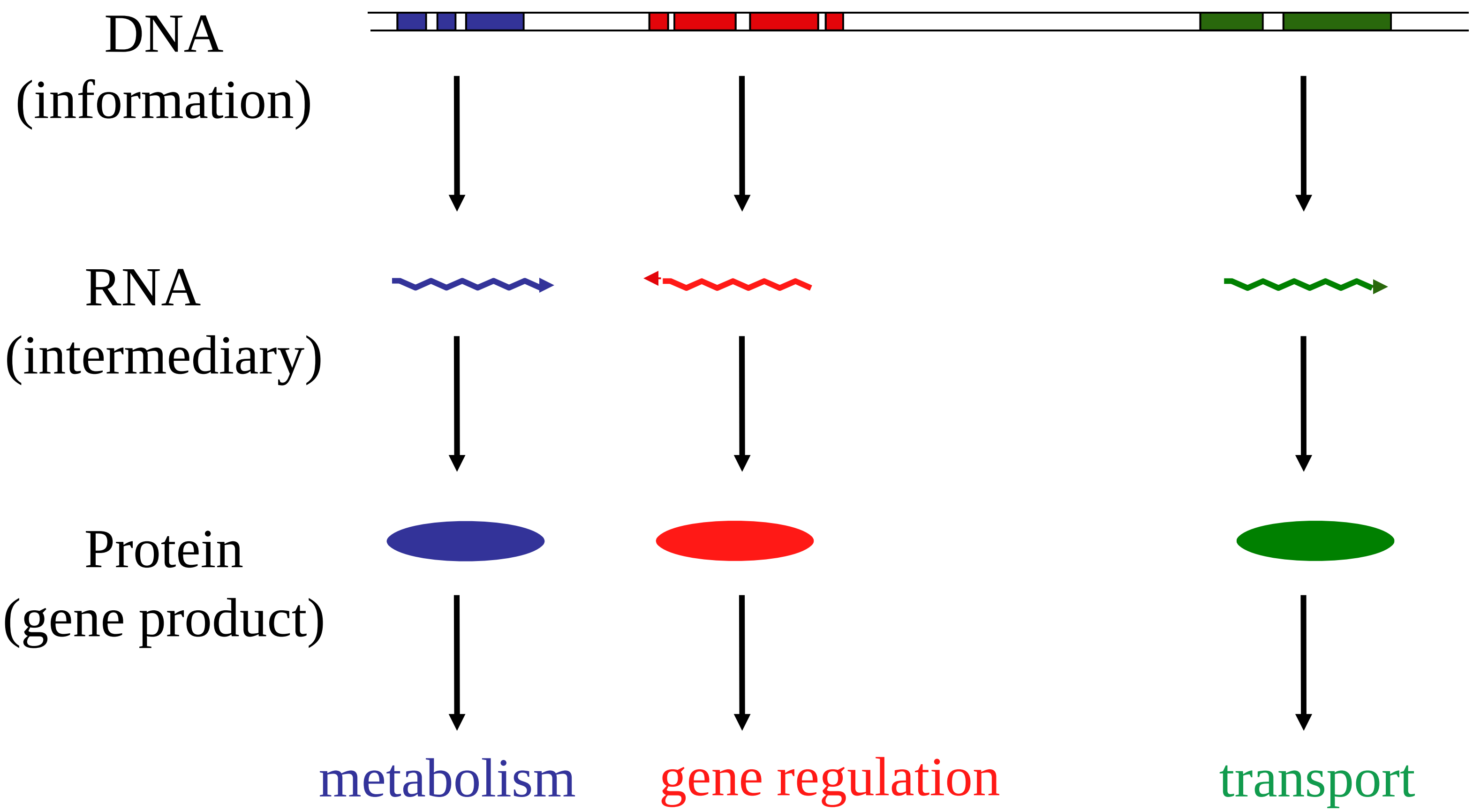
The genome contains more than protein coding genes



DNA
(information)

RNA
(intermediary)

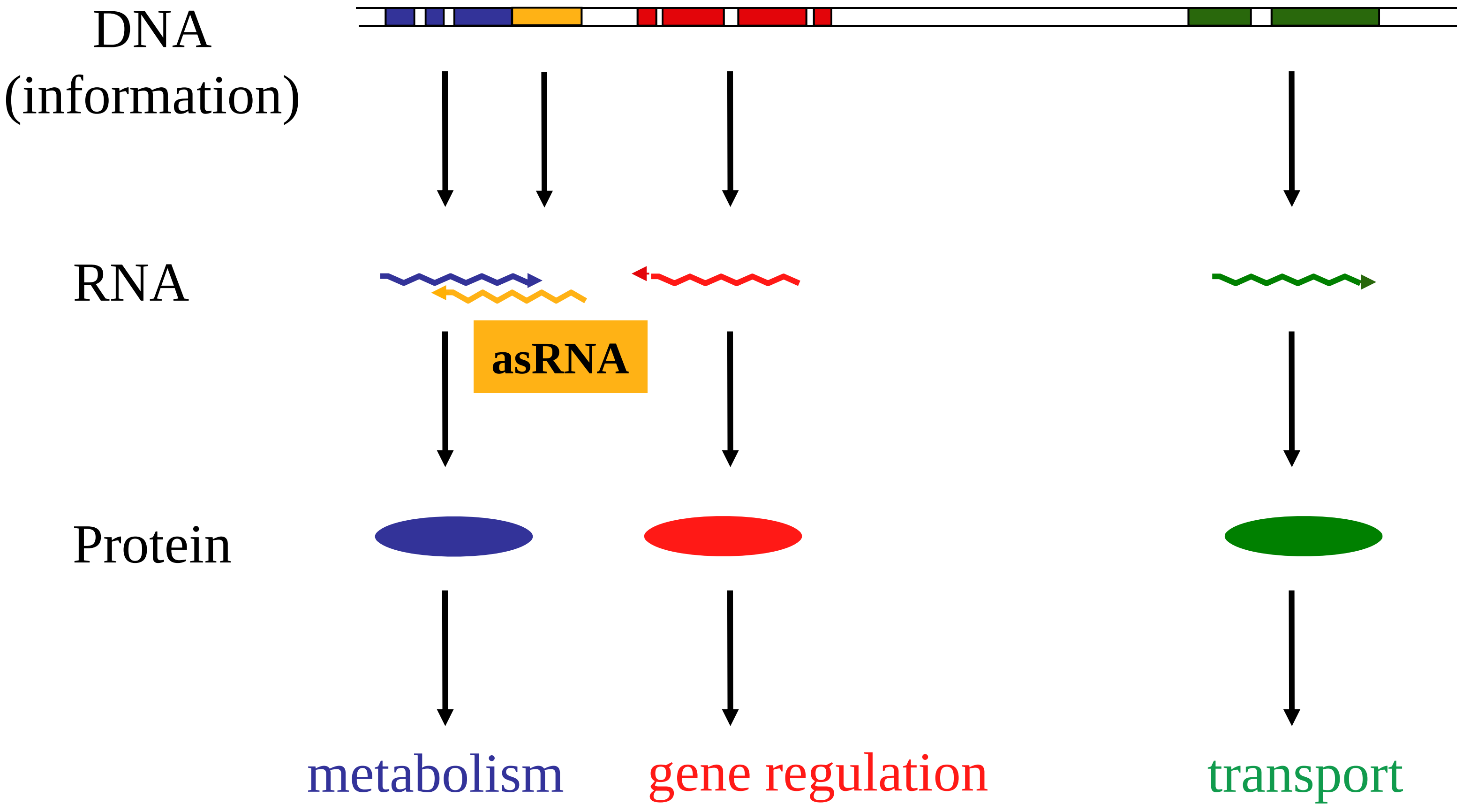
Protein
(gene product)

metabolism

gene regulation

transport

At least three types of **non-protein coding genes** exist



DNA
(information)

