGCGGTGGTGGTGGTGCAGCCTCACGGAAAGGCTTGC GGGG CGCCGCGCTCGTGTCCCTCCGTGCTCTC-CTGCGTGTGCCGCTTCCGCTTCTCCTCTCTCTCA
          ** ***** **

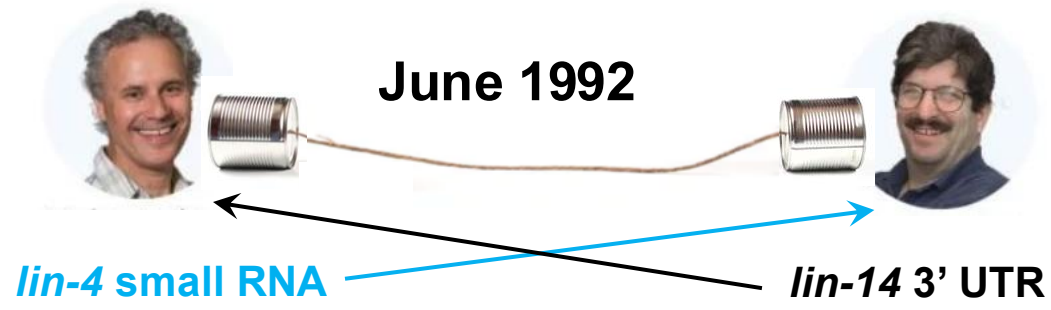
elegans      GTGCGCGGGG---GGACCGCGC---AAAAAAGAATAACGACGAAGCGACCGAATGACCCAGTCTCT TCACTTCTCTACTTTTCGATCCTCCTC---CTTCAGCTACTCCTCCATGTTCATCCA
briggsae    GTGCGCGGTGAA--GGACCGCGCAGCAAAAAAAGAATAACGACGAAGCGCCGAATGACCCAGTCTCT TCACTTCTCTACTTTTCGATCCTCCTCCTCCCTTCTTTTCTGCT-GCTTCTTCTACTCCTCCATGTTCATCCA
remanei     GTGCGCGGTGAAGGGGACTGCGGCAG---AAAAAAGAATAACGACGAAGCGACCGAATGACCCAGTCTCT TCACTTCTCTACTTTTCGATCCTCCTCATCTTATTTTCTGCT--TCTTCTTCTACTCCTCCATGTTCATCCA
vulgaris    GTGCGCGGTGAAGGGGACTGCGGCAG---AAAAAAGAATAACGACGAAGCGACCGAATGACCCAGTCTCT TCACTTCTCTACTTTTCGATCCTCCTCCCAATCTTATTTTCTGCTTCTTCTACTCCTCCATGTTCATCCA
          ***** *      **** ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** ***** *****

elegans      TCCTCCGCCC-ATCAC TCCAGAGACCCCTT-TCGGT CACTCTTTCCAATAGACTCTACCACAATCGGTG GACTC ATCACACTTACTTTCAAATATTAAACTA-TTCCTGAA-TATAATAAATCTTATAGT-----TT
briggsae    TC---CCGCCCAATCGCTCCAGAGACTCACACCGGTCACTCTAACTATTAGTCTTTCACCGCAACC GGT-----ATCAT TCCAATC---CATCCATC---CTA-TTTCTAAACTACAGTAATCC-----
remanei     TC---CCGCCCAATCGCTCCC---AGACCCCGTCCGGT CACTCT--CTATTAGACCCCTTCC TCAATCTGTGCG-----ACTC---AATCTACCAACTATTTCTGCGGTACAGTAACCCGAAGAGTATCATATTC
vulgaris    TC---CCGCCCAATCGCTCCC---AGACCCCGTCCGGT CACTCT--CTATTAGACTCTTCC TCAATCTGTGCG-----AATC---AATCTACCAACTATTTCTGCGGTACAGTAACCCGAAGAGT-----
          ** ***** ** ***** ** ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

elegans      TTAGTTTTATAGTTTTTAGATTCTAGACAATTT--CTAGAGTTTGGTTGGTTTATGGTT---TTATGCTTCCGGCCTGTTCCTGAGACCTCAAGTGTGAGTGTAATATGATGCTTCAACCTGGGCCTCGGGTACCA
briggsae    -----TTTAAAAAATCCTAAAACT-----AGAATTTTGGTTGGTTTATATGTATCAGATGCTTTCGGCCTGTTCCTGAGACCTCAAGTGTGAGCGTTTGAACTGCTTTCACGCTGGGCCTCGGGTACAG
remanei     ATCAATCATATTCATCACATTCTAGACTTTCTGAGAAAGACTTTTGGTGGTTTATTATGTT-TCTGATGCTTTCGGCCTGTTCCTGAGACCTCAAGTGTGAGCGCACTGTTTGATGCTTCAACCTGGGCCTCGGGTACAG
vulgaris    ---TATCA TATTCATCACATTCTAGACTTTCTGAGAAAGACTTTTGGTGGTTTATTATGTT-TCTATGCTTTCGGCCTGTTCCTGAGACCTCAAGTGTGAGCGCACTGTTTGATGCTTCAACCTGGGCCTCGGGTACAG
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

“Evolutionary mutagenesis” → clones from *C. briggsae*, *C. remanei*, and *C. vulgaris* rescue *lin-4(e912)*

Complementarity between *lin-4* RNA and *lin-14* 3' UTR sequences



5'GUUCCUGAGACCUCAAGUG.UGAG	<i>lin-4</i>
3'CAAG.GACUC.....UCGU-ACUC	<i>lin-14</i> 3'UTR
UAAG.GACUC.-.....ACUU	
CAAGGGACUC.-...UUUAC-GCUC	
UAAG.GACUC.-.....U.ACUC	
CAAGGGACUC.....CAU..CUU	
CAAG.GACU.-.....UGU.-UUC	
CA.GGGACUC.-.....ACUC	

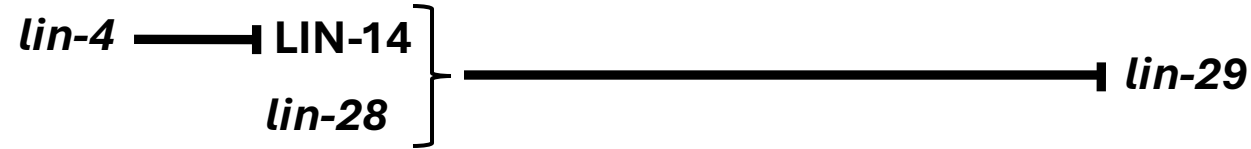
Today's perspective:

- U **CCUGAGACCUCAAGUGUGA**
.GGGACUC.....ACU...
- U **CCUGAGACCUCAAGUGUGA**
.GGGACUC.....UUACGCU...
- U **CCUGAGACCUCAAGUGUGA**
.GGGACUC.....CAU.CU...
- UC **CCUGAGACCUCAAGUGUGA**
..GGACUC.....ACU...
- UC **CCUGAGACCUCAAGUGUGA**
..GGACUC.....UCGUACU...
- UC **CCUGAGACCUCAAGUGUGA**
..GGACUU.....GU.UU...
- UC **CCUGAGACCUCAAGUGUGA**
..GGACUC.....ACU...

Lee, Feinbaum & V. Ambros (1993) The *C. elegans* heterochronic gene *lin-4* encodes small RNAs with antisense complementarity to *lin-14*. *Cell* 75

Wightman, Ha, Ruvkun (1993) Posttranscriptional regulation of the heterochronic gene *lin-14* by *lin-4* mediates temporal pattern formation in *C. elegans*. *Cell* 75

Ambros lab heterochronic activities 1993 ~ 2000



Rougvie and Ambros (1995) The heterochronic gene *lin-29* encodes a zinc finger protein that control a terminal differentiation event in *C. elegans*. *Development* 121

Moss, Lee, and Ambros (1997) The cold shock domain protein LIN-28 controls developmental timing in *C. elegans* and is regulated by the *lin-4* RNA. *Cell* 88

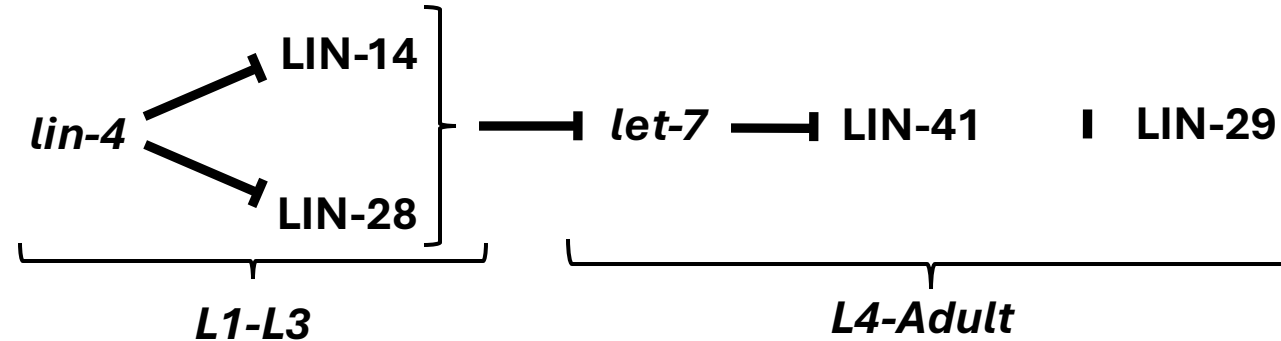
Feinbaum and Ambros (1999) The timing of *lin-4* RNA accumulation controls the timing of postembryonic developmental events in *C. elegans*. *Developmental Biology* 210

Olsen and Ambros (1999) The *lin-4* regulatory RNA controls developmental timing in *C. elegans* by blocking LIN-14 protein synthesis after the initiation of translation *Developmental Biology* 216

Slack, Basson, Liu, Ambros, Horvitz, Ruvkun (2000) The LIN-41 RBCC gene acts in the *C. elegans* heterochronic pathway between *let-7* regulatory RNA and the LIN-29 transcription factor. *Molecular Cell* 5

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1999: *lin-4* and *let-7* are the only known microRNAs, and only *C. elegans*.



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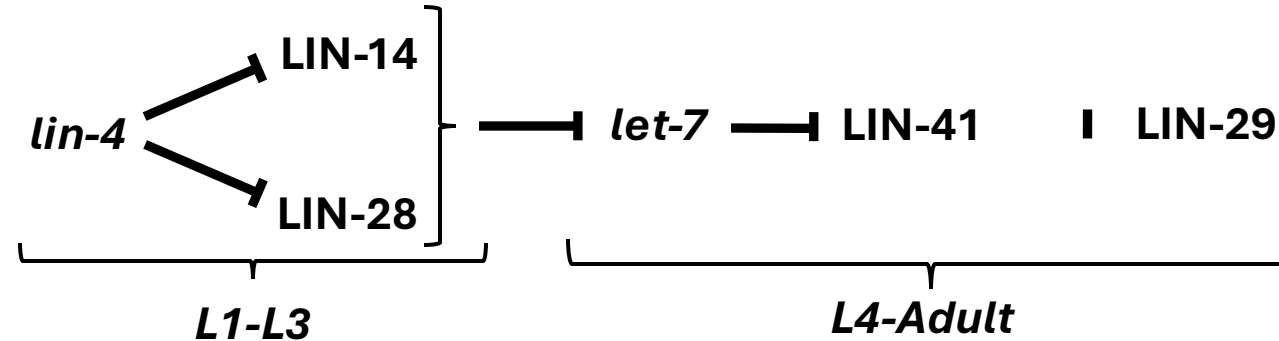
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1998 – 2001 Apprehending the scope and significance of microRNAs

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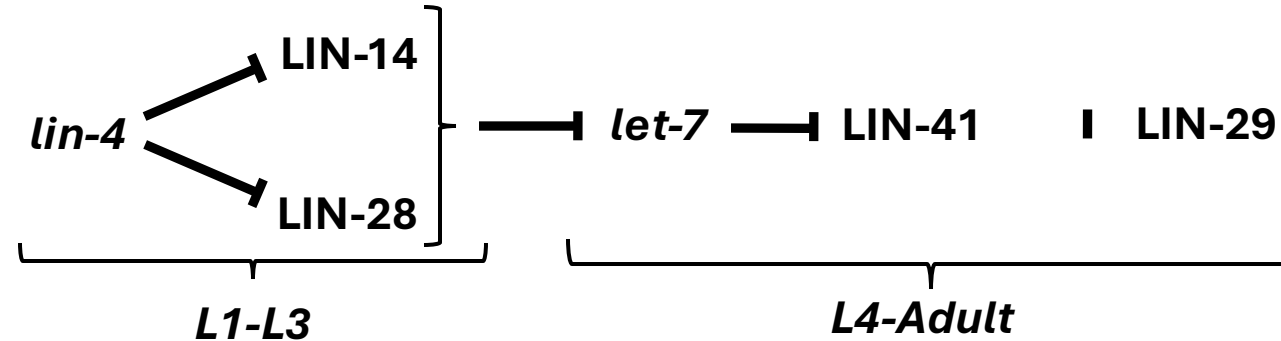
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1998 – 2001 Apprehending the scope and significance of microRNAs

Consilience of microRNA and RNAi phenomena



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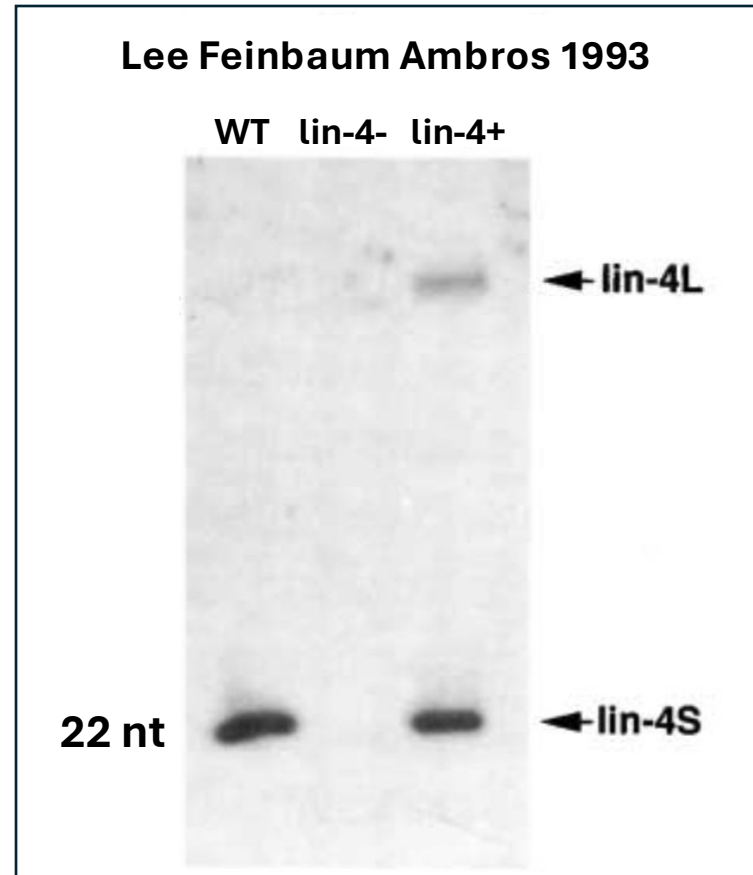
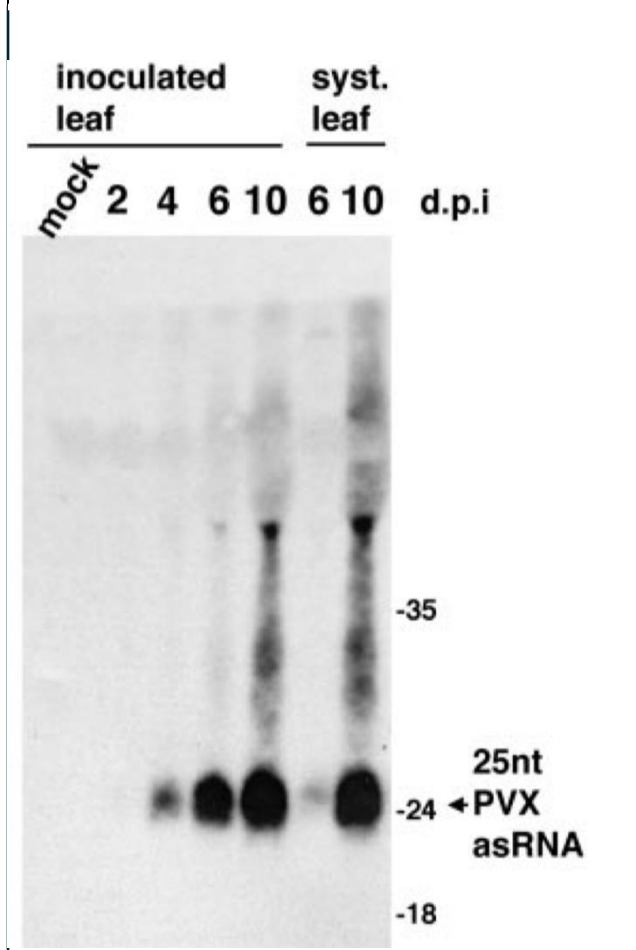
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1998 – 2001 Apprehending the scope and significance of microRNAs

