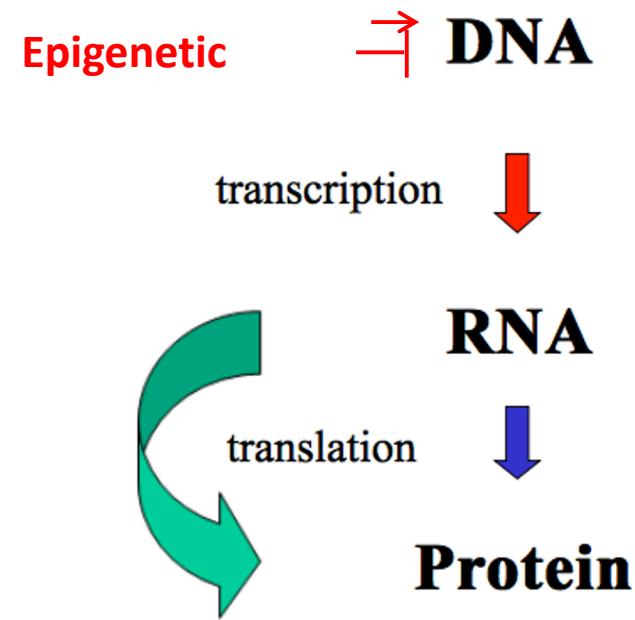


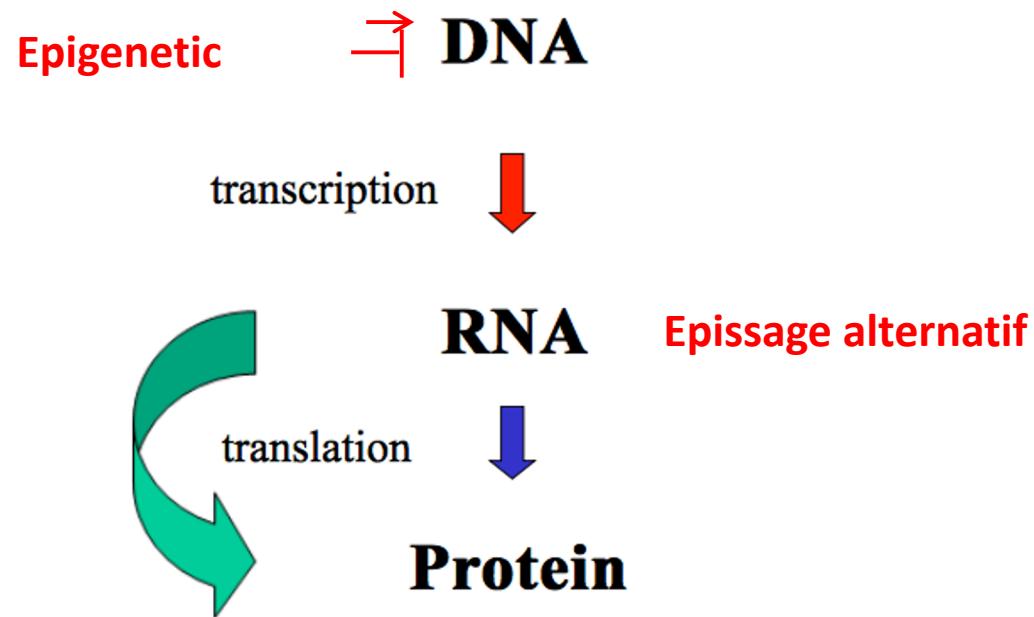
# Dynamique de la transcription

Dogme central:



# Dynamique de la transcription

Dogme central:

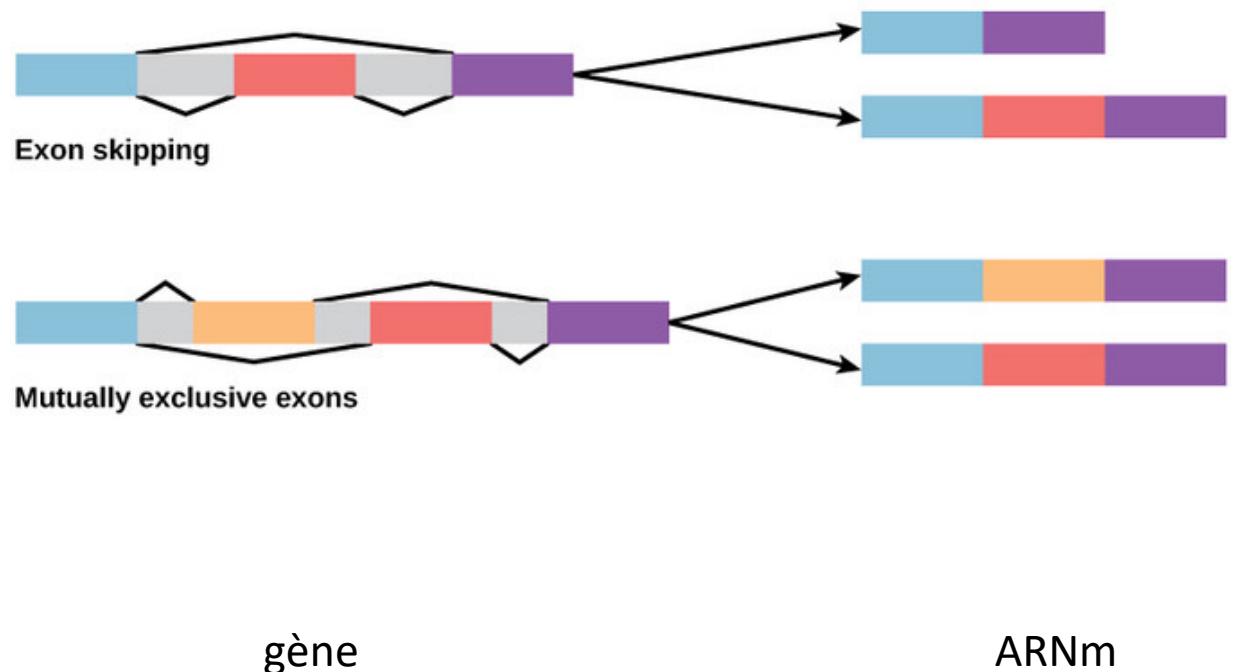


## Dynamique de la transcription

## 2- Epissage alternatif

Définition: c'est un processus qui permet, à partir d'une séquence génomique unique, de produire plusieurs ARN messagers correspondant à des protéines distinctes.

## Structure d'un gène:

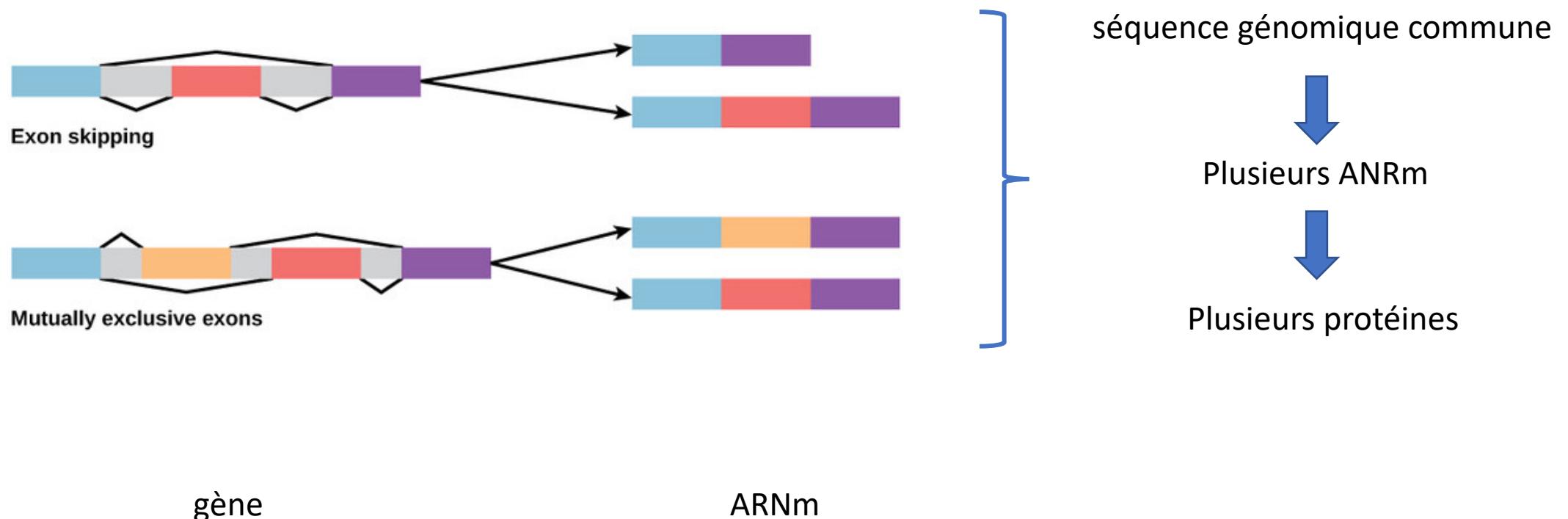


# Dynamique de la transcription

## 2- Epissage alternatif

Définition: c'est un processus qui permet, à partir d'une séquence génomique unique, de produire plusieurs ARN messagers correspondant à des protéines distinctes.