RNA

asRNA

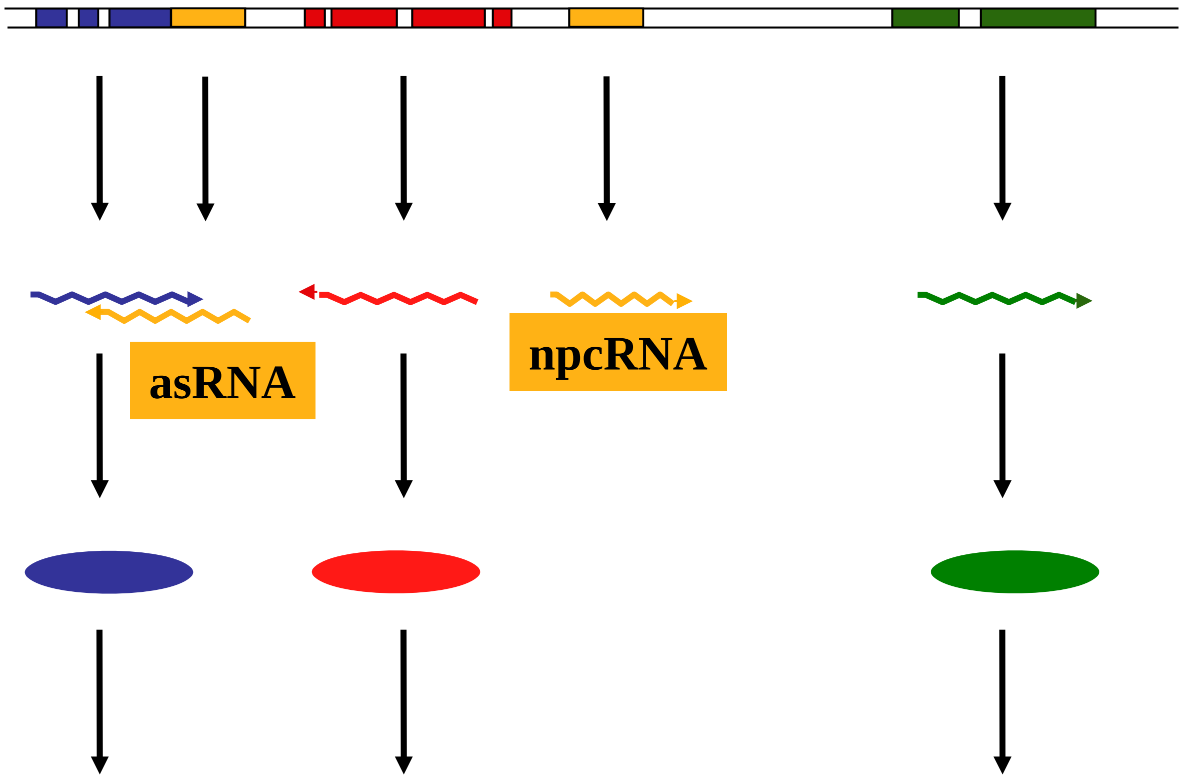
Protein

metabolism

gene regulation

transport

At least three types of non-protein coding genes exist



DNA
(information)

RNA

asRNA

npcRNA

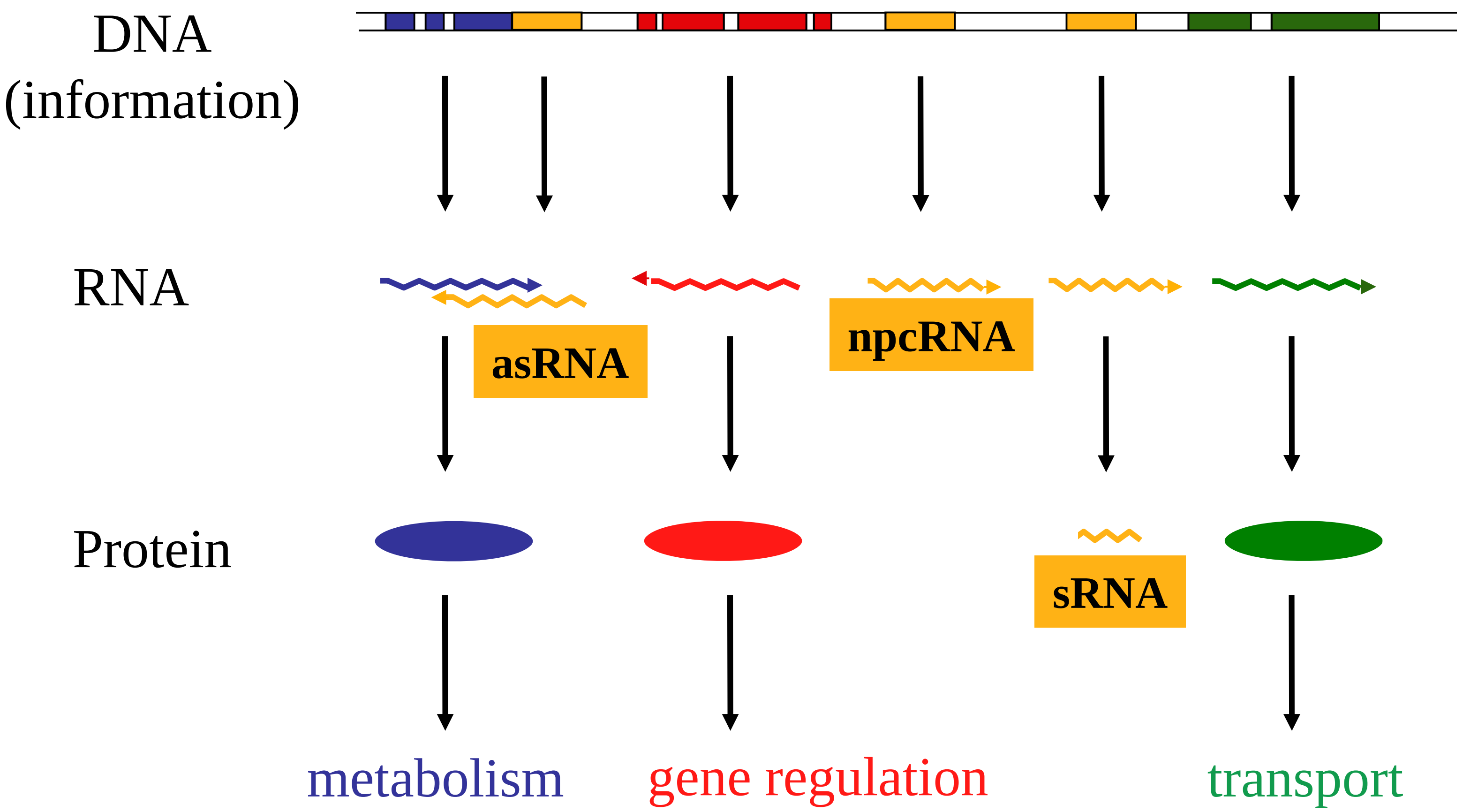
Protein

metabolism

gene regulation

transport

At least three types of non-protein coding genes exist



DNA
(information)