Consilience of microRNA and RNAi phenomena

Fire et al Mello (1999) Potent and specific genetic interference by double-stranded RNA in *Caenorhabditis elegans* *Nature*

Hamilton & Baulcombe (1999) A species of small antisense RNA in posttranscriptional gene silencing in plants *Science*



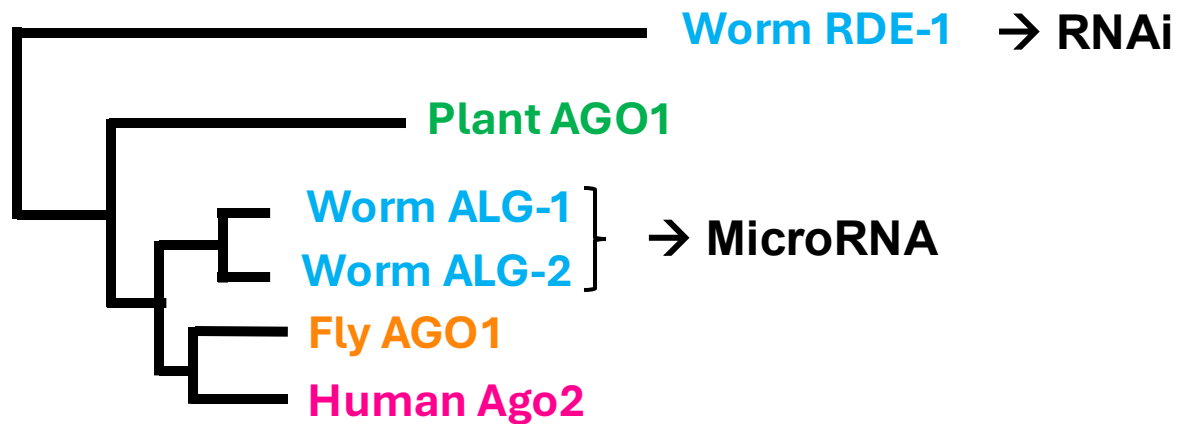
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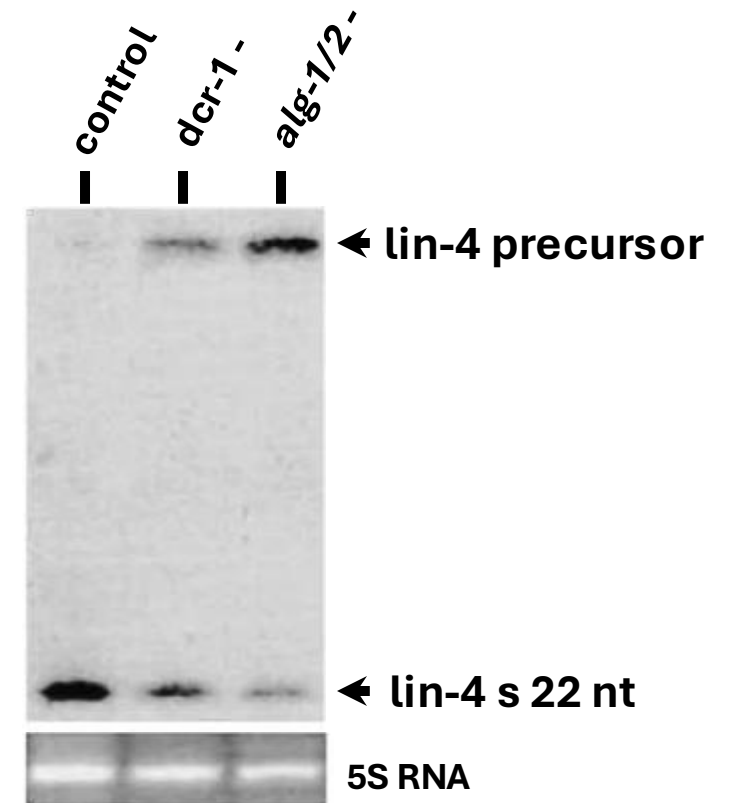
RNAi and microRNAs are mechanistically related?



Tabara et al Mello (1999) *C. elegans rde-1* is required for RNAi and encodes a conserved Argonaute family protein



Grishok et al Ruvkun Mello (2001) *C. elegans* Argonautes ALG-1 and ALG-2 are required for *lin-4* and *let-7* function



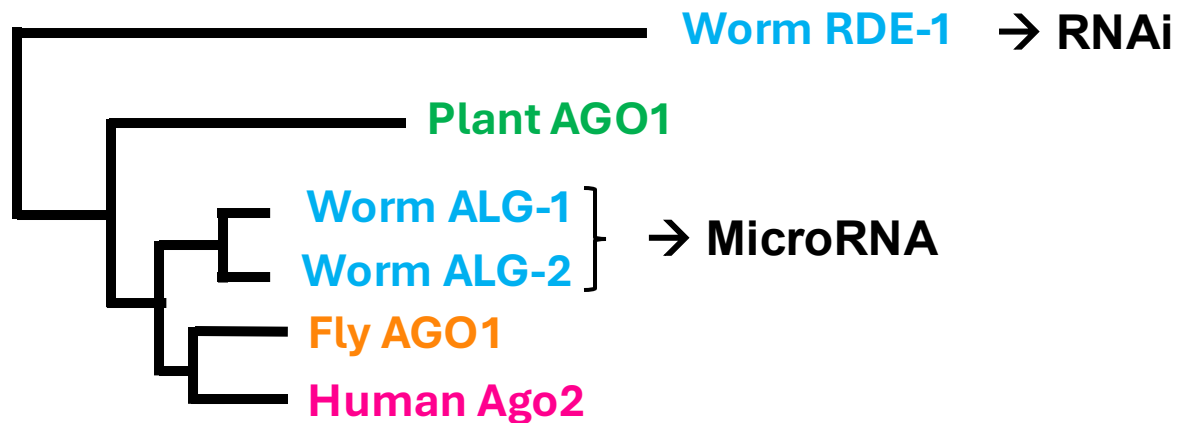
1998 – 2001 Apprehending the scope and significance of microRNAs

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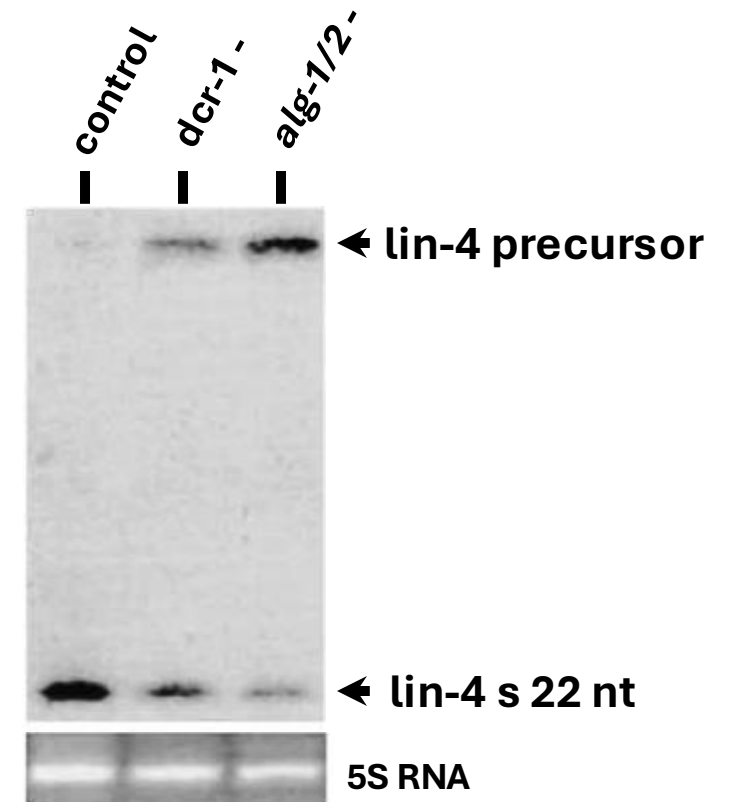
? microRNAs: Evolutionary adaptation of RNAi for gene regulation ?



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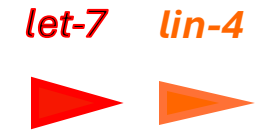
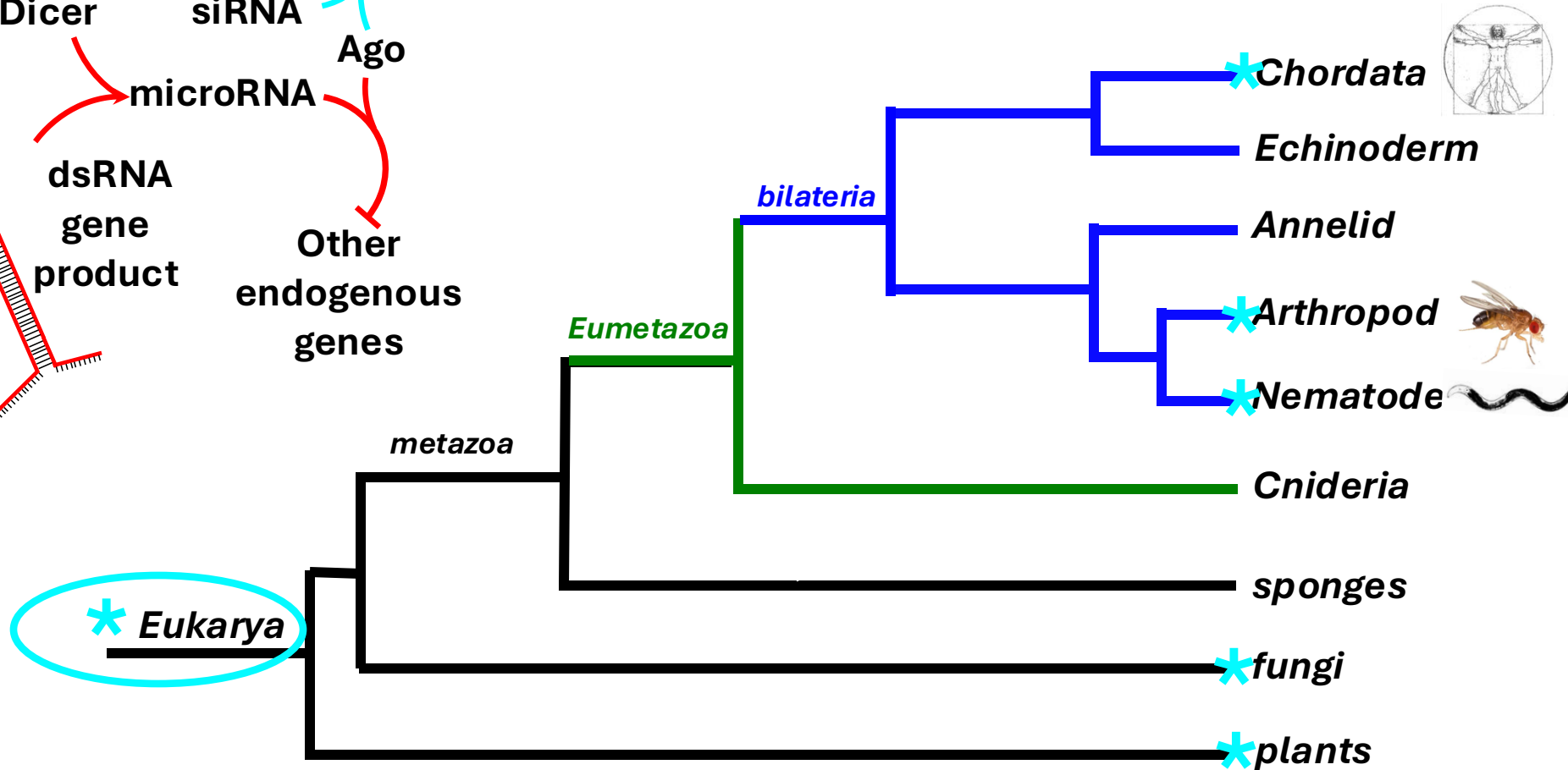
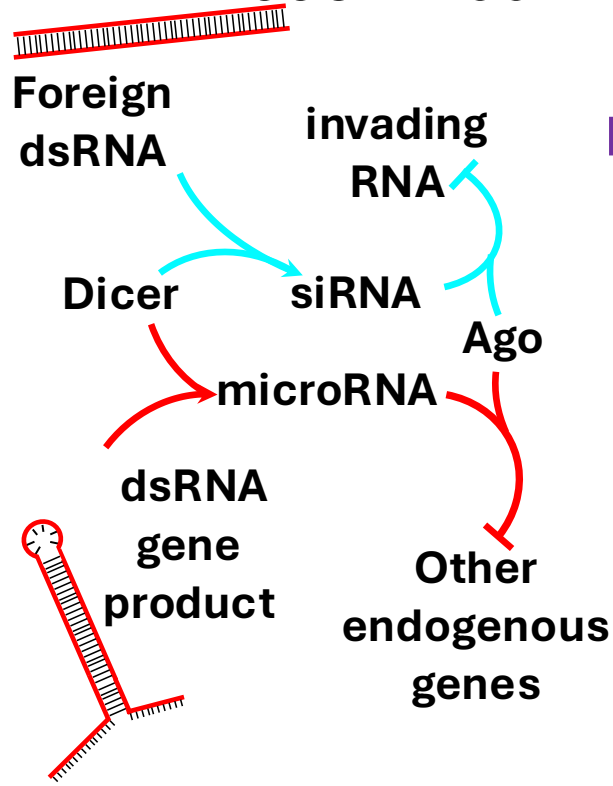


1998 – 2001 Apprehending the scope and significance of microRNAs

Consilience of microRNA and RNAi phenomena

Evolutionary adaptation of RNAi for gene regulation

*RNAi → viral defense involving small RNAs

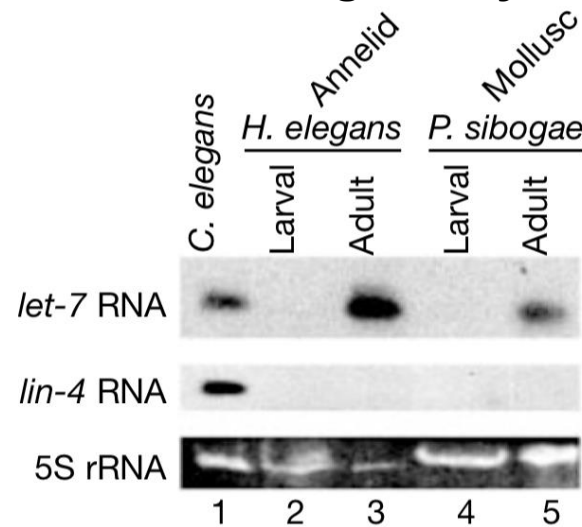


1998 – 2001 Apprehending the scope and significance of microRNAs

let-7 microRNA is ancient and derived from RNAi

***let-7* microRNA is conserved across bilaterian animals!**

Pasquinelli et al ... Ruvkun (2000) Conservation of the sequence and temporal expression of *let-7* heterochronic regulatory RNA. *Nature*