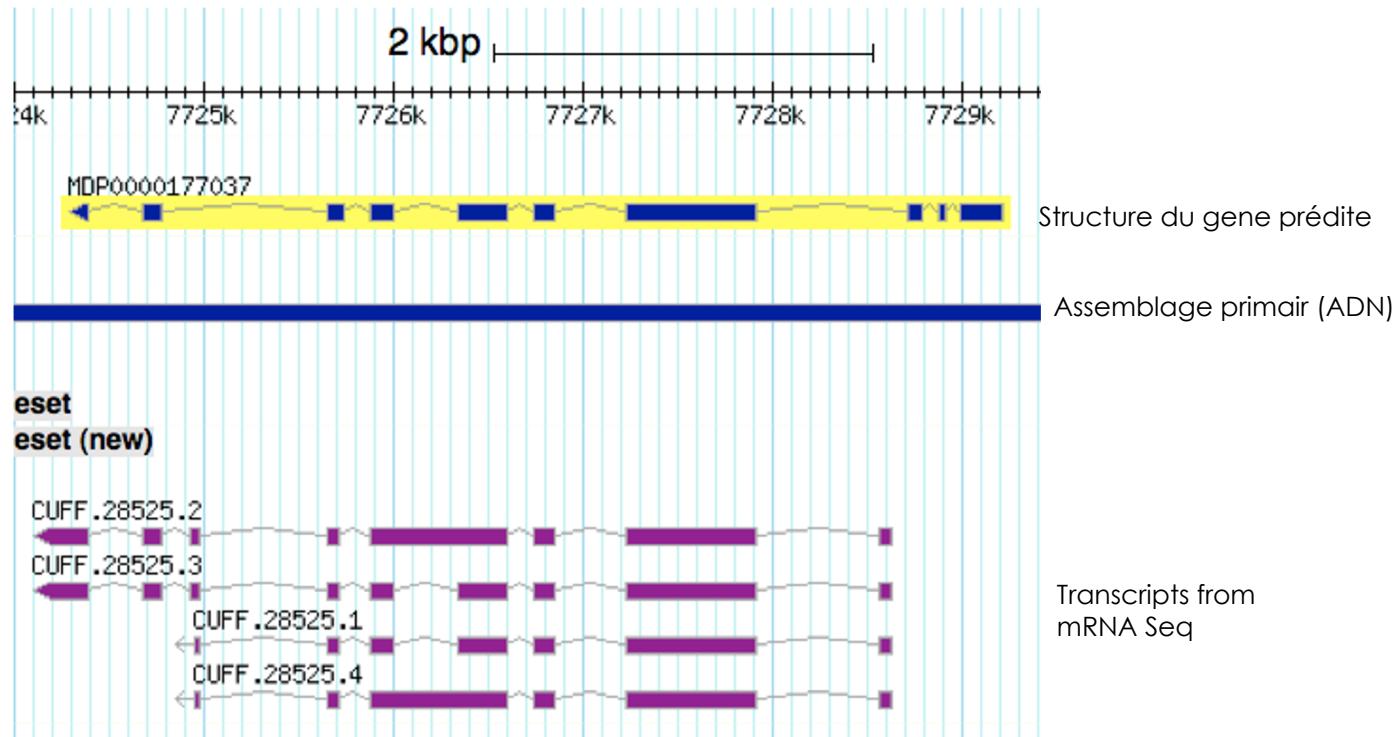
Structure d'un gène:



# Dynamique de la transcription

## 2- Epissage alternatif

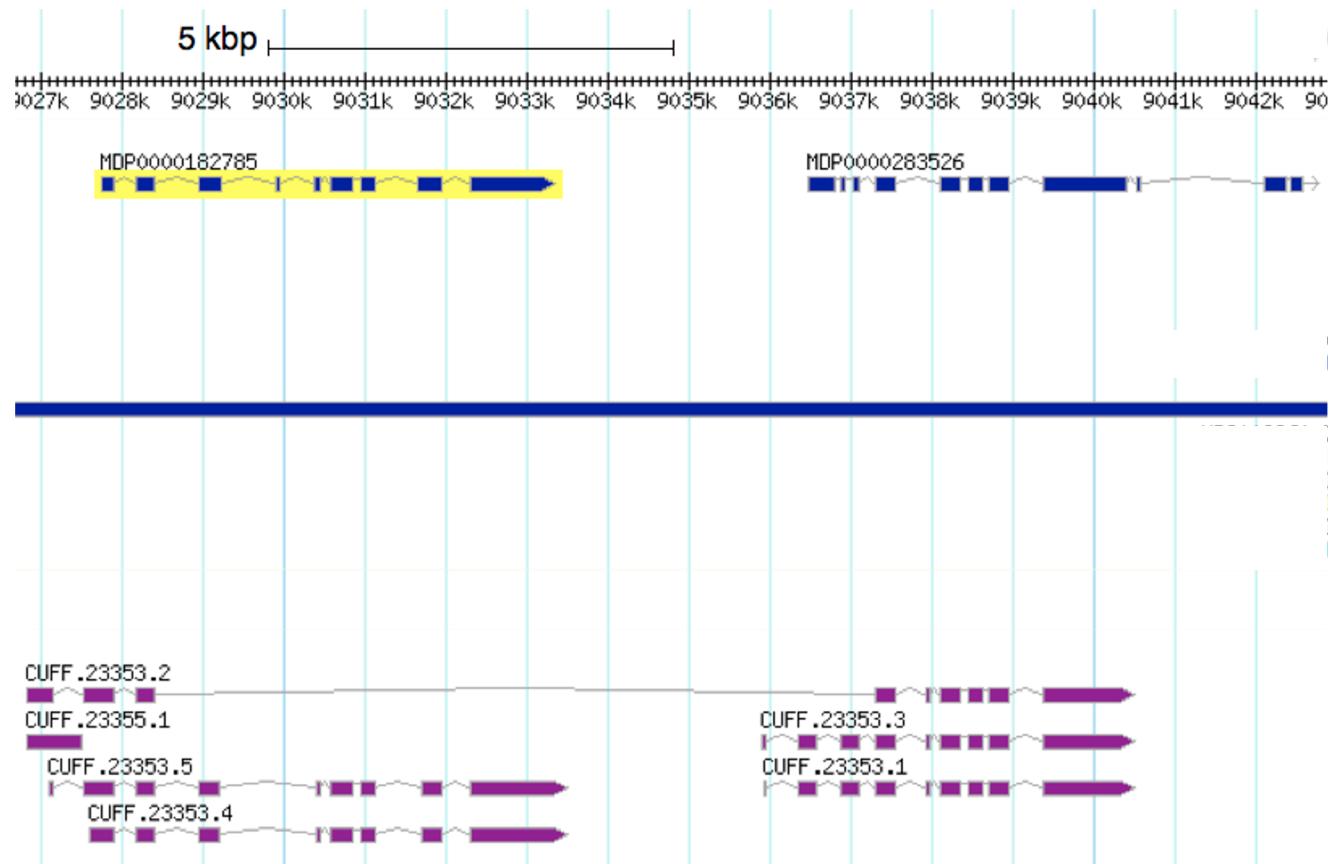
Exemple: Etude du transcriptome du pommier: 8 tissus séquencés