RNA

asRNA

npcRNA

Protein

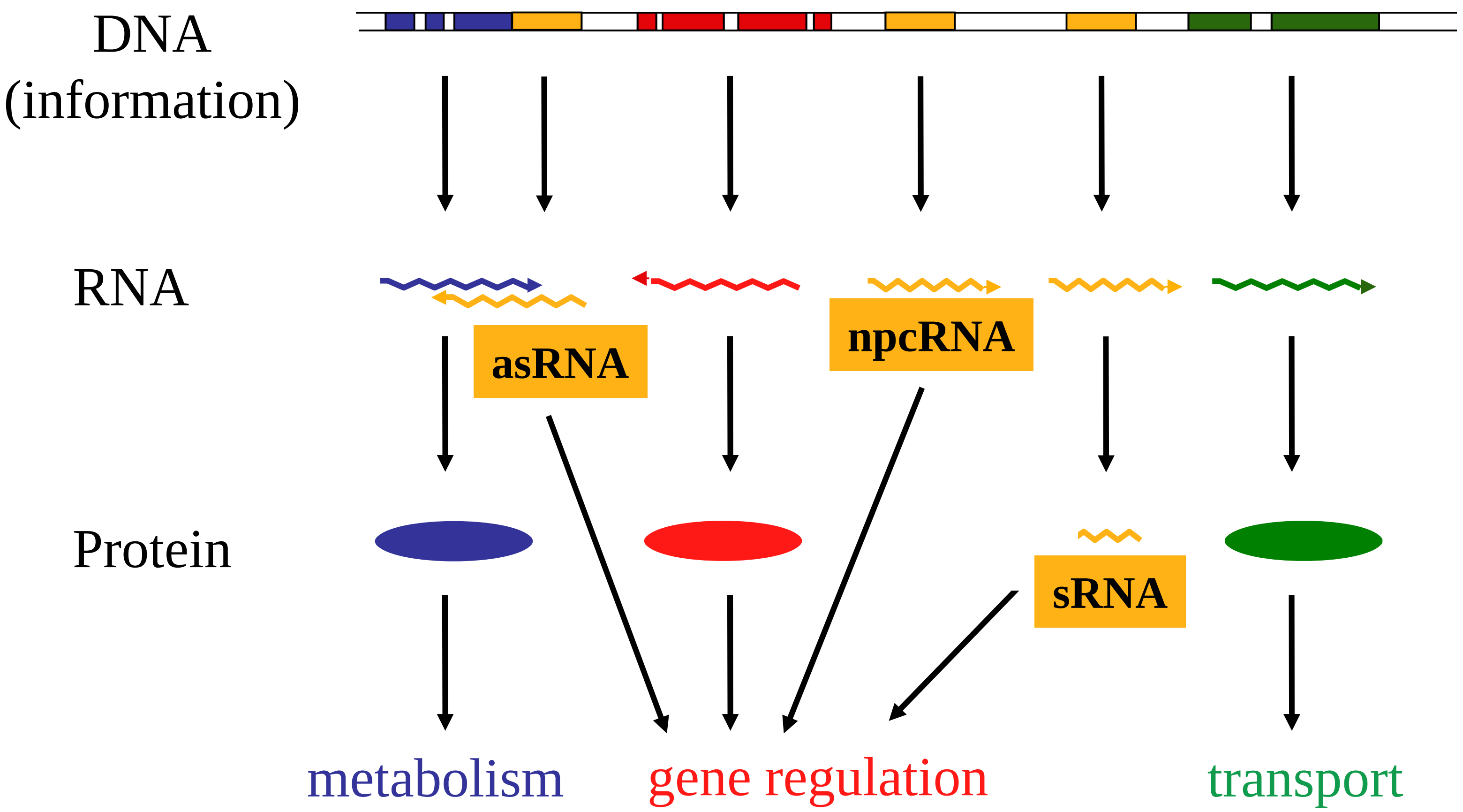
sRNA

metabolism

gene regulation

transport

At least three types of non-protein coding genes exist



DNA
(information)