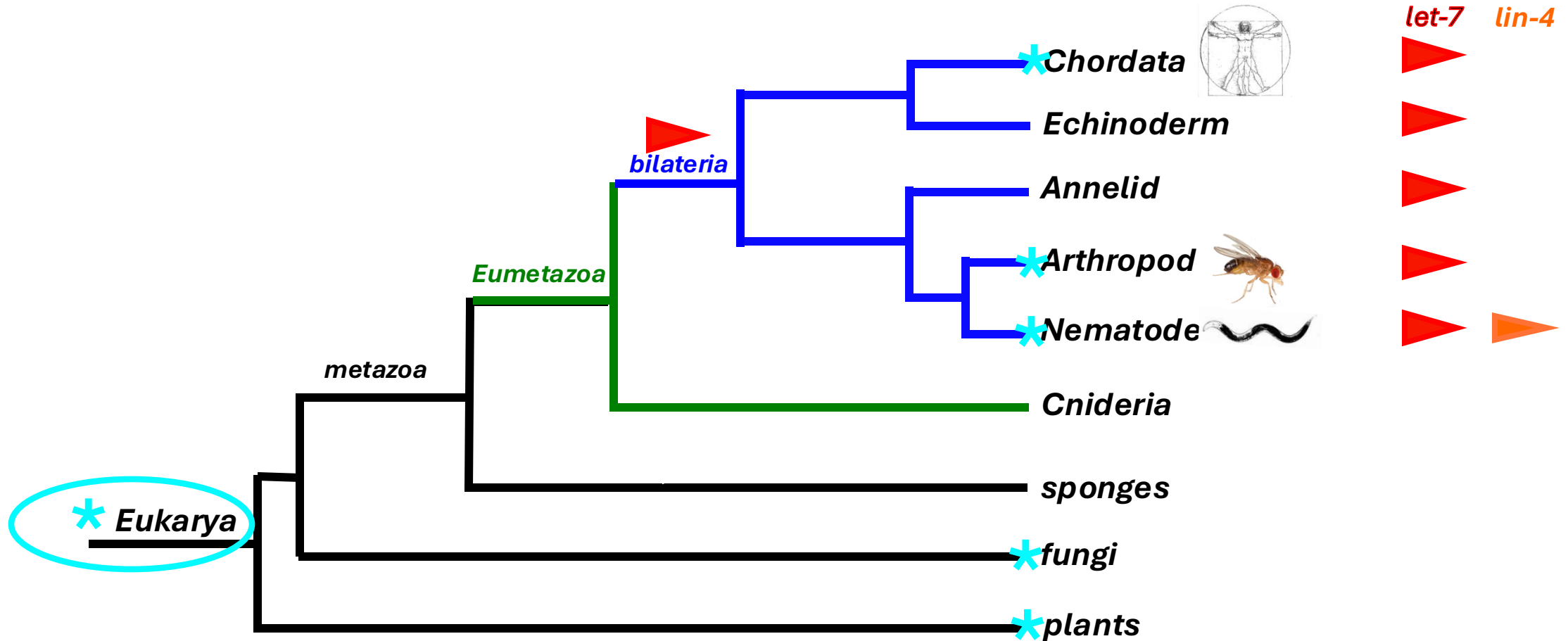


Fish *let-7a* UGAGGUAGUAGGUUGUAUAGUU
Fly *let-7a* UGAGGUAGUAGGUUGUGUGGUU
Worm *let-7a* UGAGGUAGUAGGUUGUAUGGUU

There must be other microRNAs besides *let-7* and *lin-4*!

let-7 microRNA is ancient and derived from RNAi

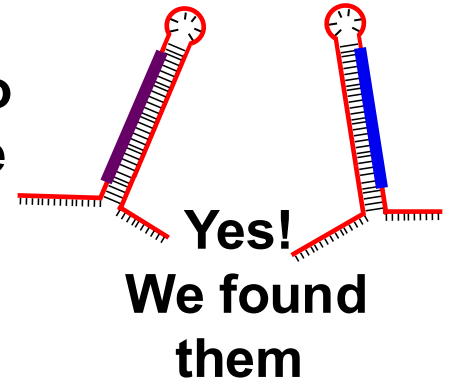
let-7 microRNA is conserved across bilaterian animals!



There must be other microRNAs besides *let-7* and *lin-4*!

circa 2000 ...
Cloning and sequencing small RNAs
(Rosalind and Victor)

C. elegans RNA → ~ 22 nt RNA → ~ 22 nt cDNA → Library of clones → ~22 nt sequences → Match to genome



We should have realized
There must be other labs doing this!

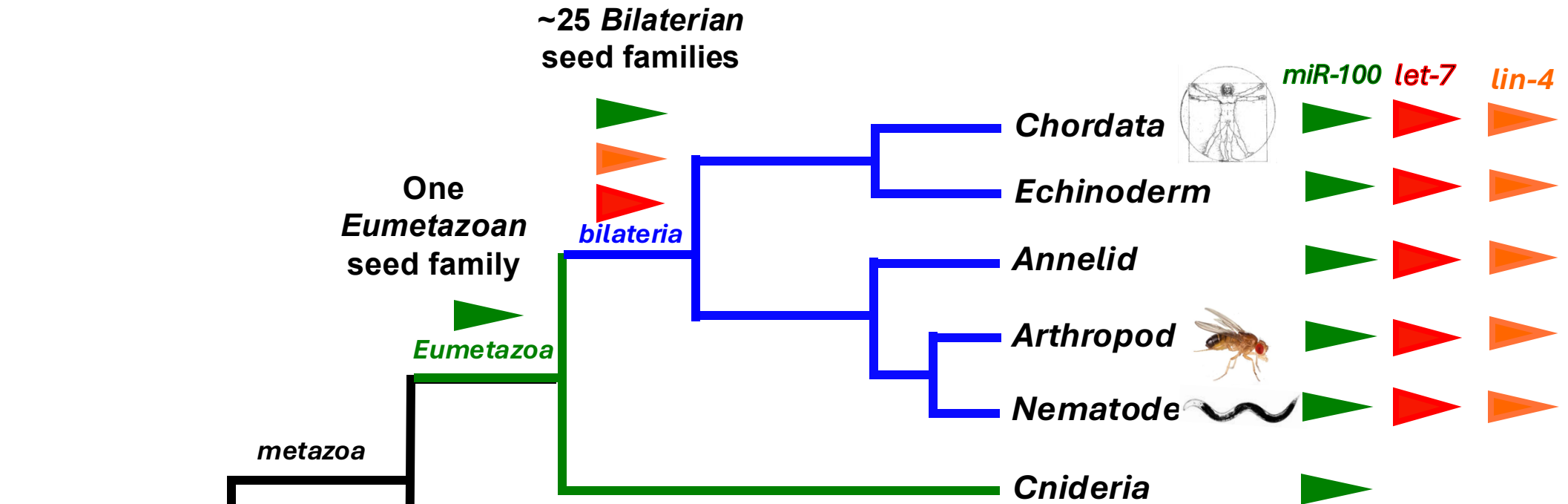
By the skin of our teeth →

Science Oct 2001: 3 papers
Many microRNAs in worms, flies, mammals
Lee and Ambros
Lau et al Bartel
Lagos-Quintana et al Tuschl

MicroRNAs across Eukaryotes

Hsa-mir-100 AACCCGUA GAUCCGAACUUGUG
 Cel-mir-52 CACCCGUA CAUAUGUUUCCGUGCU

'Seed' nt 2-8

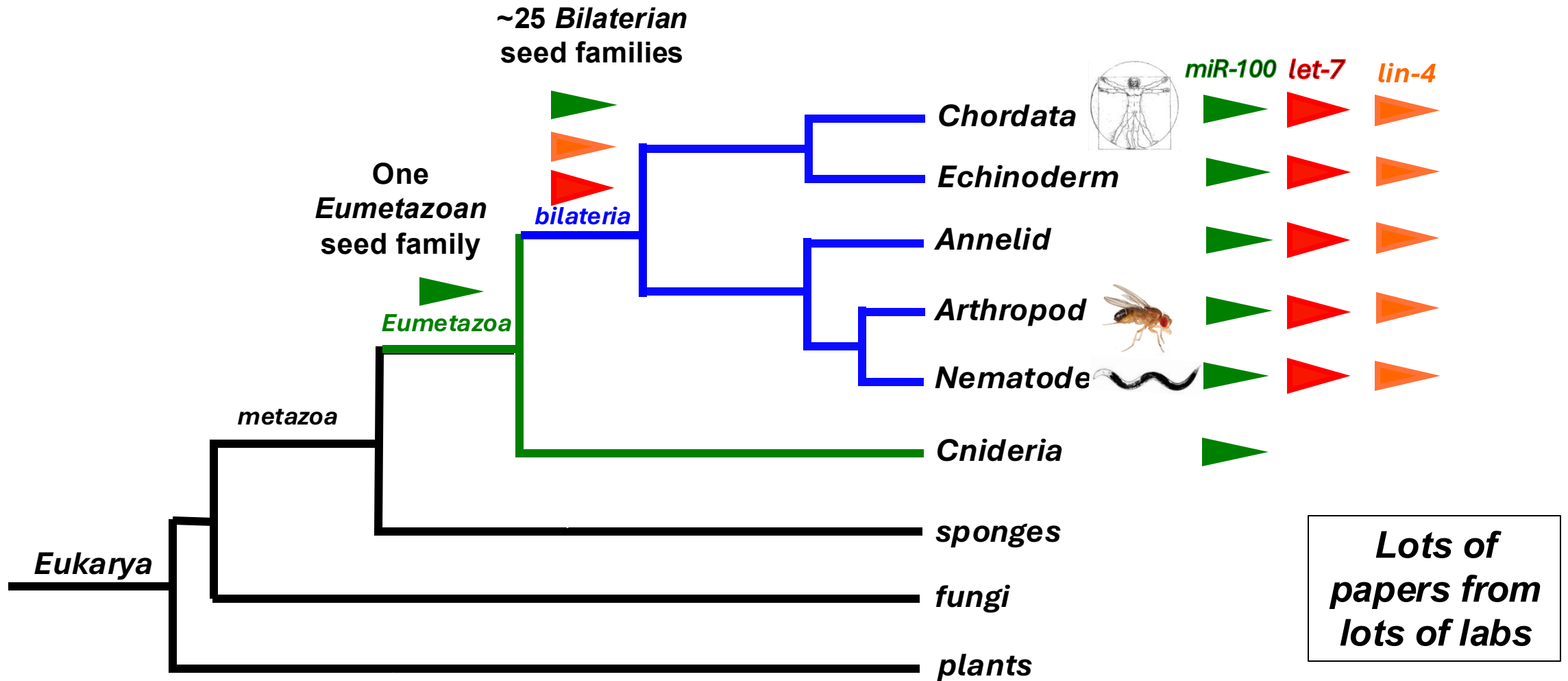


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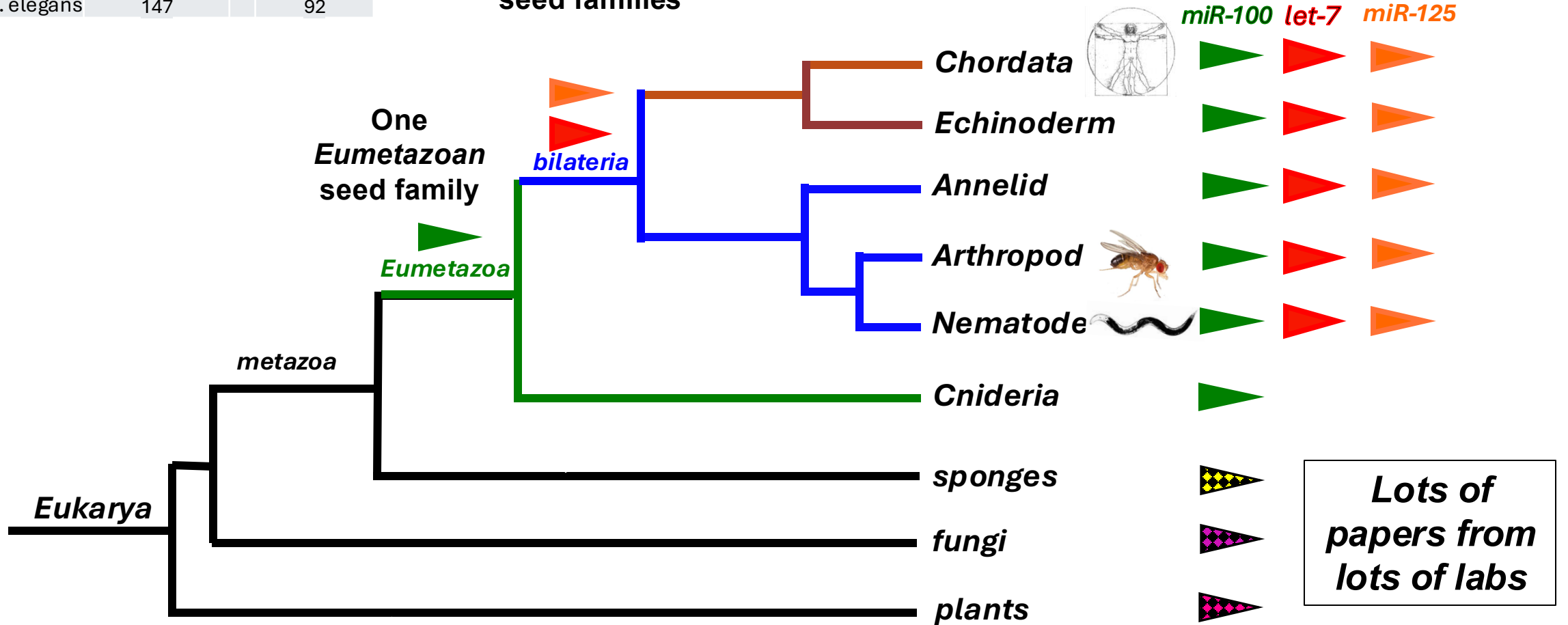
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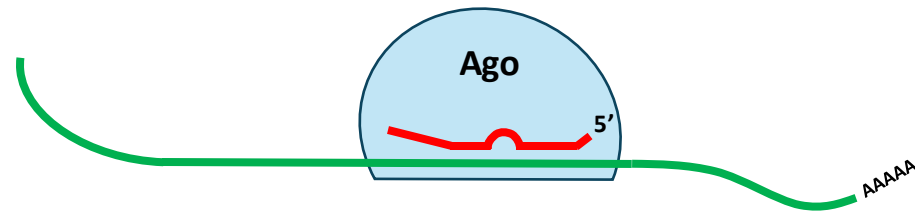
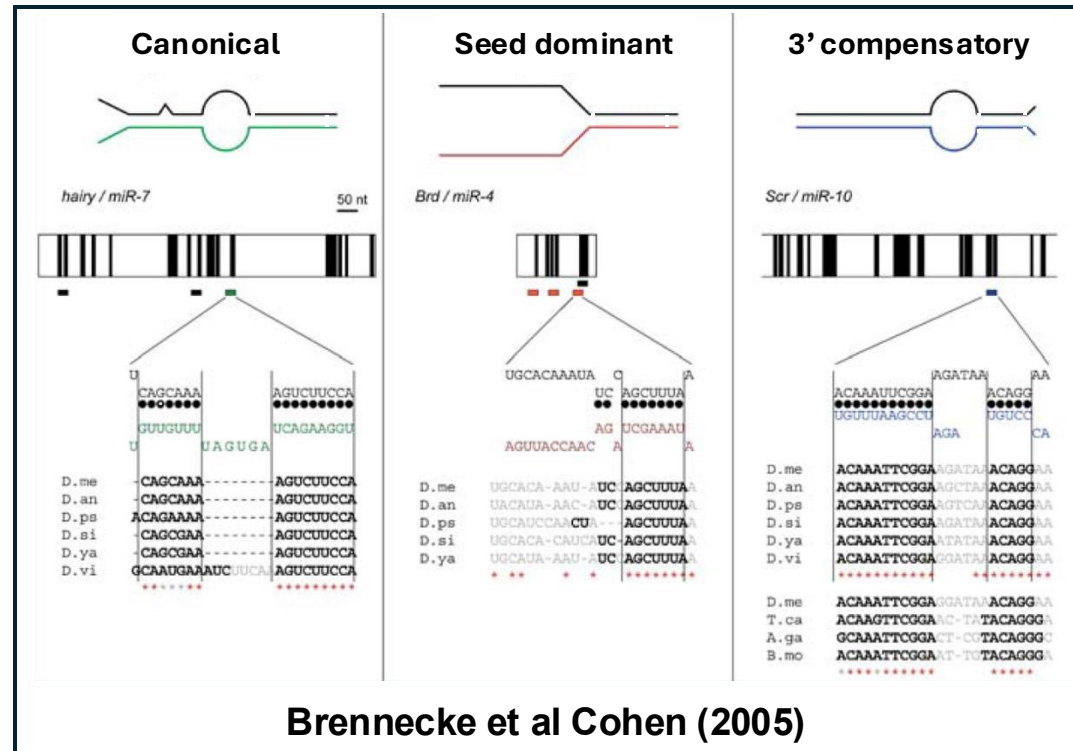
'Seed' nt 2-8

	microRNA loci	seed families
H. sapiens	575	273
D. melanogaster	163	101
C. elegans	147	92

~25 *Bilaterian*
seed families



How do microRNAs recognize their mRNA targets?