# Dynamique de la transcription

## 2- Epissage alternatif

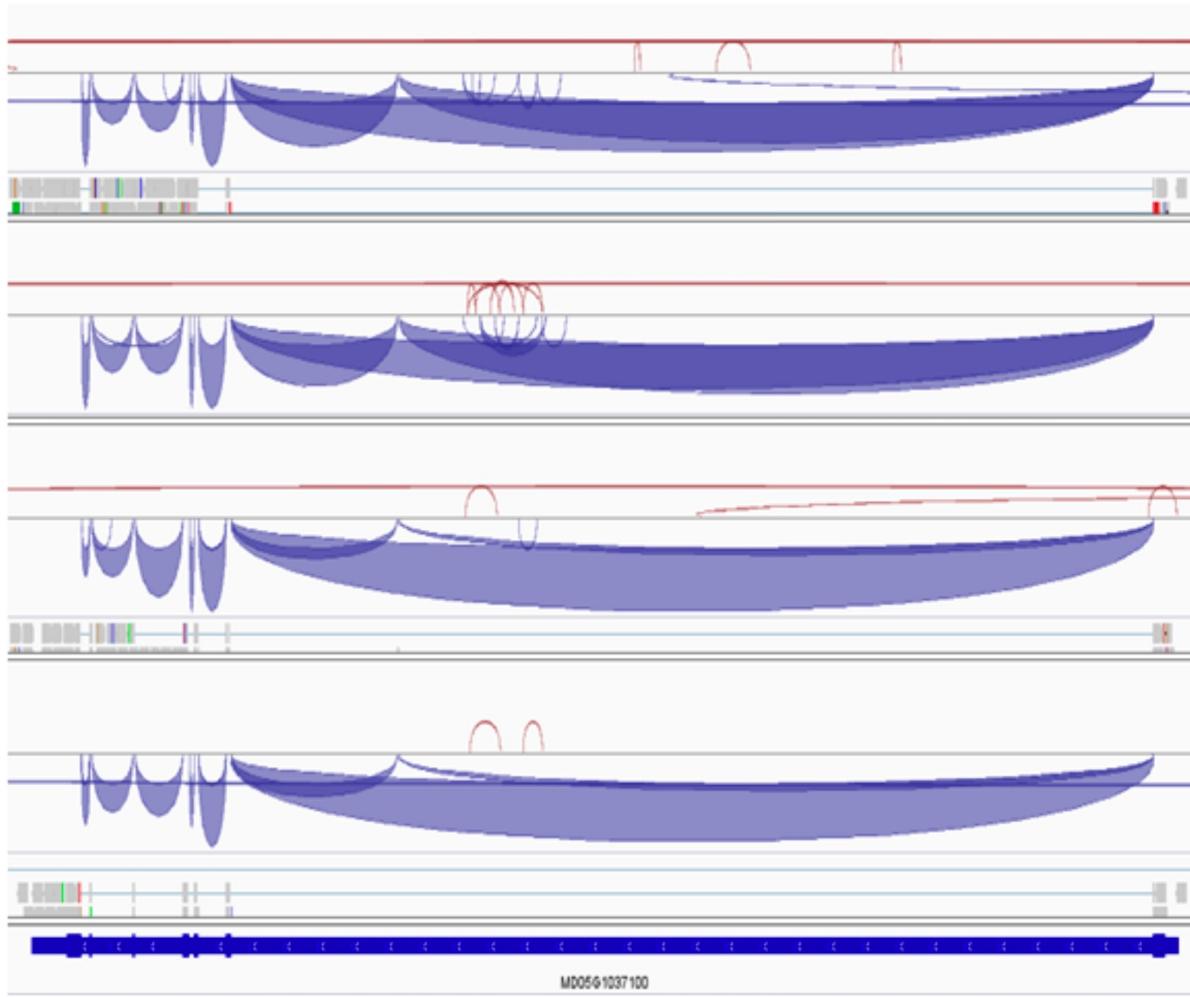
Exemple: Etude du transcriptome du pommier: 8 tissus séquencés