RNA

asRNA

npcRNA

Protein

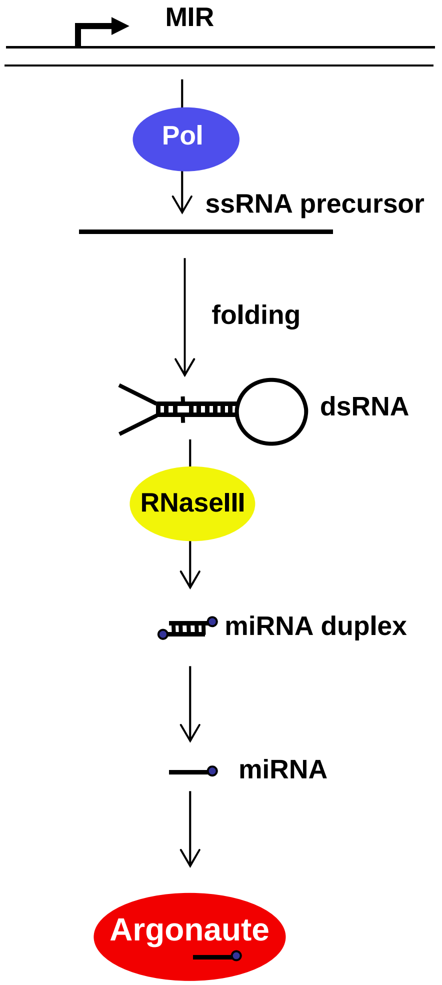
sRNA

metabolism

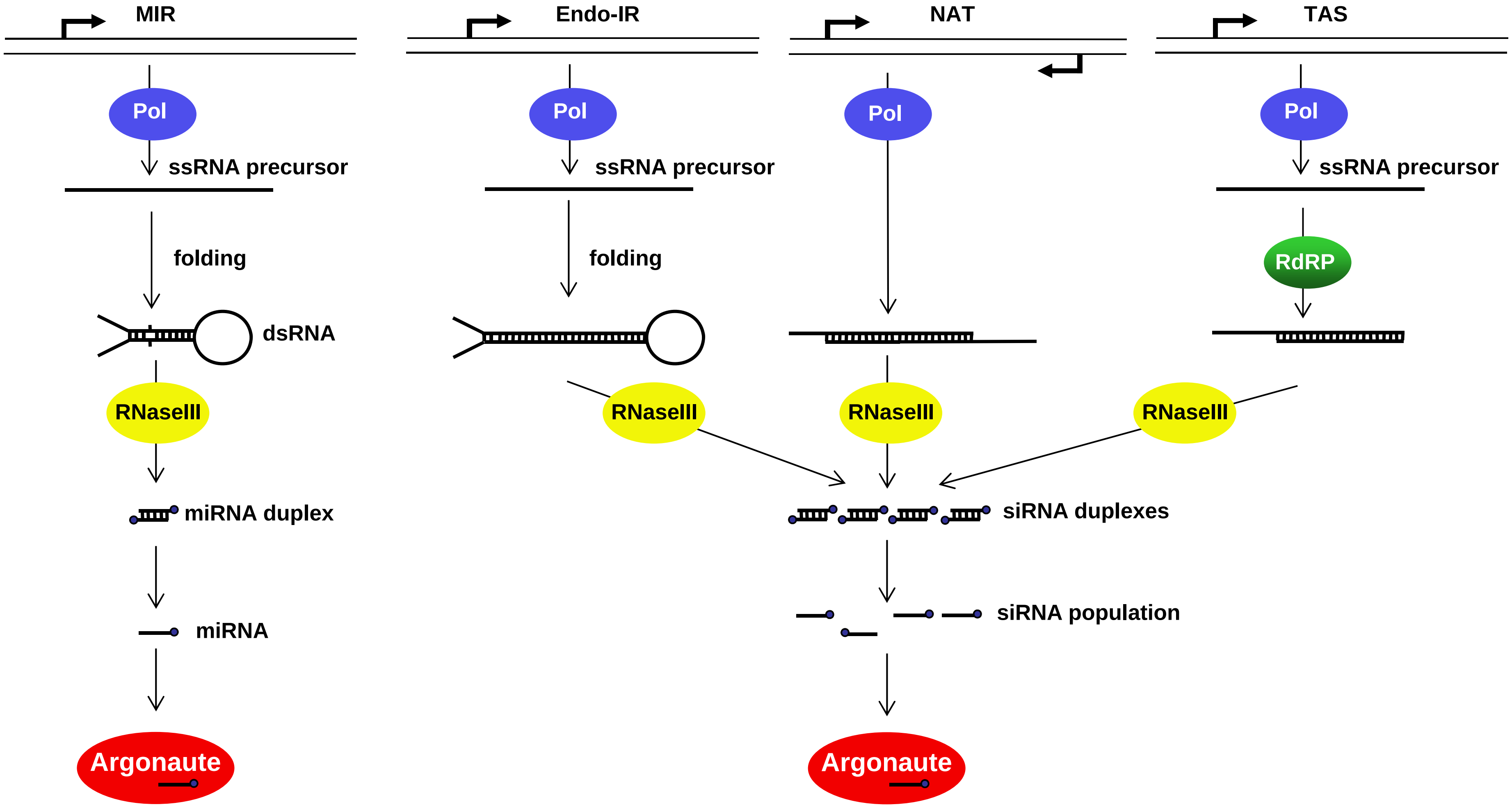
gene regulation

transport

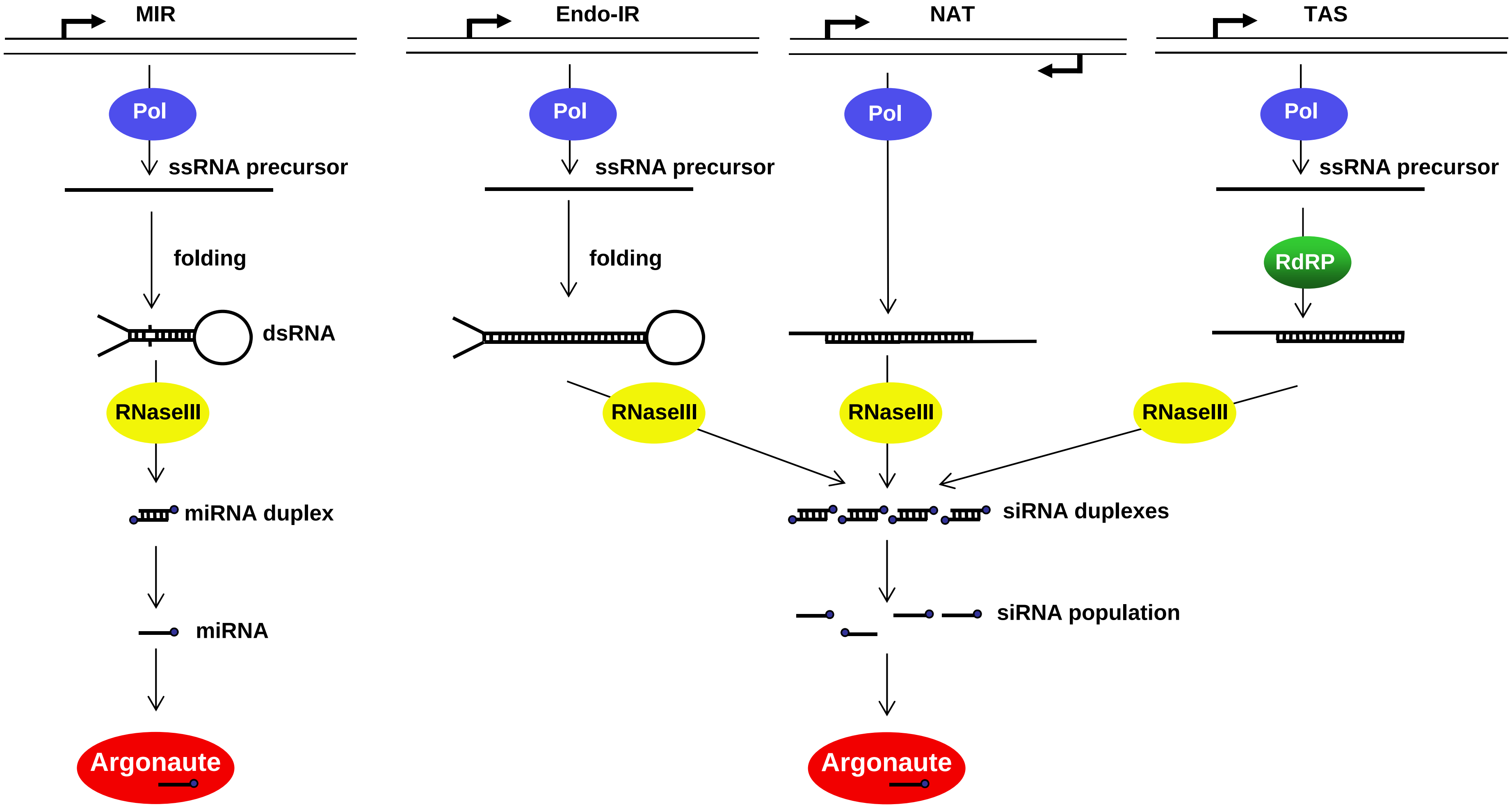
Plants contain miRNA and multiple types of siRNA



Plants contain miRNA and multiple types of siRNA



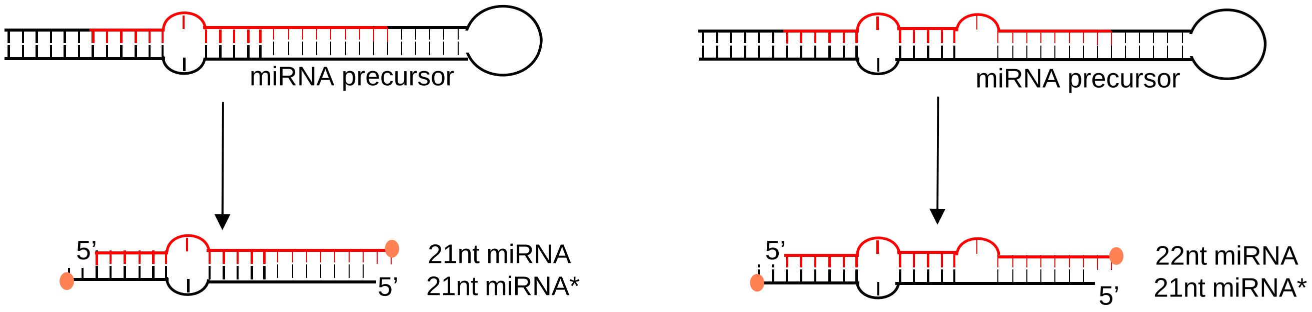
Plants contain miRNA and multiple types of siRNA



21-22-nt mi/siRNA guide PTGS while 24-nt siRNA guide TGS

Different DCL produced small RNA of different sizes

DCL1 -> 21-nt miRNA (19-25-nt depending on the structure of the stem-loop)



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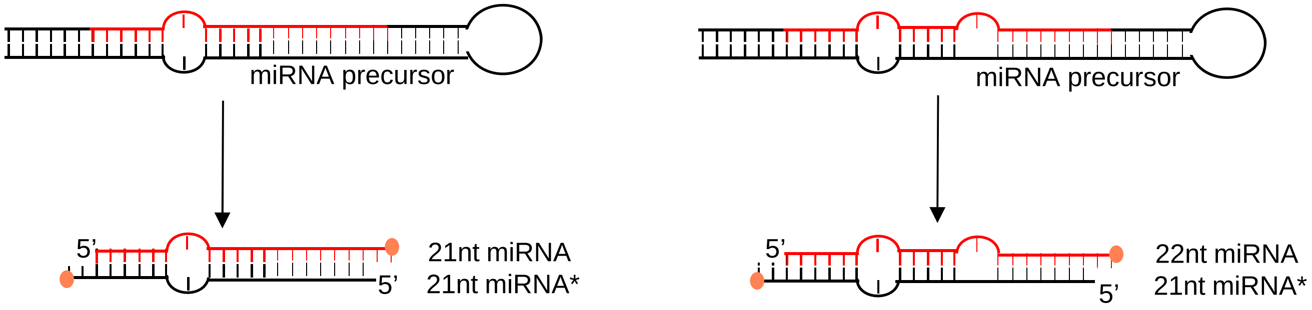
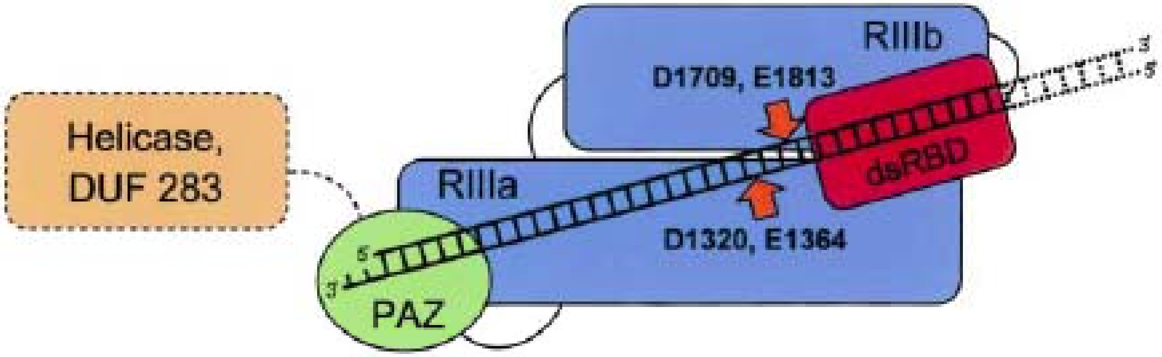


DCL2, DCL3 and DCL4 act as rulers

DCL4 -> 21-nt siRNA

DCL2 -> 22-nt siRNA

DCL3 -> 24-nt siRNA



DCL1 is essential for plant development

Wild-type

✕

null *dcl1*

hypomorphic *dcl1*

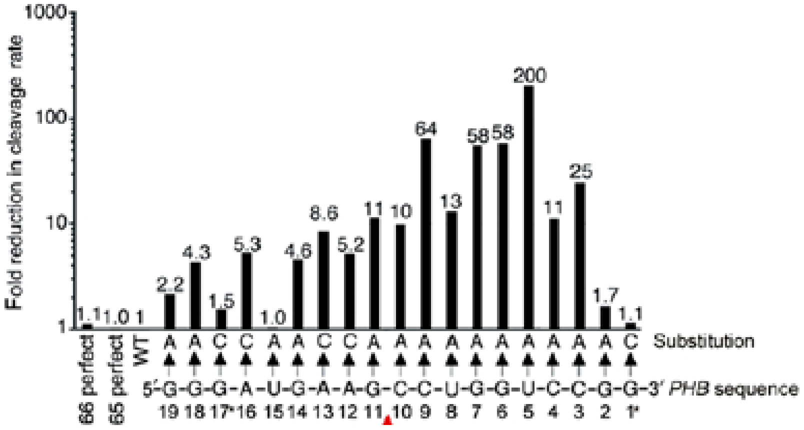
miRNAs guide translational repression

In animals, miRNA regulate thousands of targets by translational repression.

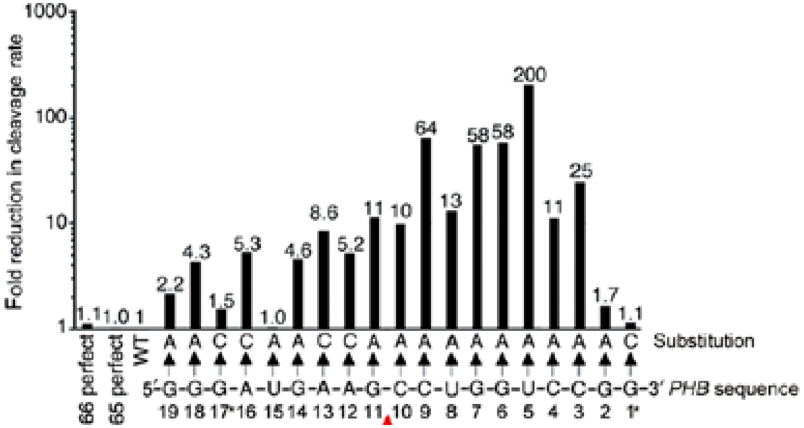
In plants, only 4 miRNA targets regulated by translational repression have been identified. However, no systematic proteomic analyses have been performed.