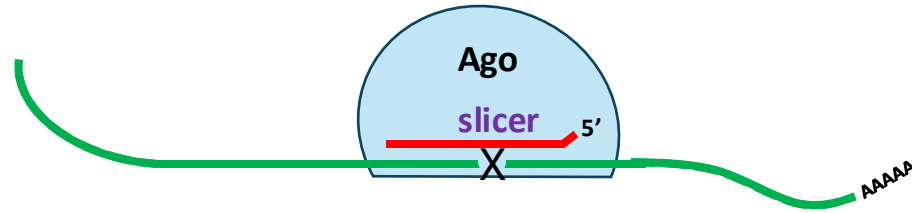


Partial complementarity – seed match (+)

How do microRNAs repress their mRNA targets?

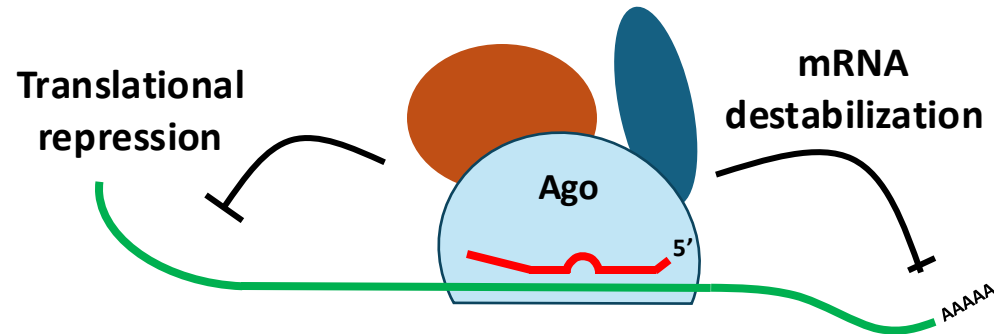
In animals, microRNAs generally do not slice their mRNA targets

RNAi:



Full complementarity → mRNA is destroyed

MicroRNAs:

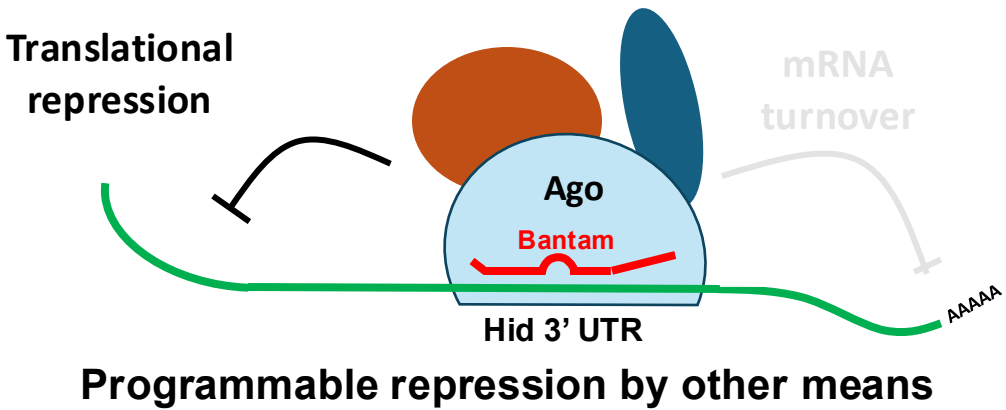


Partial complementarity – seed match (+): No Slicing

Programmable repression by other means:

Translational repression without mRNA target destabilization

Bantam ---| Hid → apoptosis

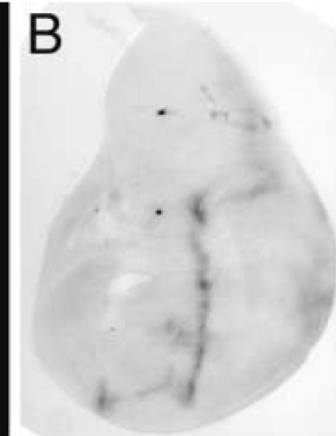


Brennecke et al Cohen (2003)

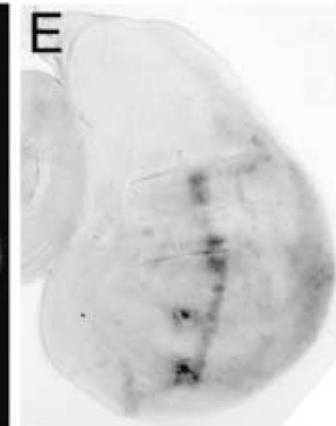
Hid protein

Hid mRNA

No
Bantam
miRNA

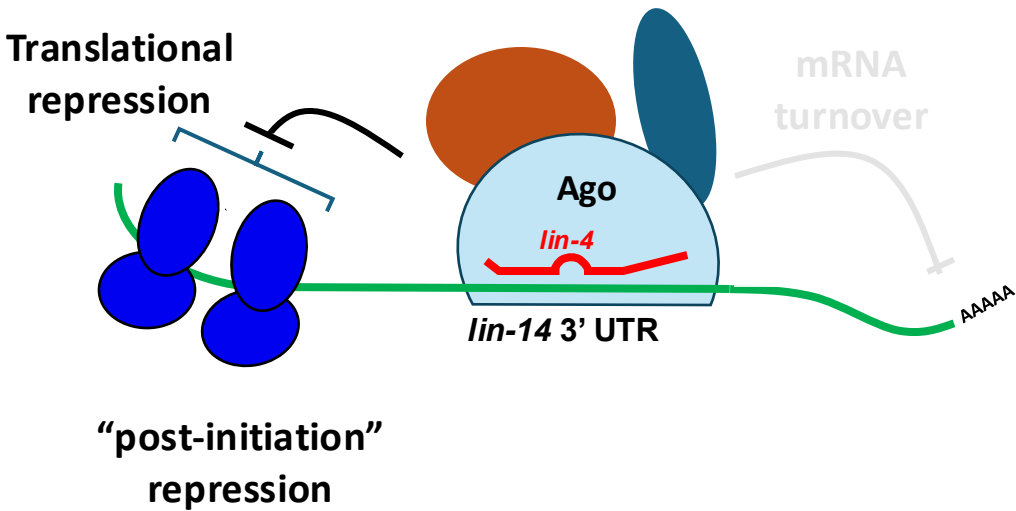


Bantam
microRNA
expressed

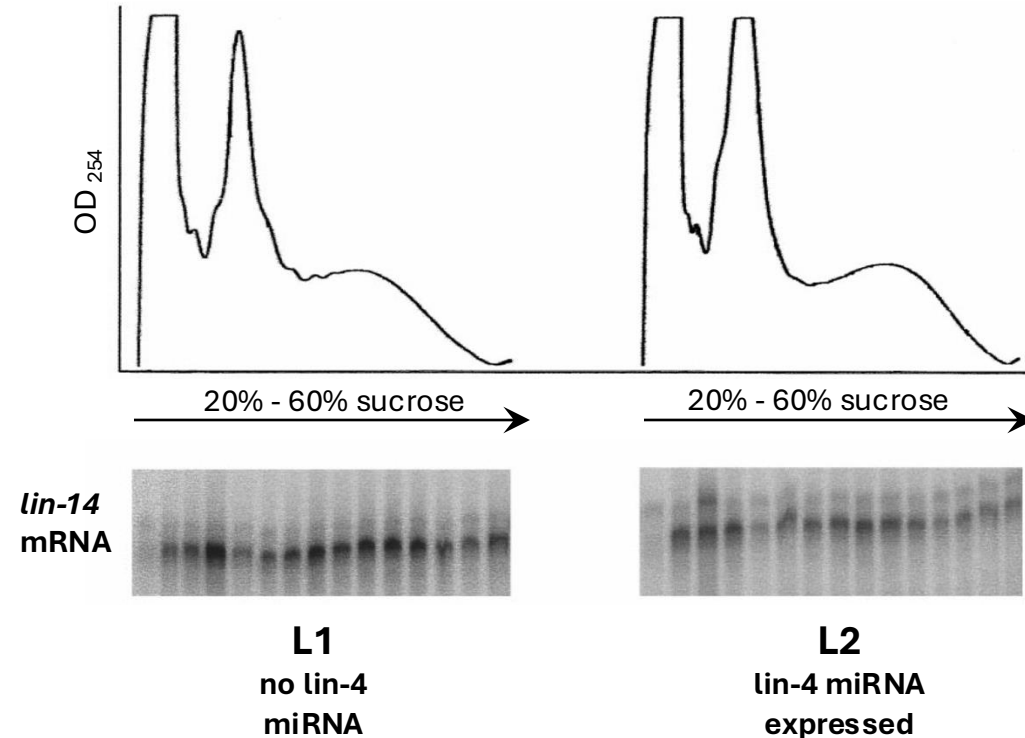


Translational repression without mRNA target destabilization

lin-4 ---| LIN-14 → early cell fates



Philip H. Olsen and Victor Ambros (1999)
Developmental Biology 216



Phil's conclusions supported and refined by:

Stadler et al Fire (2012) Contributions of mRNA abundance, ribosome loading, and post- or peri-translational effects to temporal repression of *C. elegans* heterochronic miRNA targets. *Genome Research* 12

Identification of microRNA -- target regulatory circuits

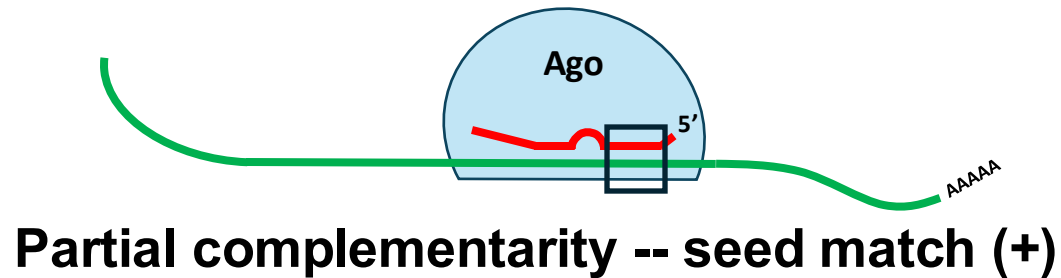
Computational searches for seed matches in annotated mRNAs

In many animals each microRNA seed can match hundreds of genes

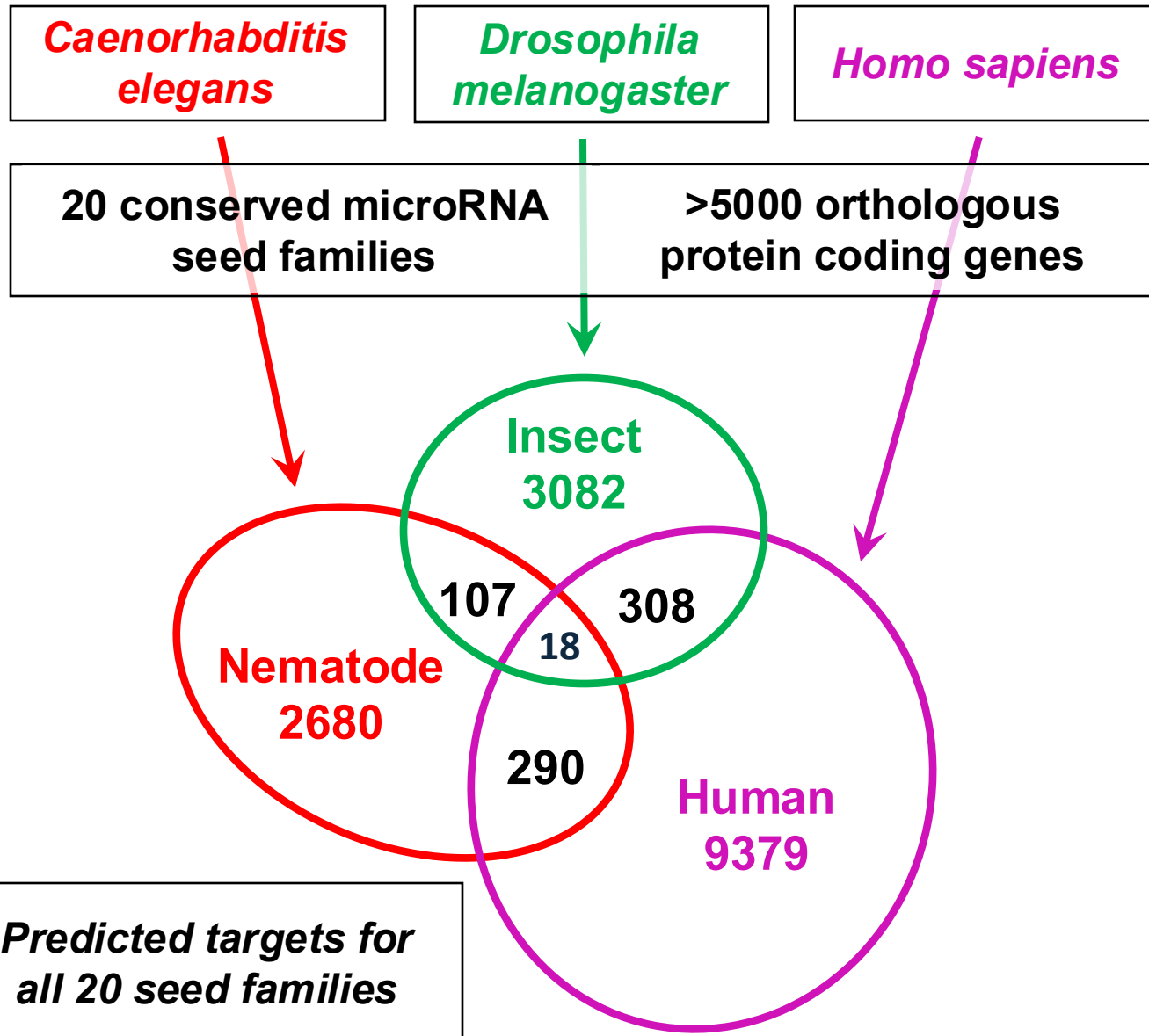
<i>C. elegans let-7</i>	→	201 sites	in	134 genes
<i>D. melanogaster let-7</i>	→	113 sites	in	94 genes
<i>H. sapiens let-7</i>	→	5479 sites	in	4140 genes

Targetscan.org

↑
Search in 3' UTR sequences for
complementarity to nt 2-8 of the
microRNA



Evolutionary patterns of of miRNA--target interactions



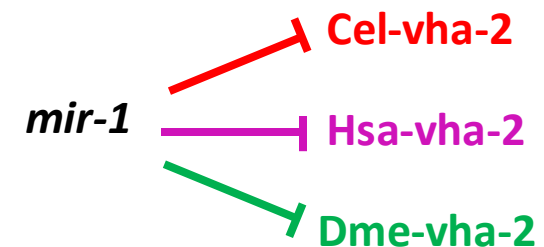
Substantial Evolutionary Fluidity in microRNA targeting

(which microRNAs regulate which genes)

Thought to reflect roles for loss and gain of microRNA target sites as evolutionarily adaptive