-> many more targets may exist in plants

miRNAs guide target RNA cleavage



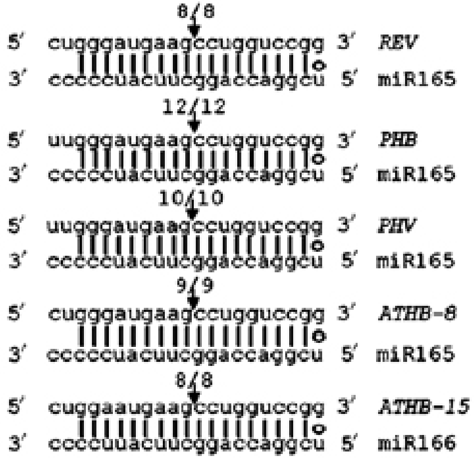
miRNAs guide target RNA cleavage

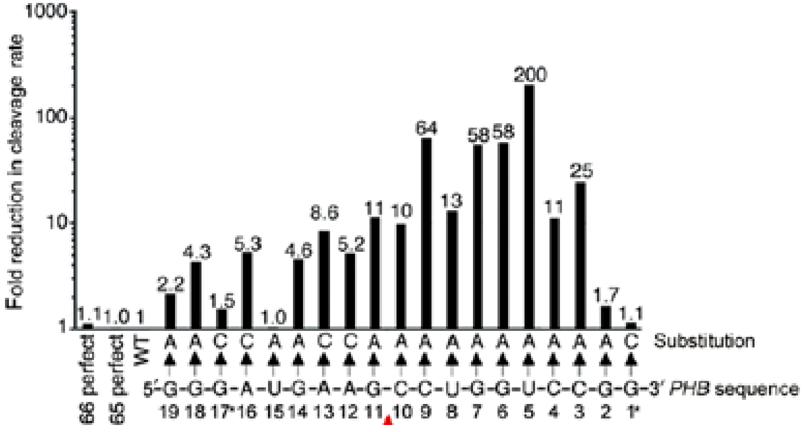


Algorithms allowing up to 3 mismatches confidently predicted hundreds of miRNA targets regulated by cleavage in plants

However, bioinformatics is insufficient to predict all miRNA targets

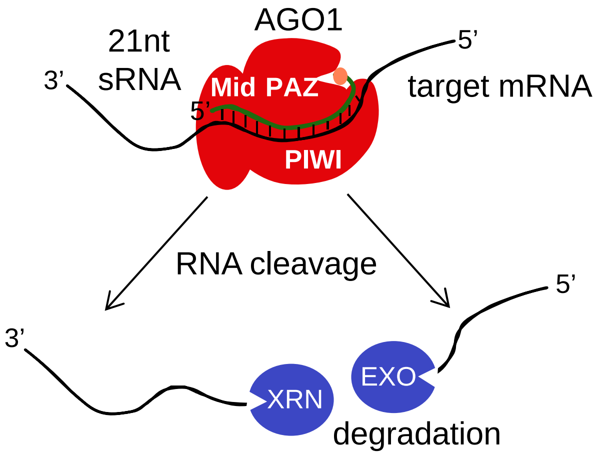
miRNAs guide target RNA cleavage



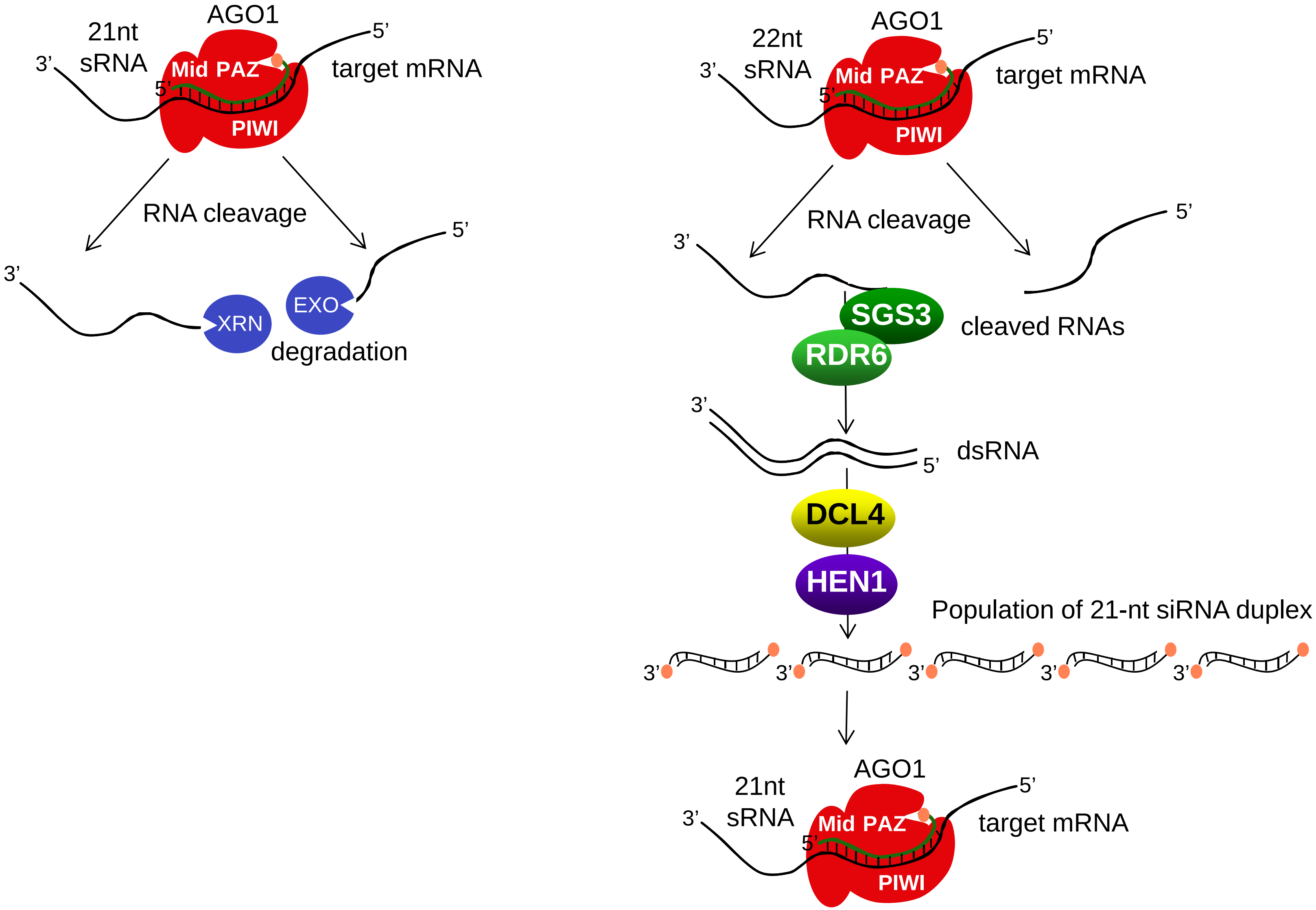


Genetics idendified miRNA targets with up to 5 mismatches

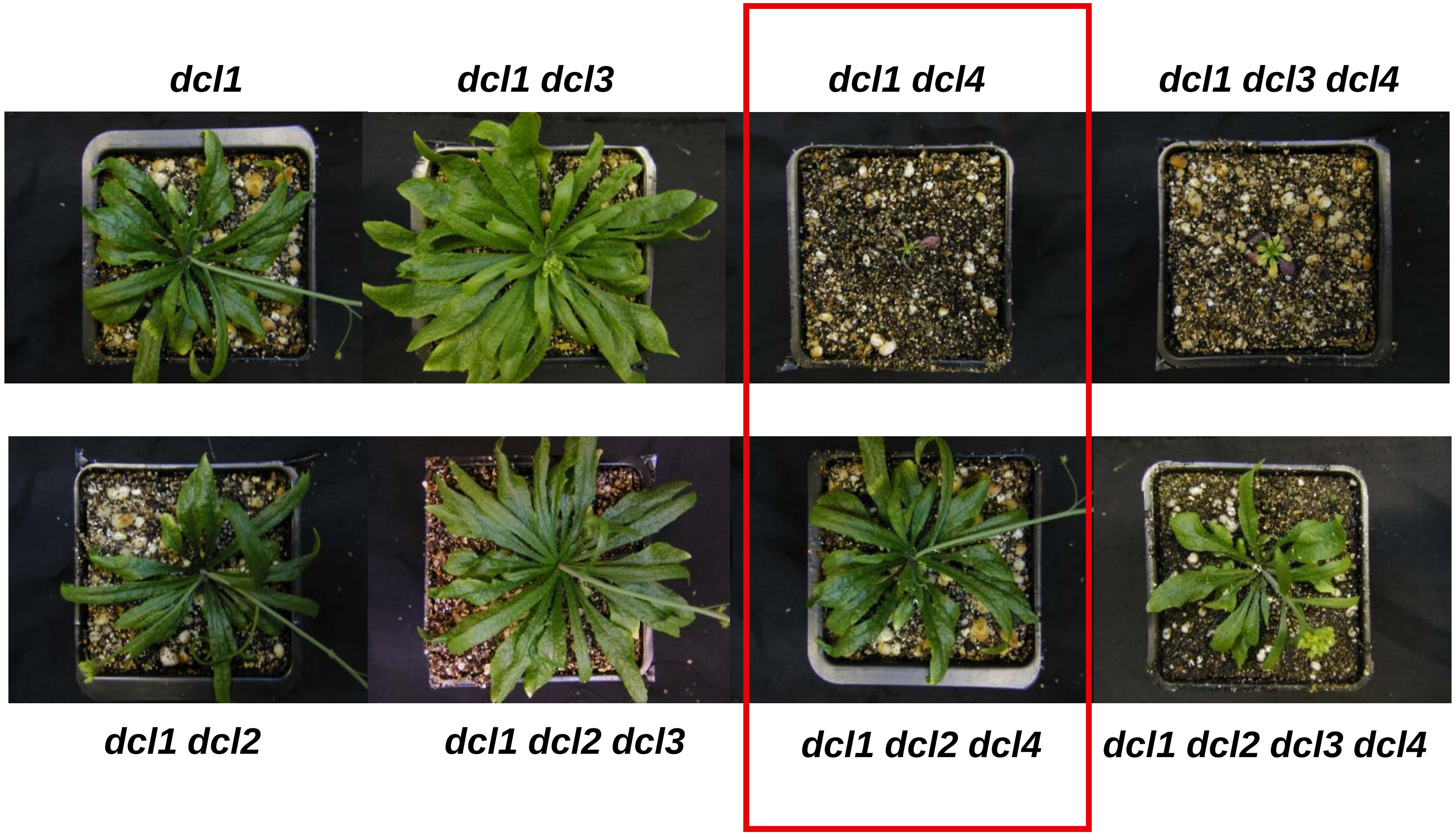
21-nt-guided cleavage products are degraded



21-nt-guided cleavage products are degraded while 22-nt-guided cleavage products produce secondary siRNA

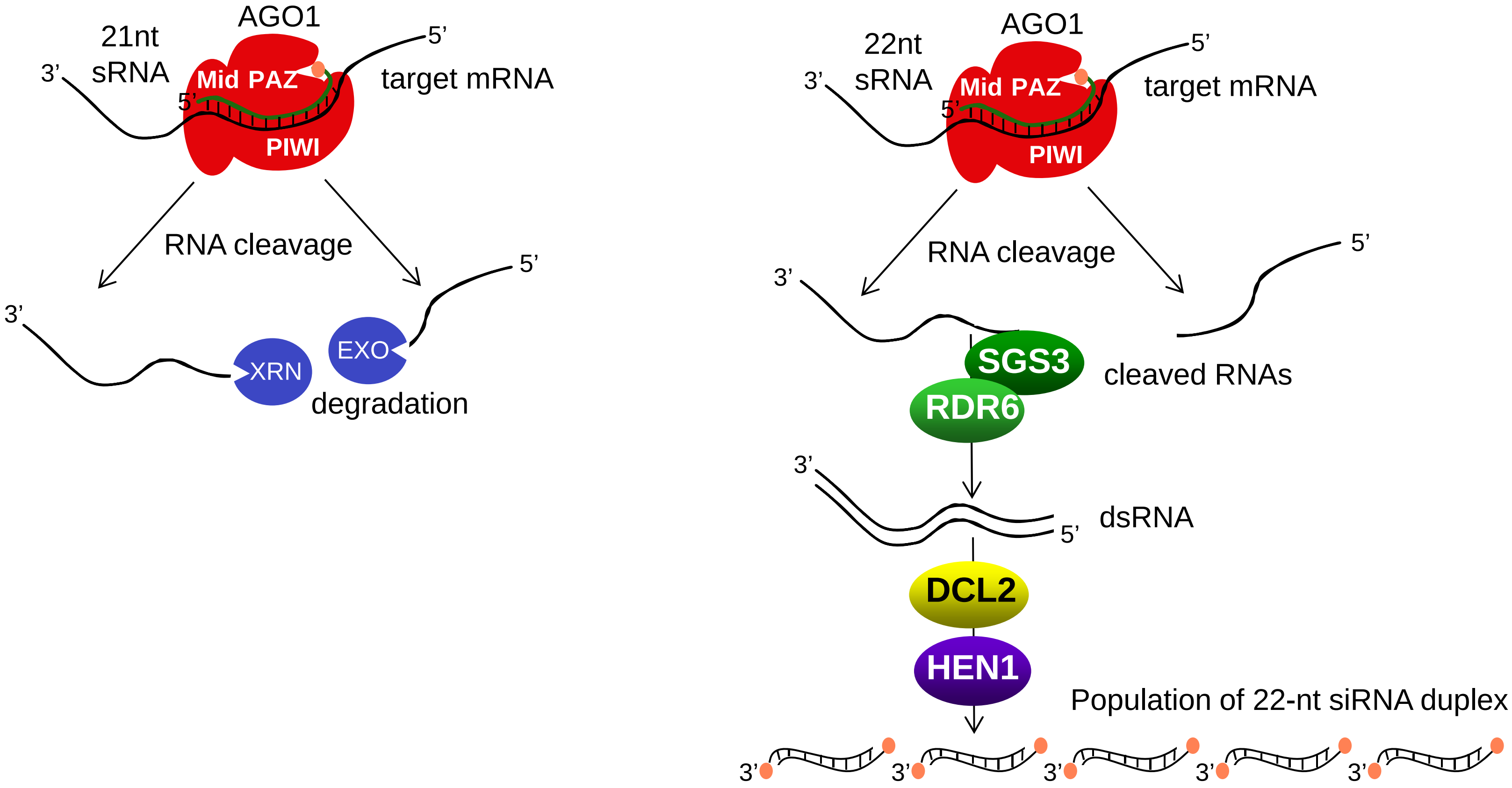


DCL2 : one nt size change makes a big difference



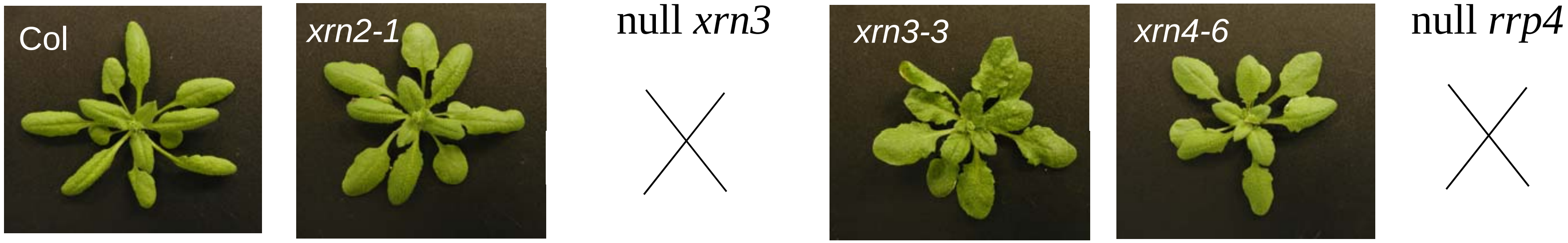
DCL2 imperfectly substitutes to DCL4 and produces 22-nt instead of 21-nt

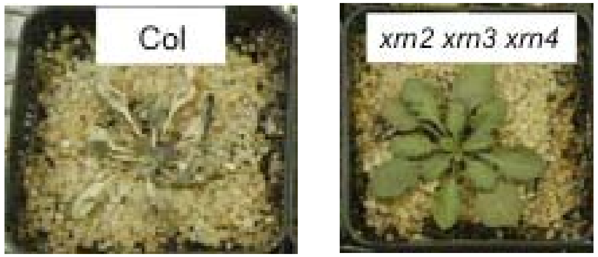
21-nt-guided cleavage products are degraded while 22-nt-guided cleavage products produce secondary siRNA