Also, certain instances of

Deep conservation of targeting



Chen and Rajewsky, 2006

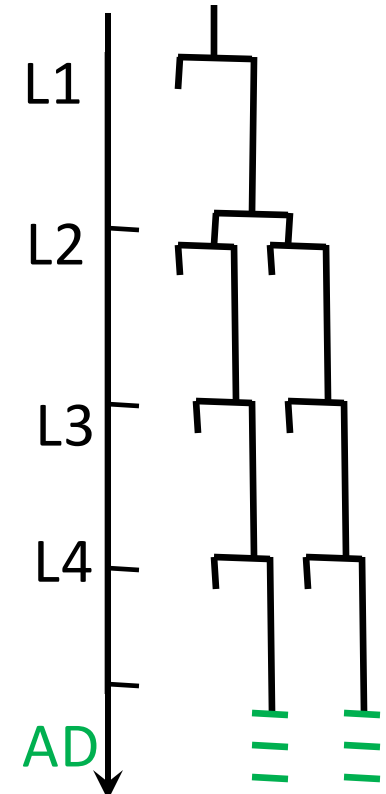
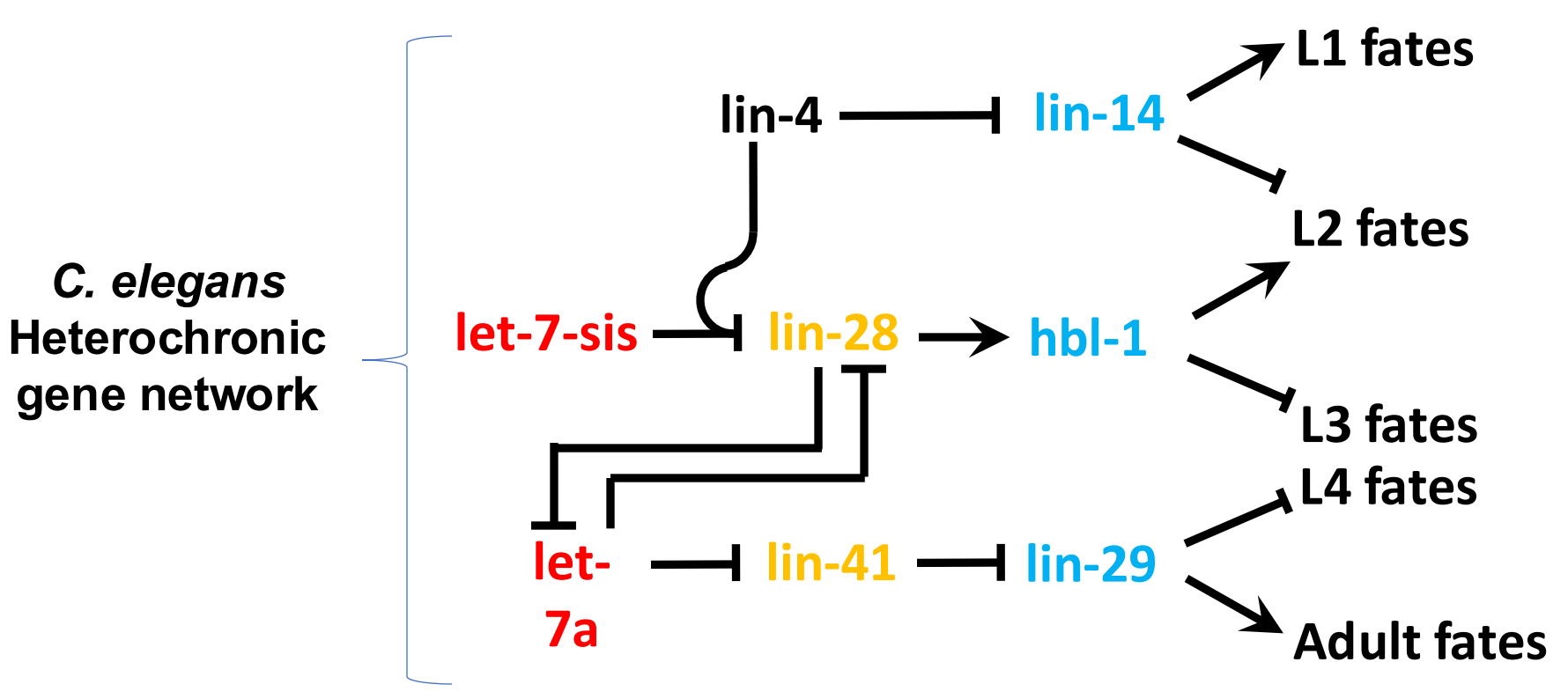
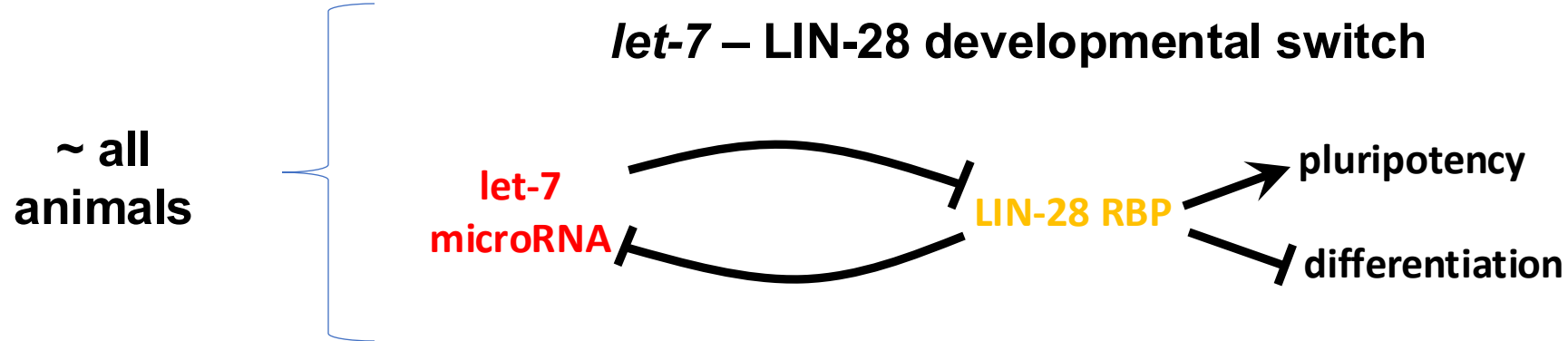
From Chen and Rajewsky, 2006

Evolutionarily conserved microRNA -- target regulatory circuits

let-7 – LIN-28 developmental switch

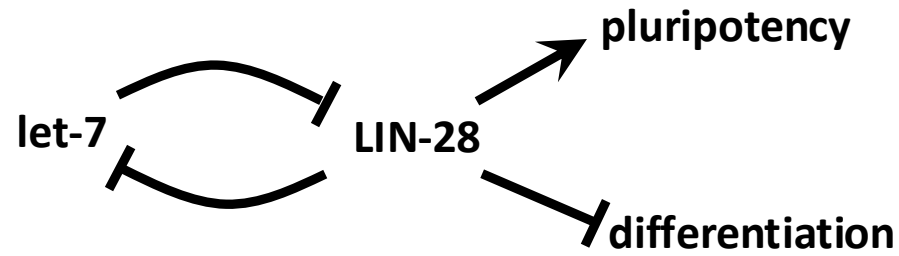


Evolutionarily conserved microRNA -- target regulatory circuits



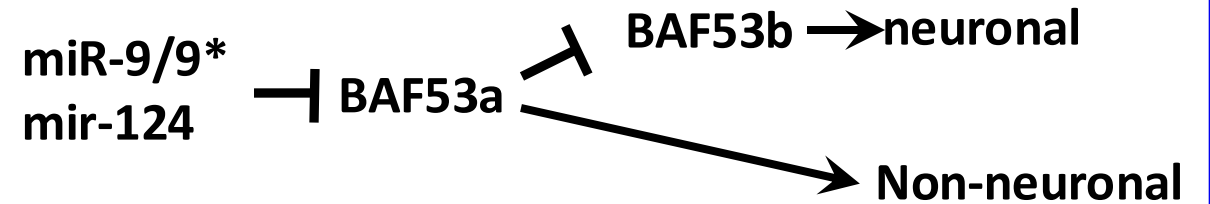
Developmental and Physiological roles of microRNAs in animals

Developmental switches



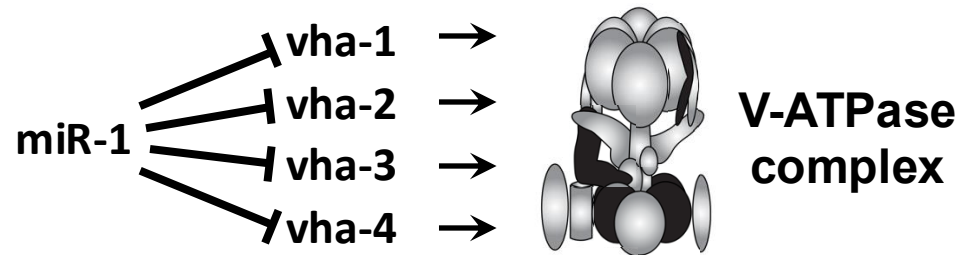
Tsialikas & Romer-Siebert (2015) *Development*

Reinforcing (even reprogramming) cell type



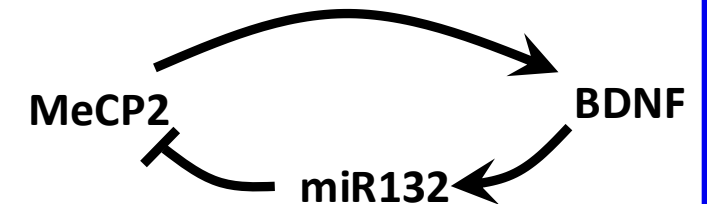
Tang, Yoo, Crabtree (013) *Curr Opin Genet Dev.*

Coordinating components of functional modules



Gutiérrez-Pérez et al, Cochella (2021) *Sci Adv*

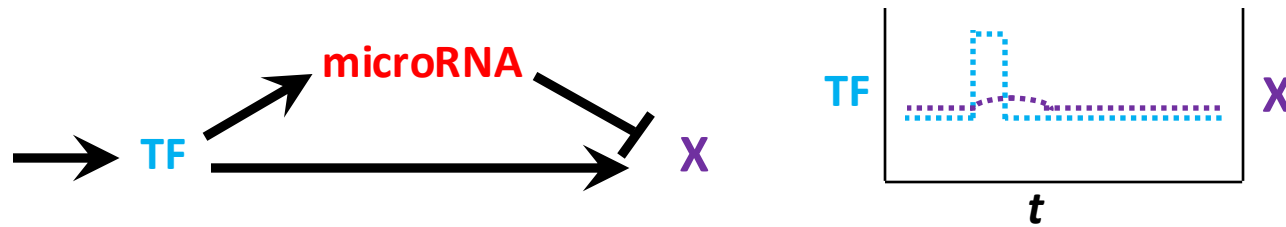
Buffering GRN noise



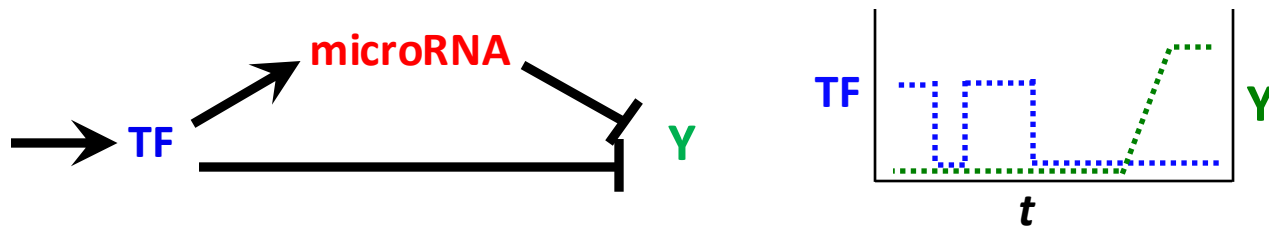
Klein et al Goodman (2007) *Nat Neuro*

Developmental and Physiological roles of microRNAs in animals

Cassidy et al, Carthew (2019) *Cell*



Martinez et al, Walhout (2008) *Genes Dev.*



Buffering GRN noise

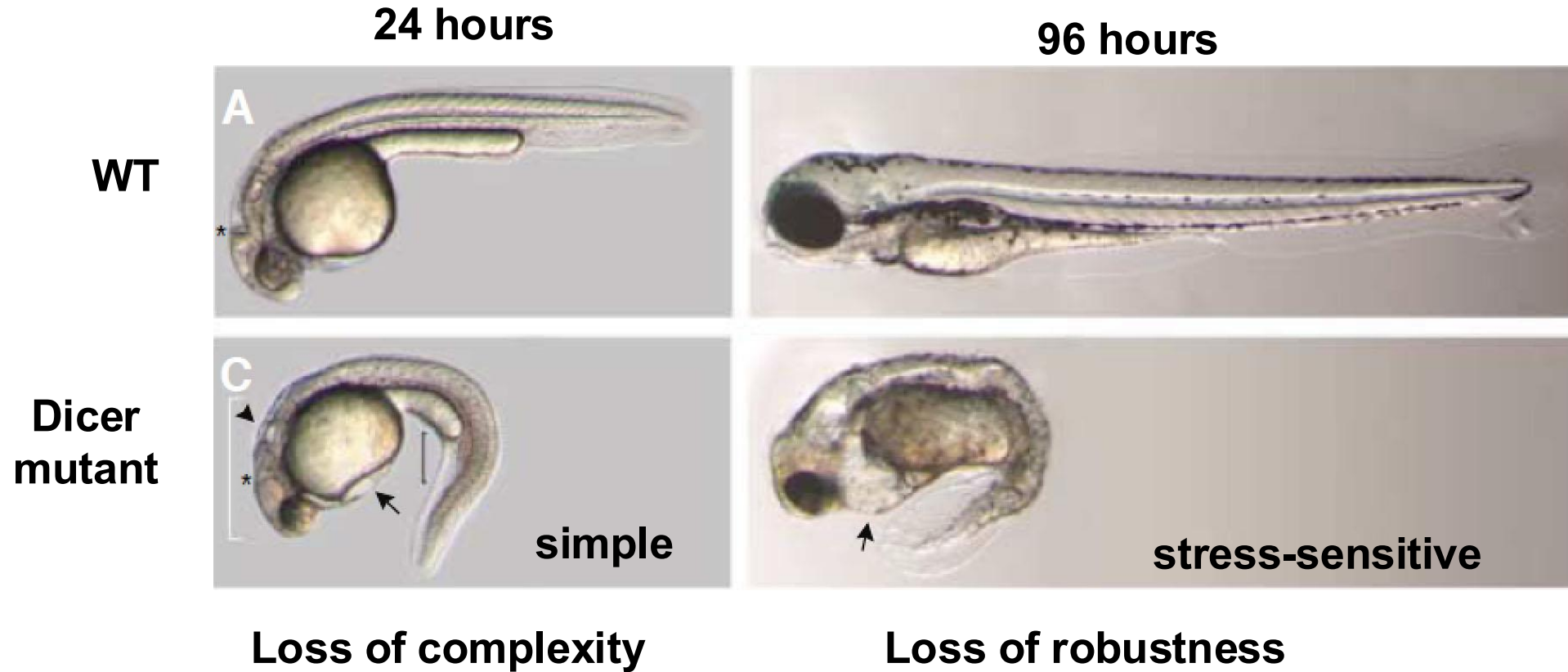


Klein et al Goodman (2007) *Nat Neuro*

Developmental and Physiological roles of microRNAs in animals

What happens to a fish embryo without microRNAs?

It makes a fish!



Giraldez et al, Schier (2005) *Science*

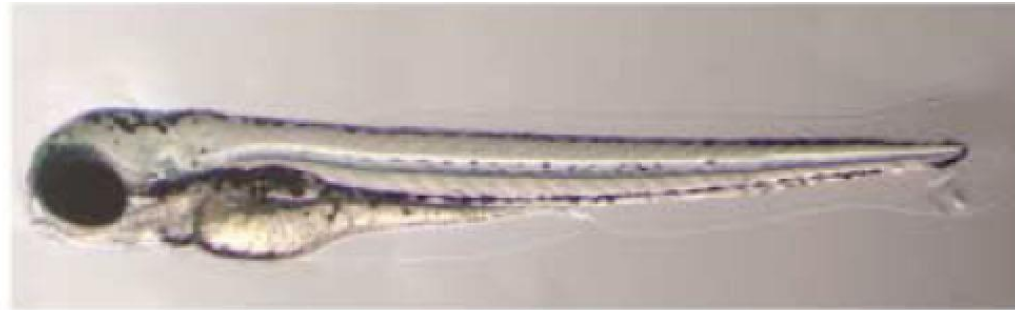
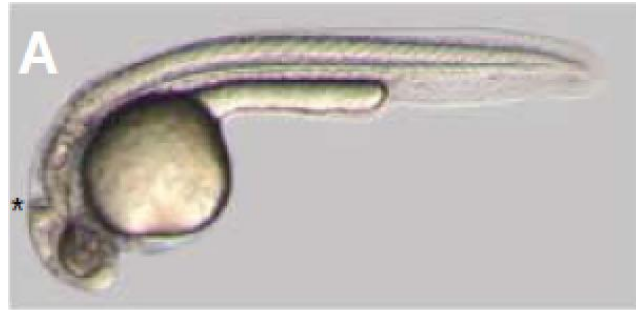
microRNAs: What are they good for?

Promote developmental cell type complexity
Confer physiological and developmental robustness

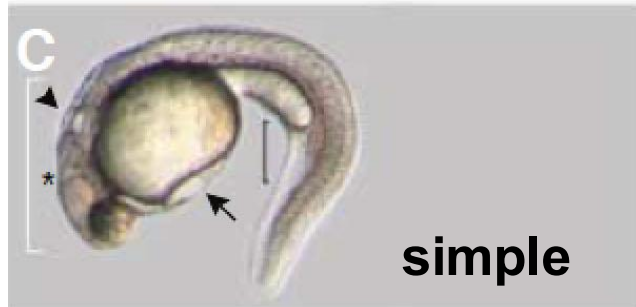
24 hours

96 hours

WT



Dicer mutant



Loss of complexity

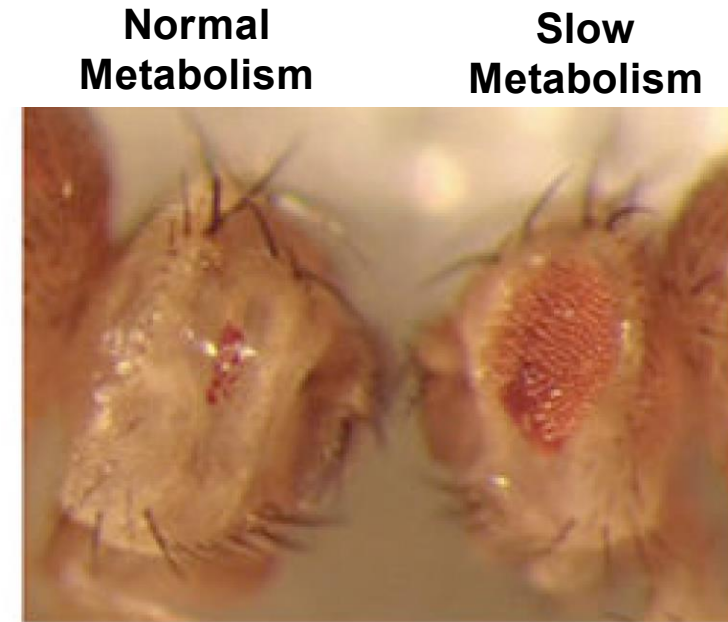
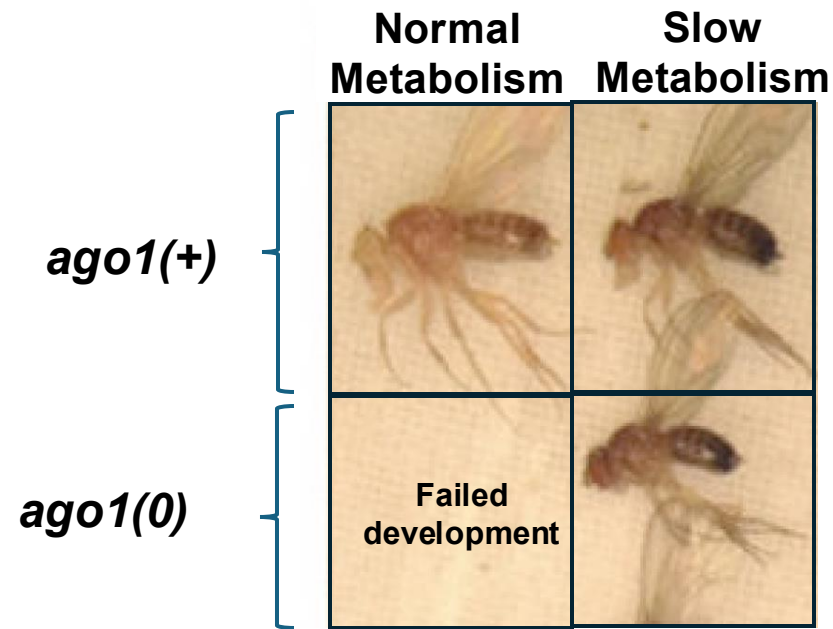
Loss of robustness

Giraldez et al, Schier (2005) *Science*

microRNAs: What are they good for?

Flies without microRNAs

- Promote developmental cell type complexity
- Confer physiological and developmental robustness
- Enable rapid high-energy growth and development



Ago1 Mosaics

MicroRNAs promote organismal complexity and stress-resilient living

Promote developmental cell type complexity

Confer physiological and developmental robustness

Enable rapid high-energy growth and development

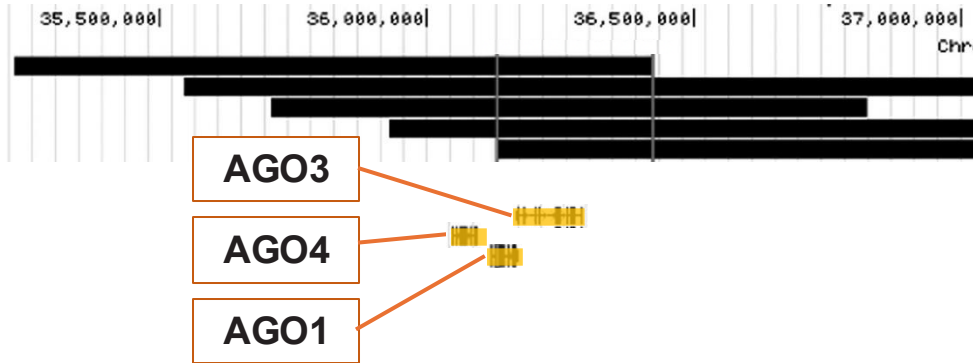
MicroRNAs in Human Disease

Stress Resilience \leftrightarrow Disease

Human Argonaute mutations that cause Neurodevelopmental Disorder (NDD)

Tokita et al (2015) Deletions of the AGO1/AGO3/AGO4 gene cluster in NDD patients

Broad disruptions of microRNA regulation by impairing multiple Argonaute proteins

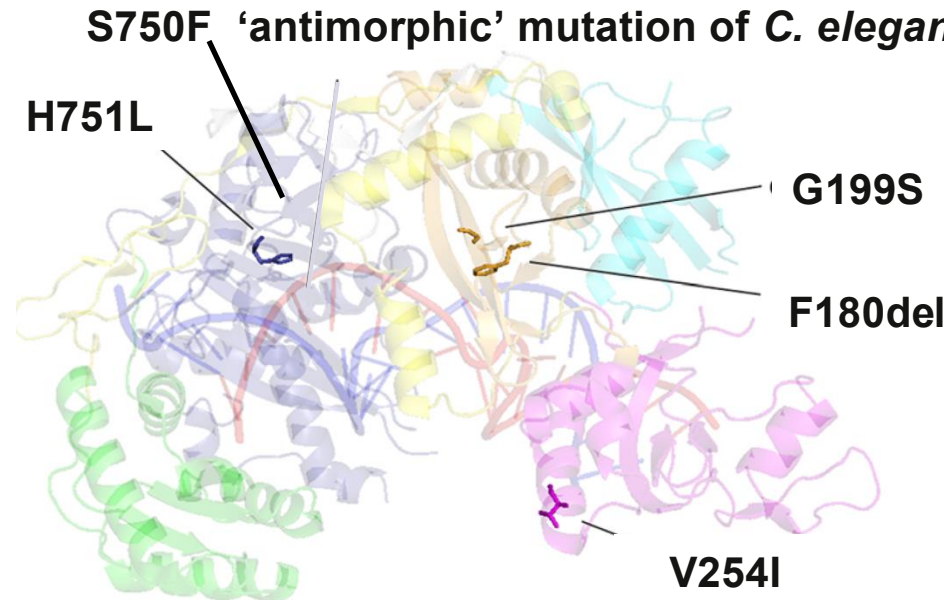


Deletion of multiple microRNA Argonaute genes can cause Neurodevelopmental Disorder (NDD)

Schalk et al. (2021) Human AGO1 variants in NDD

Lessel et al. (2020) Human AGO2 variants in NDD

Could the single amino acid variants somehow broadly disrupt microRNA regulation?



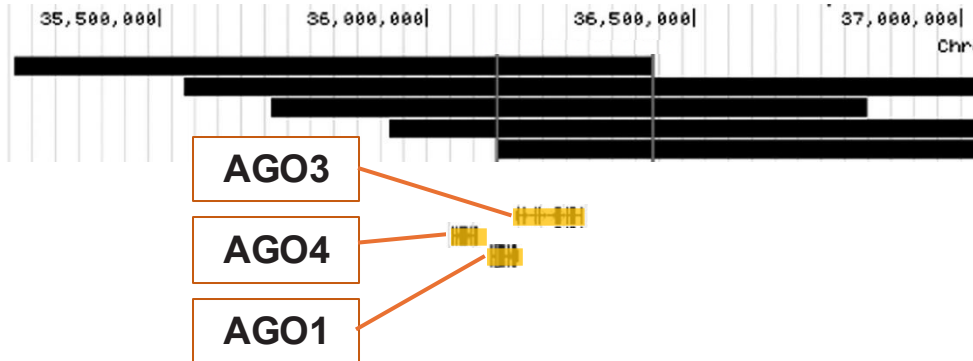
A single amino acid change in just one microRNA Argonaute can cause Neurodevelopmental Disorder (NDD)

Zinovyeva et al Ambros (2014) Mutations in conserved residues of *C. elegans* microRNA Argonaute ALG-1

Argonaute Syndrome

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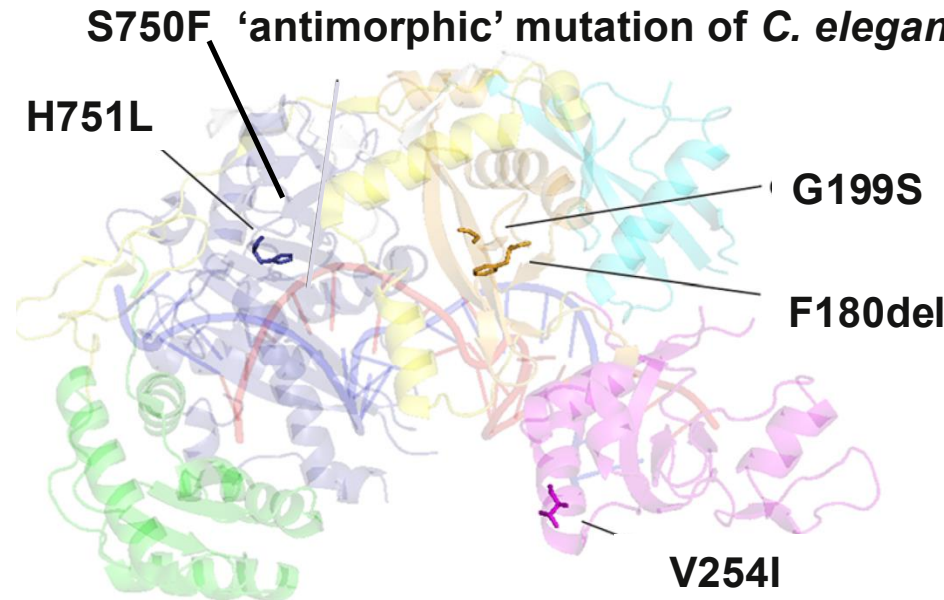


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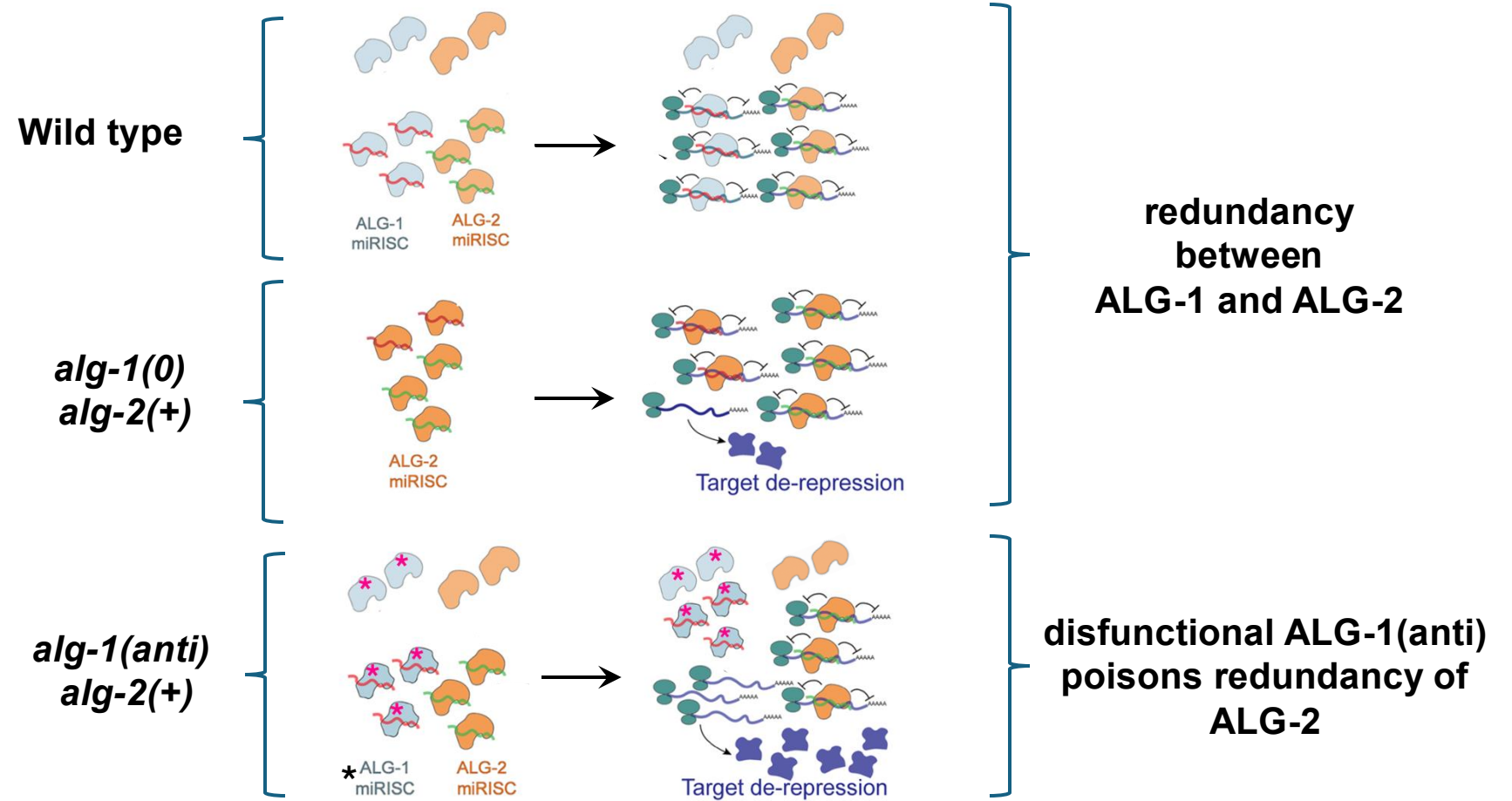
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C. elegans ALG-1 'antimorphic' mutations are worse than absence of ALG-1