In *dcl1 dcl4*, which lacks 21-nt siRNAs, 22-nt siRNAs made by DCL2 promote secondary 22-nt siRNAs, which promote tertiary 22-nt siRNAs, which promote…

XRN and Exosome are essential for plant development





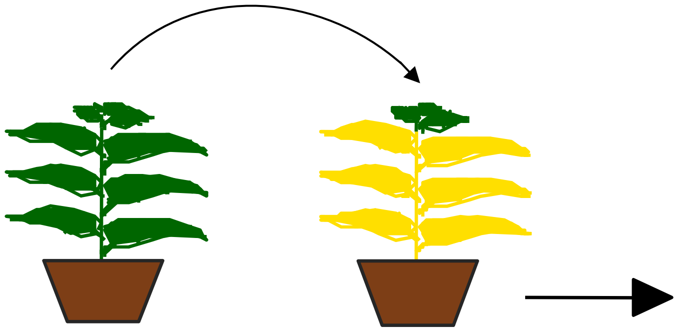
Partial impairment of the XRN pathway promotes drought stress resistance

Collaboration Laurent Nussaume, CEA

siRNA of all sizes are mobile

Progression of silencing

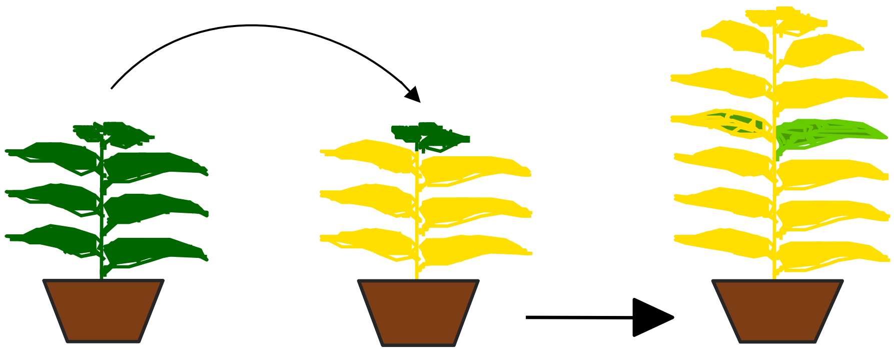
PTGS produces a sequence-specific systemic silencing signal



NS scion

PTGS stock

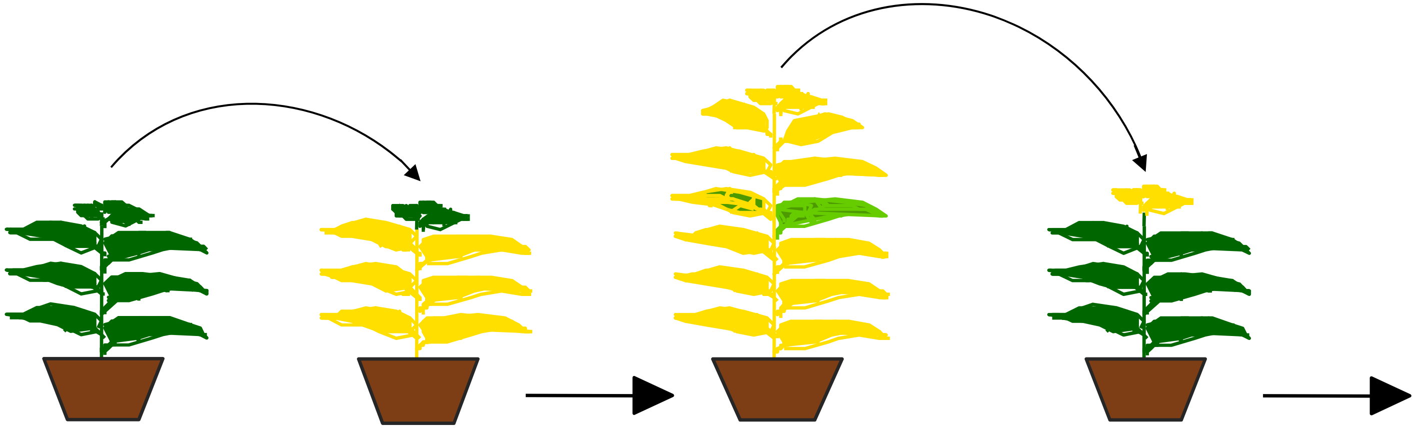
PTGS produces a sequence-specific systemic silencing signal