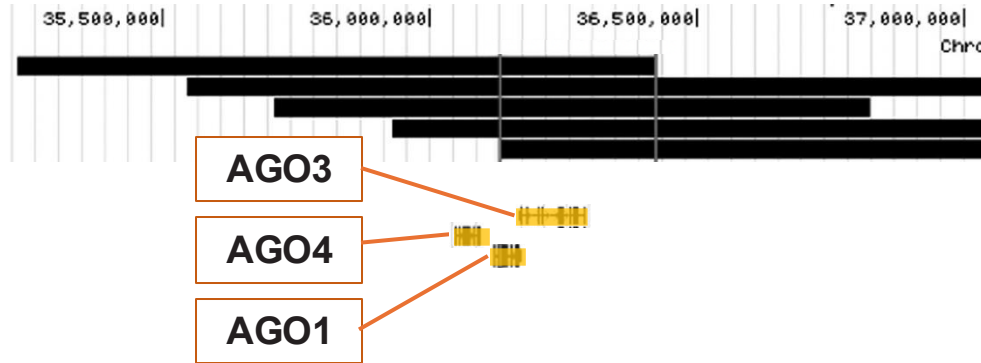
Nematodes have 2 microRNA Argonautes ALG-1 and ALG-2

Zinovyeva et al Ambros (2014) Mutations in conserved residues of *C. elegans* microRNA Argonaute ALG-1

Modeling human microRNA Argonaute NDD mutations in *C. elegans* ALG-1

Tokita et al (2015) Deletions of the AGO1/AGO3/AGO4 gene cluster in NDD patients

Broad disruptions of microRNA regulation



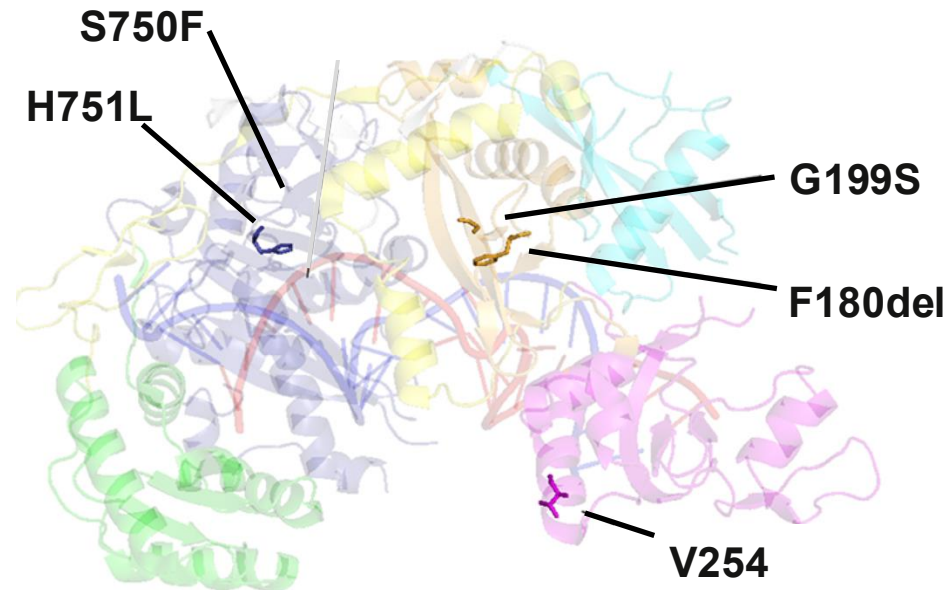
Deletion of multiple microRNA Argonaute genes can cause Neurodevelopmental Delay (NDD)

Schalk et al. (2021) Human AGO1 variants in NDD

Lessel et al. (2020) Human AGO2 variants in NDD

Argonaute Syndrome

Could the mutant protein 'poison' the redundancy of other human Argonautes?

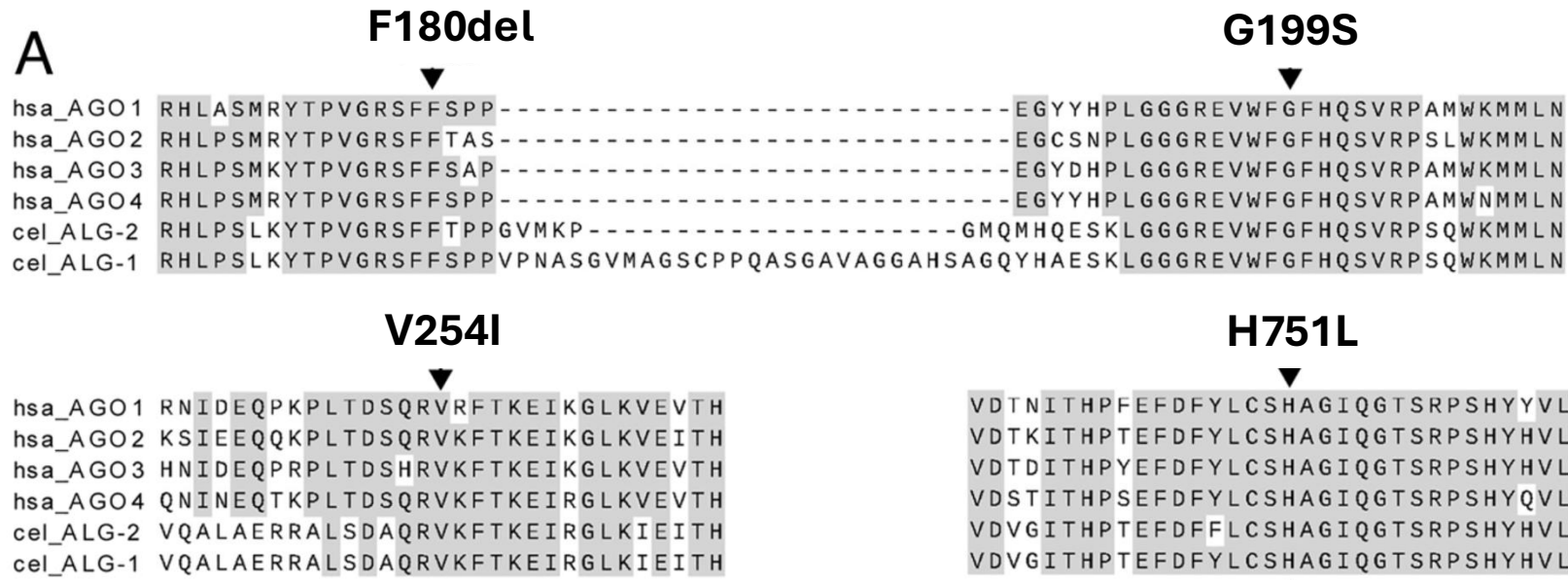


A single amino acid change in just one microRNA Argonaute can cause Neurodevelopmental Delay (NDD)

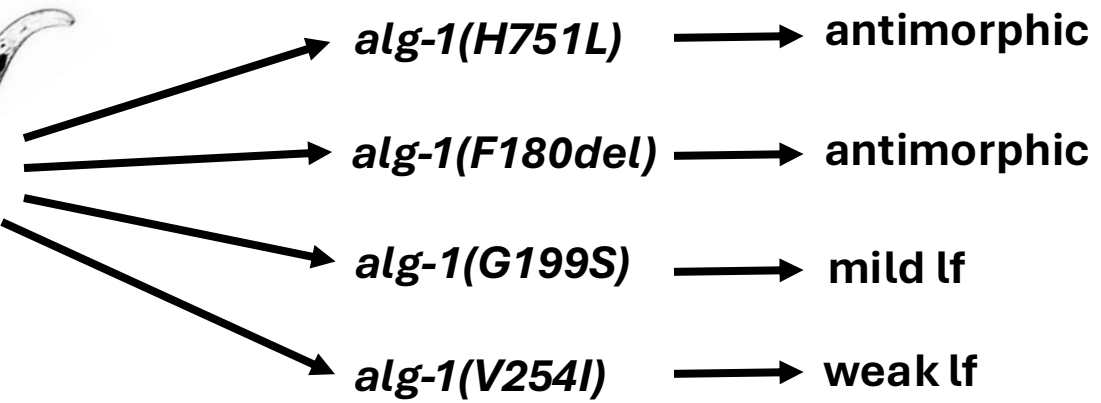
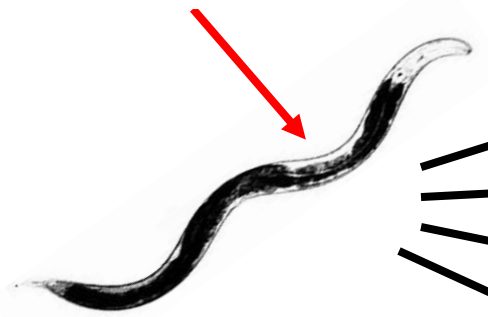
Zinovyeva et al Ambros (2014) Mutations in conserved residues of *C. elegans* microRNA Argonaute ALG-1

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Duan, Li, Panzade, Piton, Zinovyeva, Ambros (2024) *PNAS*



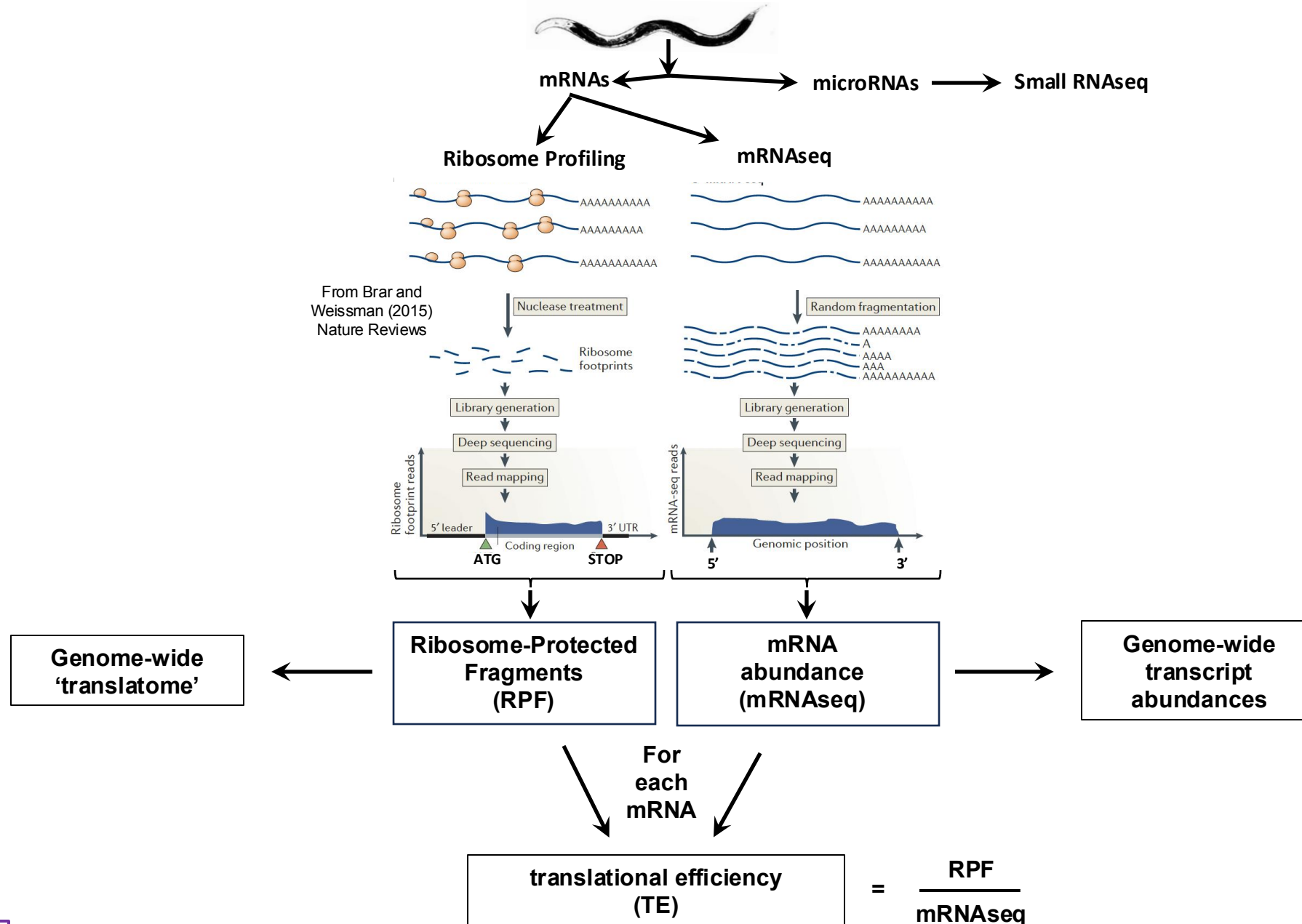
CRISPR/Cas



Developmental phenotypes
Heterochronic; viability

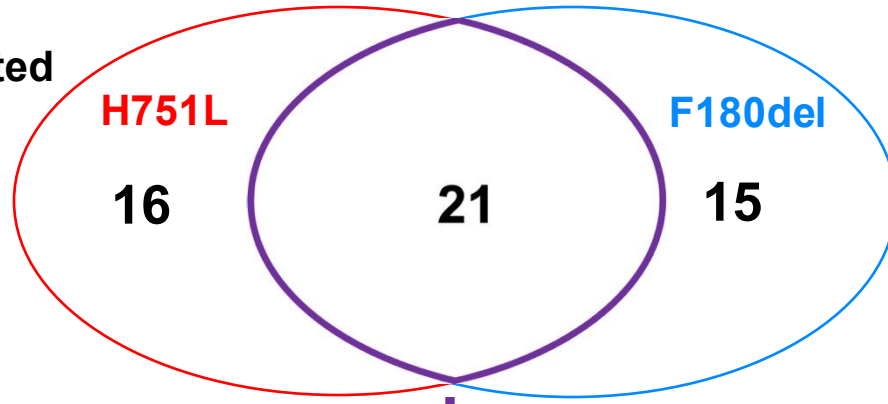
Molecular phenotypes
microRNAs; mRNAs

Molecular phenotypes of *C. elegans* *alg-1(NDD)* mutants



ALG-1(NDD) mutations can have variant-specific downstream consequences

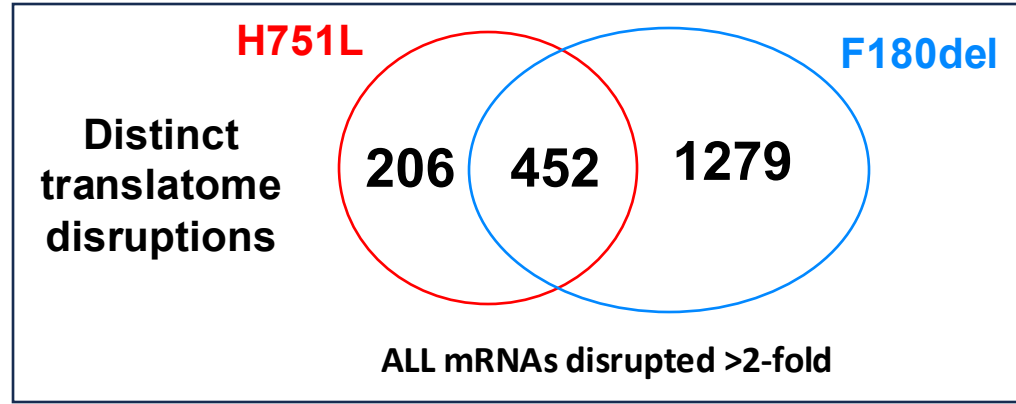
Distinct sets of functionally disrupted microRNAs



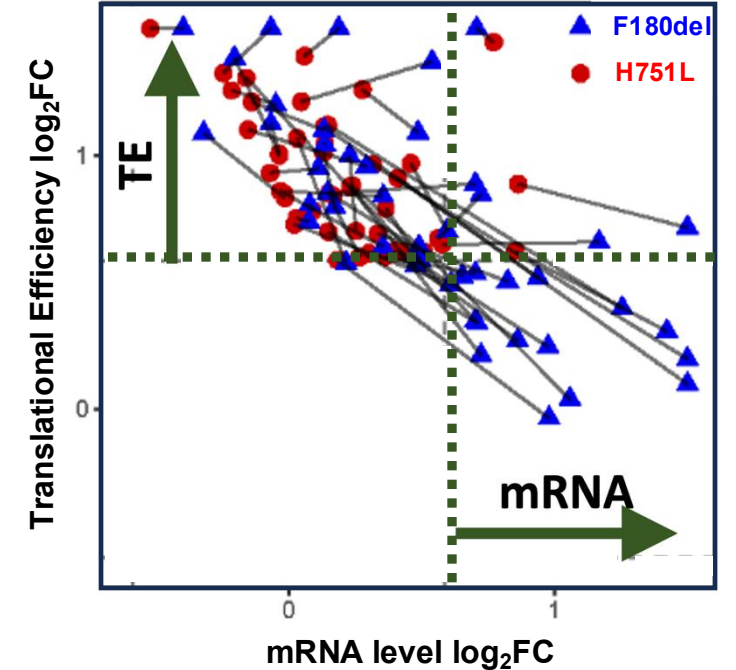
21 miRNAs disabled by both mutations

Seed match mRNA targets that are de-repressed in both mutants

Modes of de-repression?
Translational Efficiency (TE) and/or mRNA stability

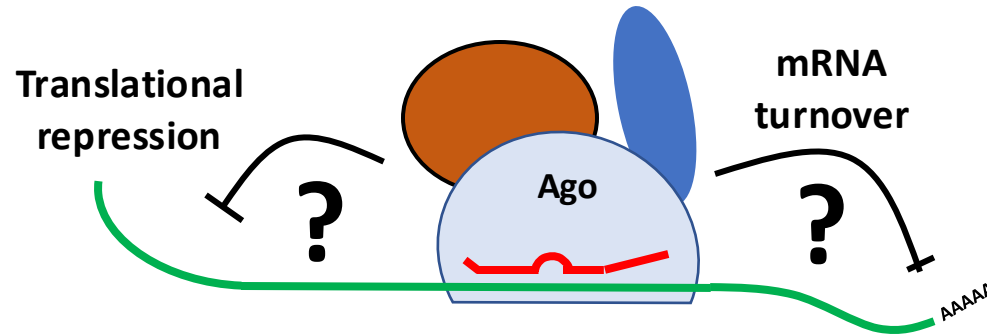
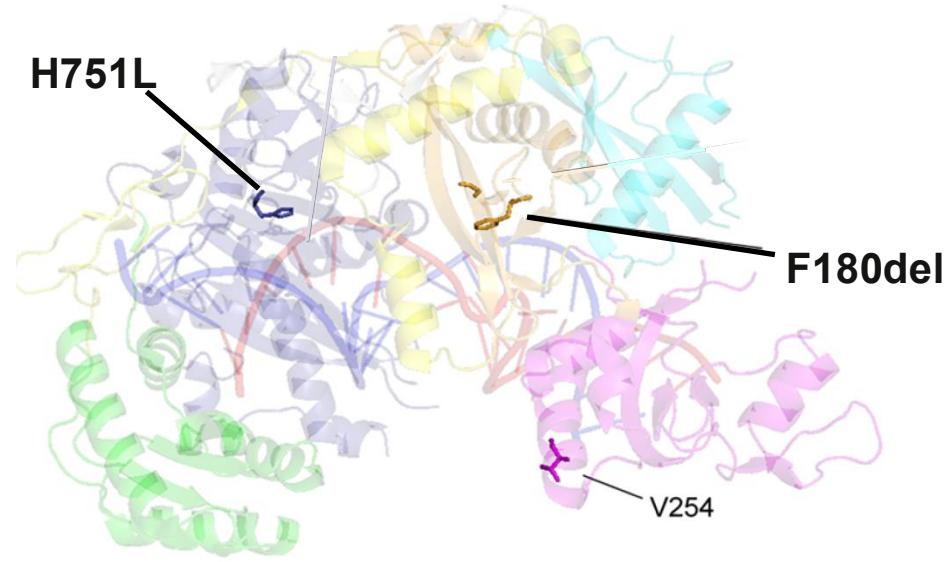
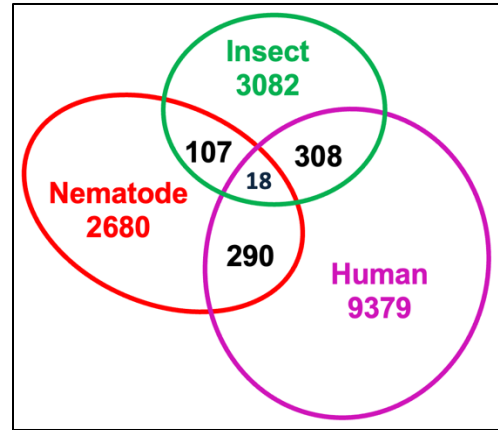


Distinct impairments of mRNA translational repression vs stability



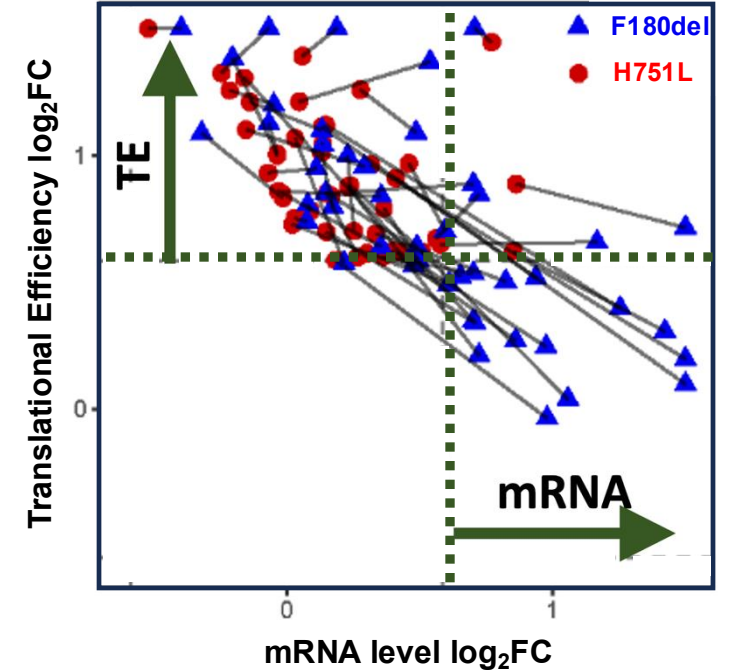
ALG-1(NDD) mutations with distinct variant-specific downstream consequences

	microRNA loci	seed families
H. sapiens	575	273
D. melanogaster	163	101
C. elegans	147	92



Structural and biochemical basis for functional differences amongst variants

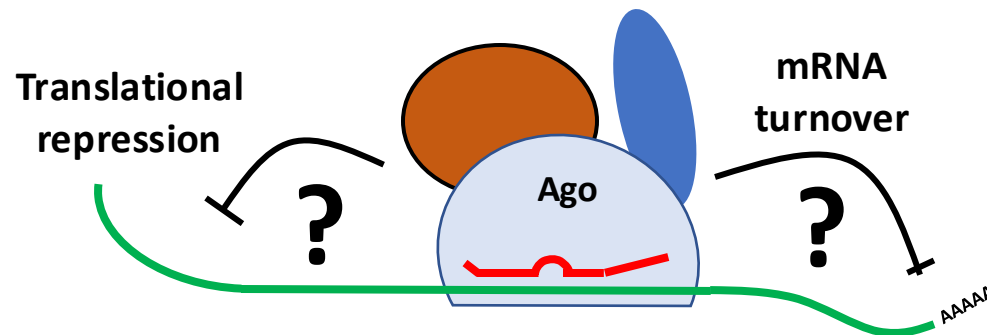
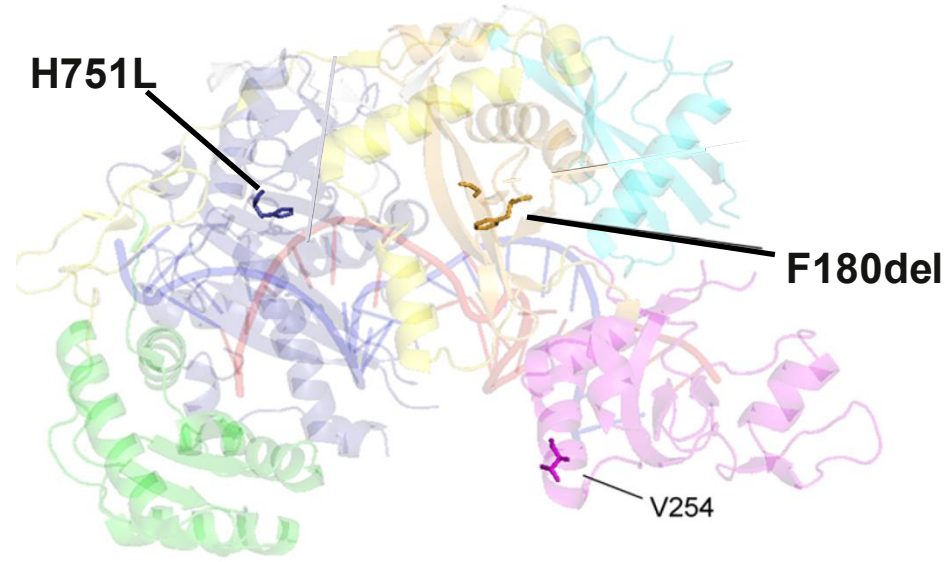
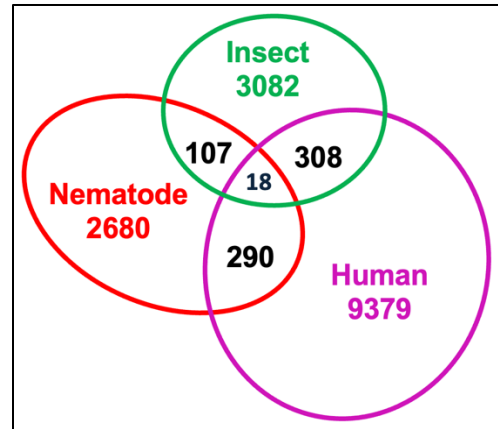
Distinct impairments of mRNA translational repression vs stability



Synergism: Model Organism Genetics \leftrightarrow Human Genetics

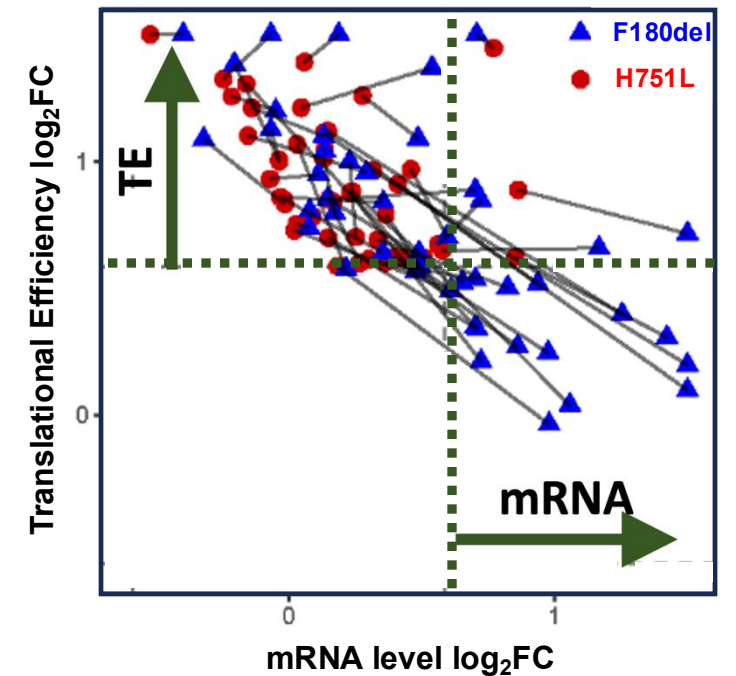
Basic Science Opportunities: Novel avenues of investigation of microRNA Argonaute mechanisms

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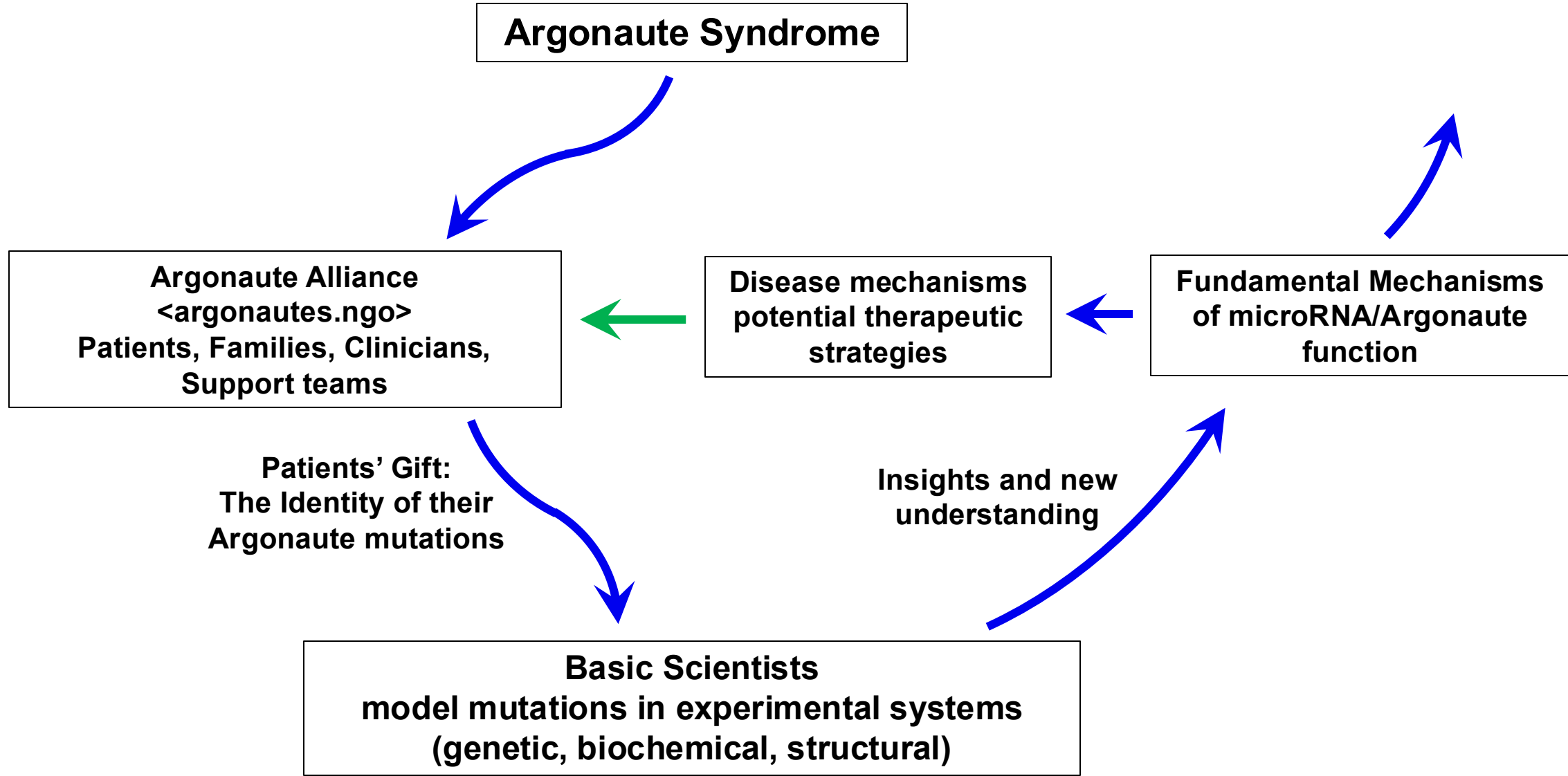


Structural and biochemical basis for functional differences amongst variants

Distinct impairments of mRNA translational repression vs stability



Synergism Among Basic Scientists, Patients, and families



The Marvelous Story of microRNAs Continues to Unfold

THANK YOU!

to **YOU ALL**
for being here today

to **ROSALIND LEE and RHONDA FEINBAUM**
for discovering *lin-4* microRNA

to **GARY RUVKUN**
for sharing struggles,
discoveries, rewards



Most of all ..

to **CANDY LEE**
for everything