NS scion

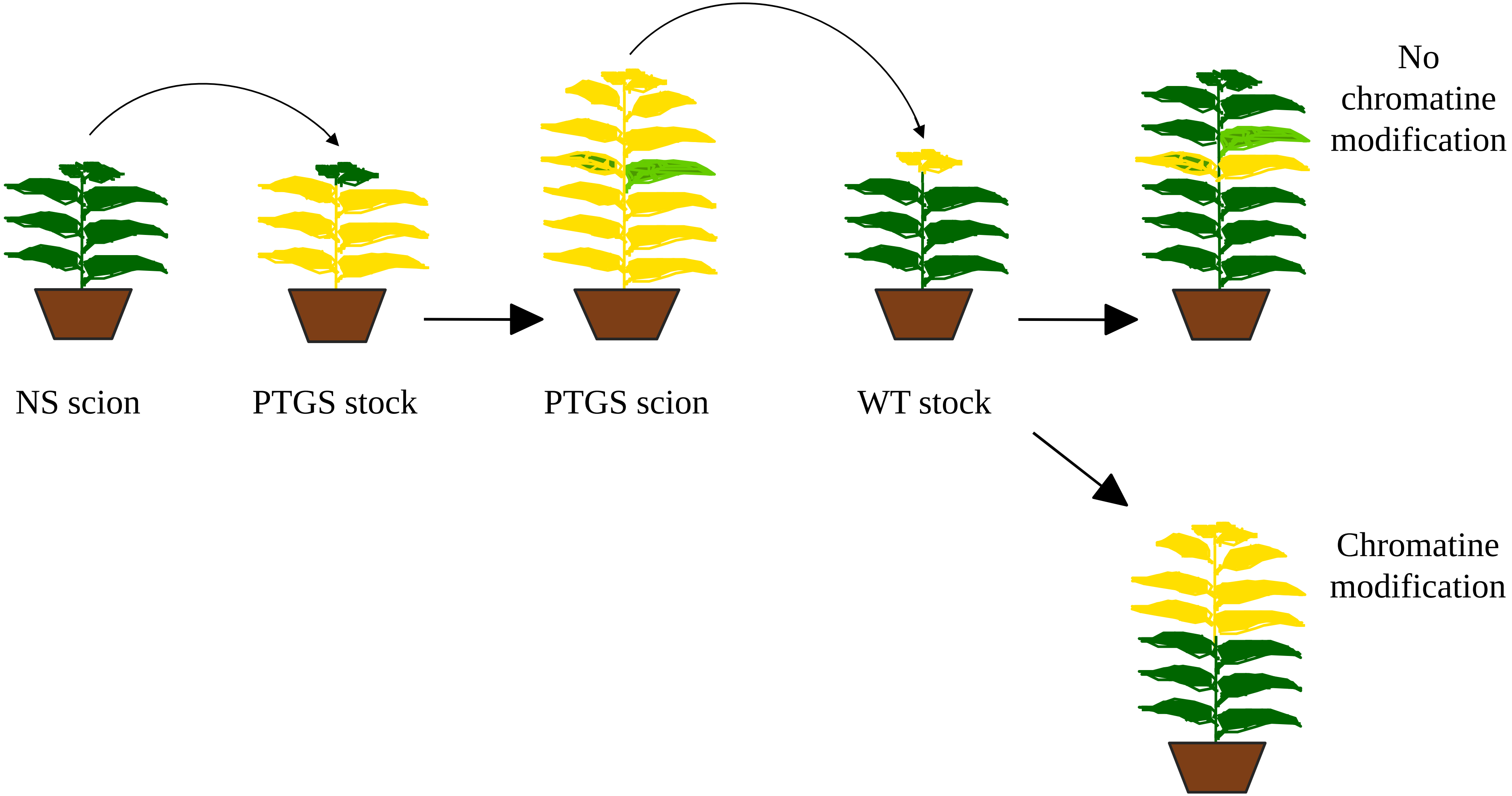
PTGS stock

PTGS maintainance requires chromatine modification



NS scion PTGS stock PTGS scion WT stock

PTGS maintainance requires chromatine modification



NS scion

PTGS stock

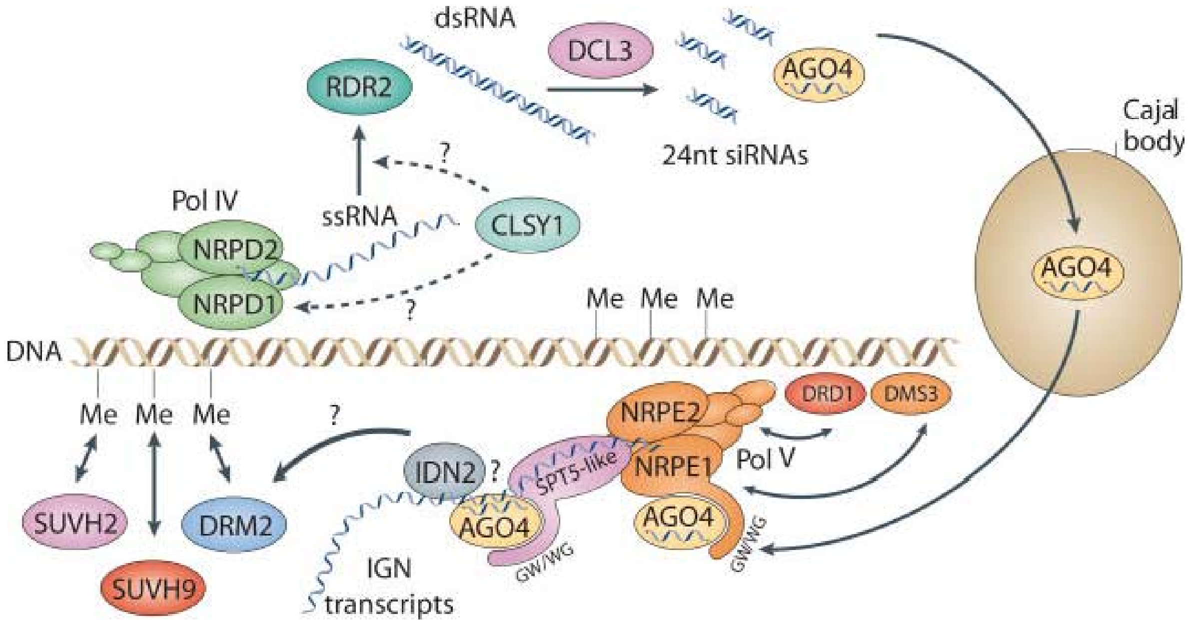
PTGS scion

WT stock

No chromatine modification

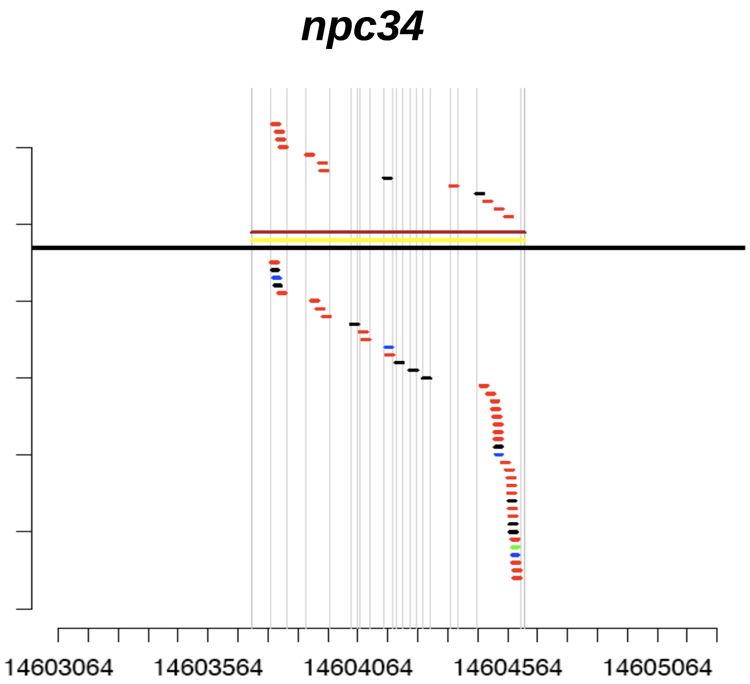
Chromatine modification

24-nt siRNAs guide RNA cleavage and DNA methylation



RNA precursors of DCL3-dependent 24-nt siRNAs are labile

Very few have been cloned



24nt siRNAs

Transcript

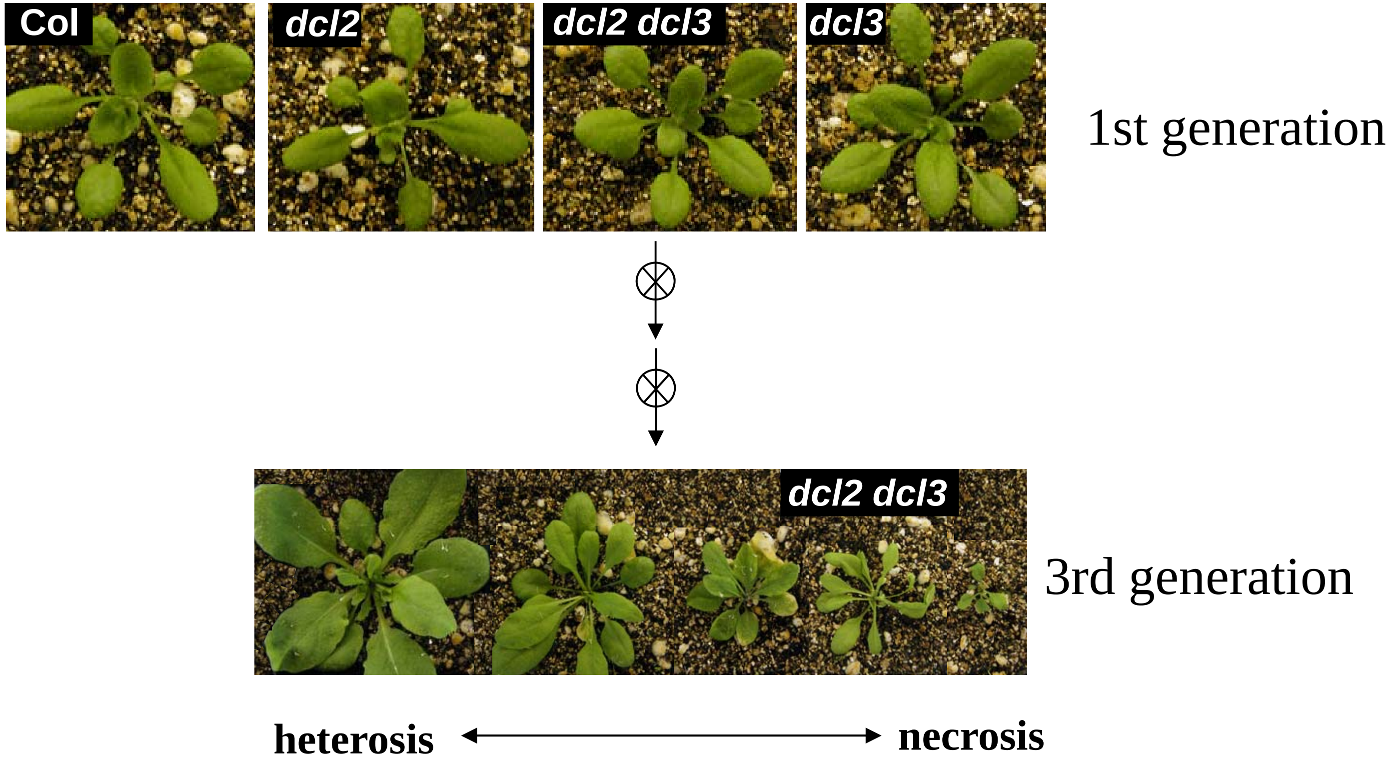
Genomic locus

NPC34 chromatin is marked by epigenetic marks linked to PcG repression

DCL2 and DCL3 act redundantly to prevent genomic shocks

dcl2 (Col) x *dcl3* (Col) -> viable *dcl2 dcl3*

dcl2 (Ws) x *dcl3* (Col) -> epigenetically unstable *dcl2 dcl3*



LabEx project 3 : Epigenetics and RNA-mediated regulation

Is it possible to specifically modify the RNA repertoire by modifying the RNA machinery and/or its cellular localization to improve plants' epigenetic potential ?

Work packages

In this project we will explore epigenetic mechanisms using a combination of cell biology , genetics and genomics.

1. Molecular identification of epigenetic targets

2. Subcellular architecture and trafficking dynamics of non-coding RNAs

People involved :

ISV Lab: RNA regulators

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F. Bardou
A.Moreno
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J-S Parent
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Bioinformatics : Daniel Gautheret at Orsay-PXI and
Hadi Quesneville / Matthias Zynnicki at URGI