# Dynamique de la transcription

## 2- Epissage alternatif

Exemple: rôle biologique



ENDO1

ENDO2

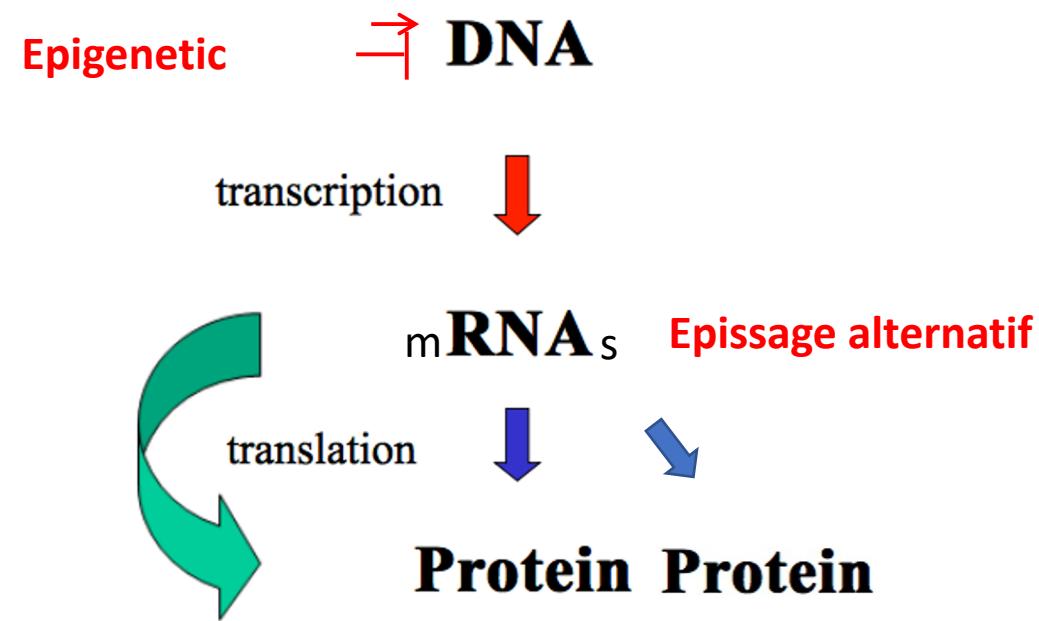
ECO1

ECO2



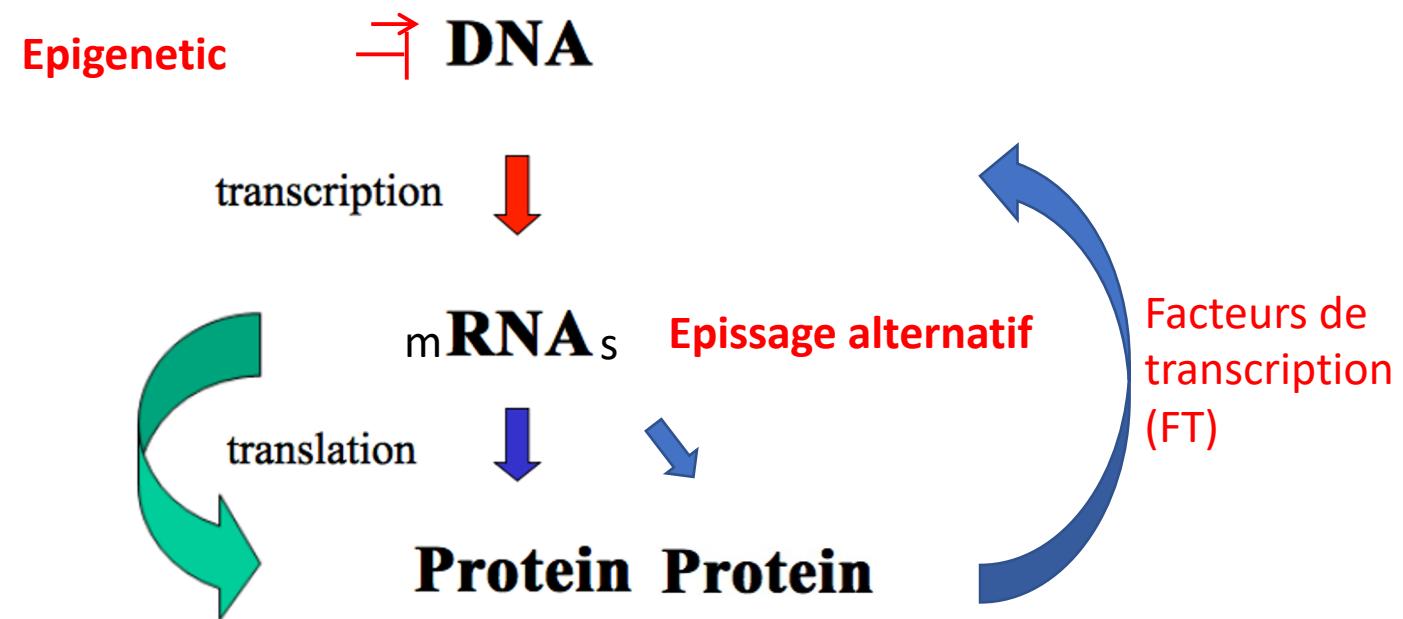
# Dynamique de la transcription

Dogme central:



# Dynamique de la transcription

Dogme central:

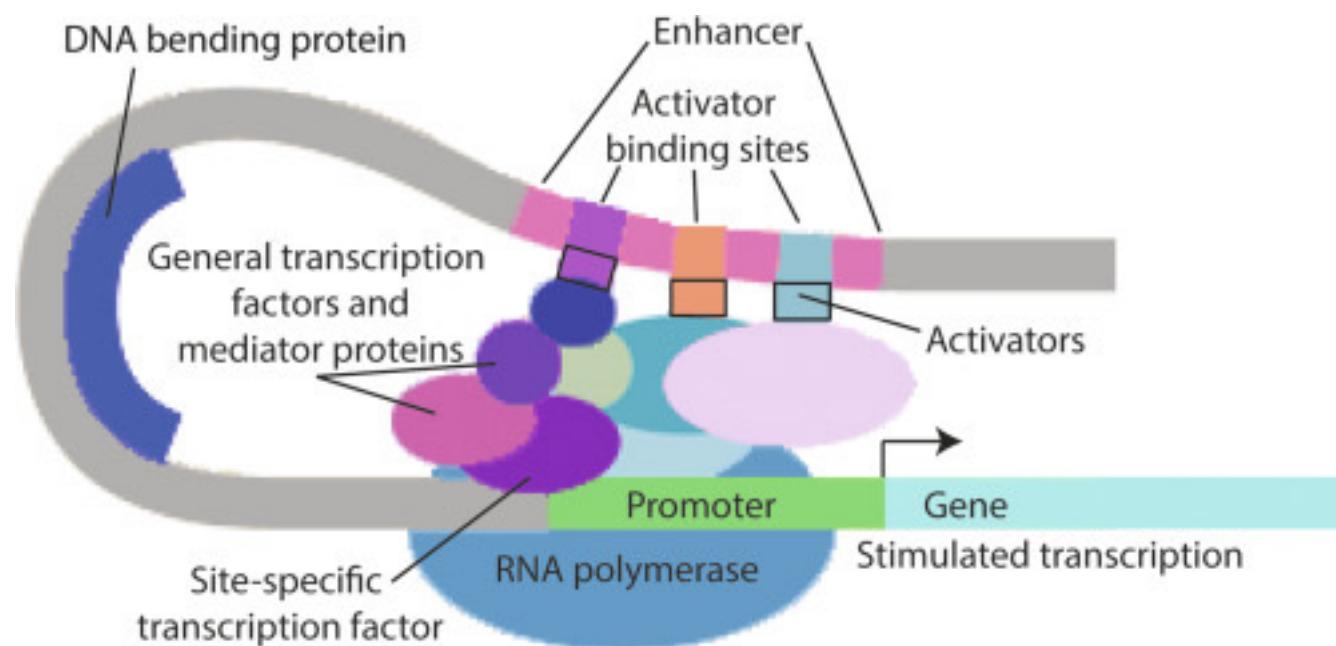


# Dynamique de la transcription

Facteurs de transcription:

C'est une protéine nécessaire à l'initiation ou à la régulation de la transcription d'un gene.  
Elle interagit avec l'ADN et l'ARN-polymérase.

→ Activateurs ou répresseurs du complexe transcriptionnel. Ils se fixent en se fixant sur les séquences régulatrices (promoteurs) en amont du gène à transcrire



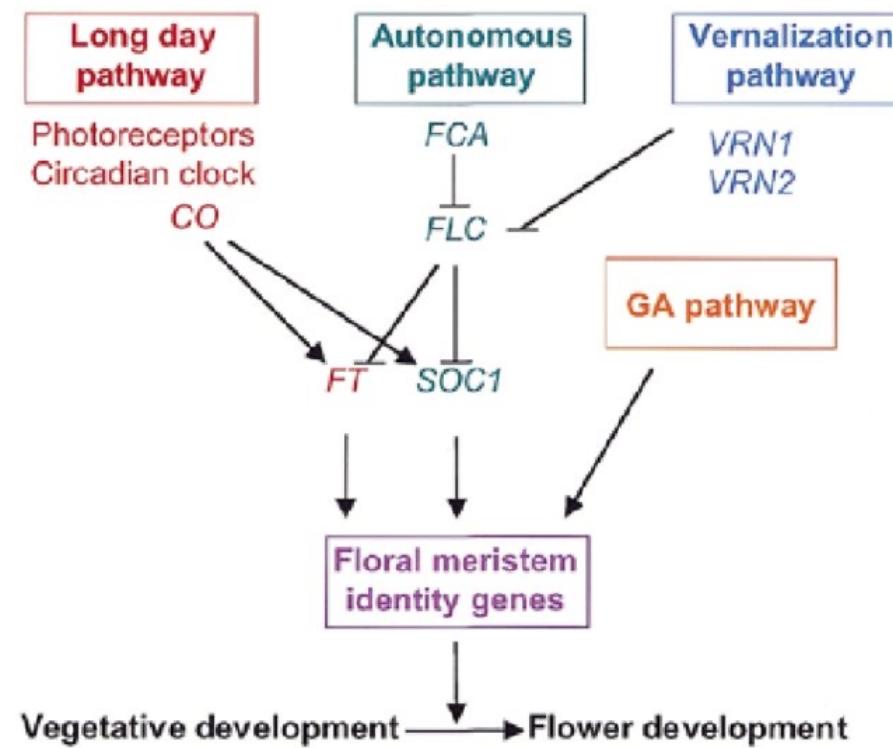
# Dynamique de la transcription

Facteurs de transcription:

Exemple: initiation florale chez les plantes

SOC1: MADS box TF (activator)

FLC: MADS box TF (repressor)



# Dynamique de la transcription

Rôle des micropeptides:

Des peptides (dérivés de la nourriture (digestion de protéines...), de l'environnement, synthétiques...) peuvent influencer l'expression de certains gènes en modifiant leur environnement épigénétique

Exemples:

- Lunasin – 43 aa – dérive du soja. Cet aa peut inhiber l'acétylation des histones H3 et H4 via une suite de 8 aa chargés négativement (Asp) à la fin de sa séquence.
- Un mélange de peptides dérivés de la cuisine chinoise traditionnelle (soft-shelled turtle) module l'expression de 101 miRNA dans les cellules gastriques cancéreuses. Certains de ces miRNA ont des effets bénéfiques sur la croissance des tumeurs → effet anti-cancereux.

REVIEW

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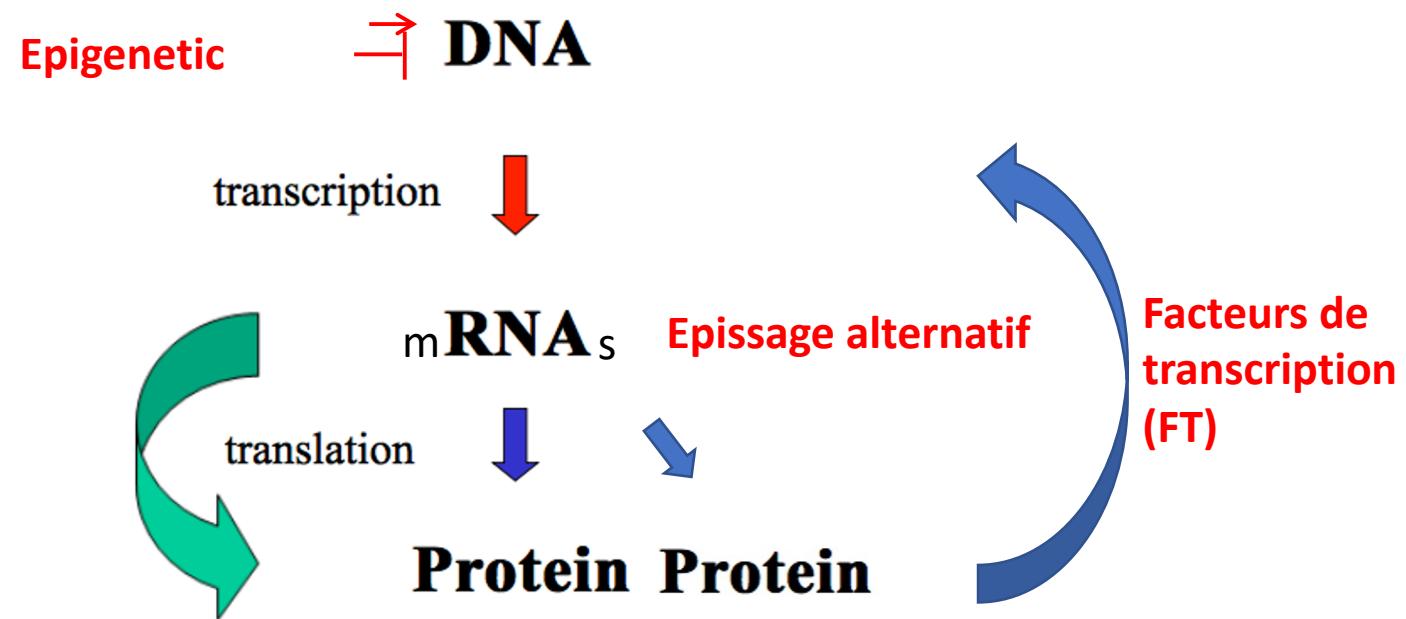
## Peptides as epigenetic modulators: therapeutic implications



Yorick Janssens<sup>1</sup>, Evelien Wynendaele<sup>1</sup>, Wim Vanden Berghe<sup>2</sup> and Bart De Spiegeleer<sup>1\*</sup>

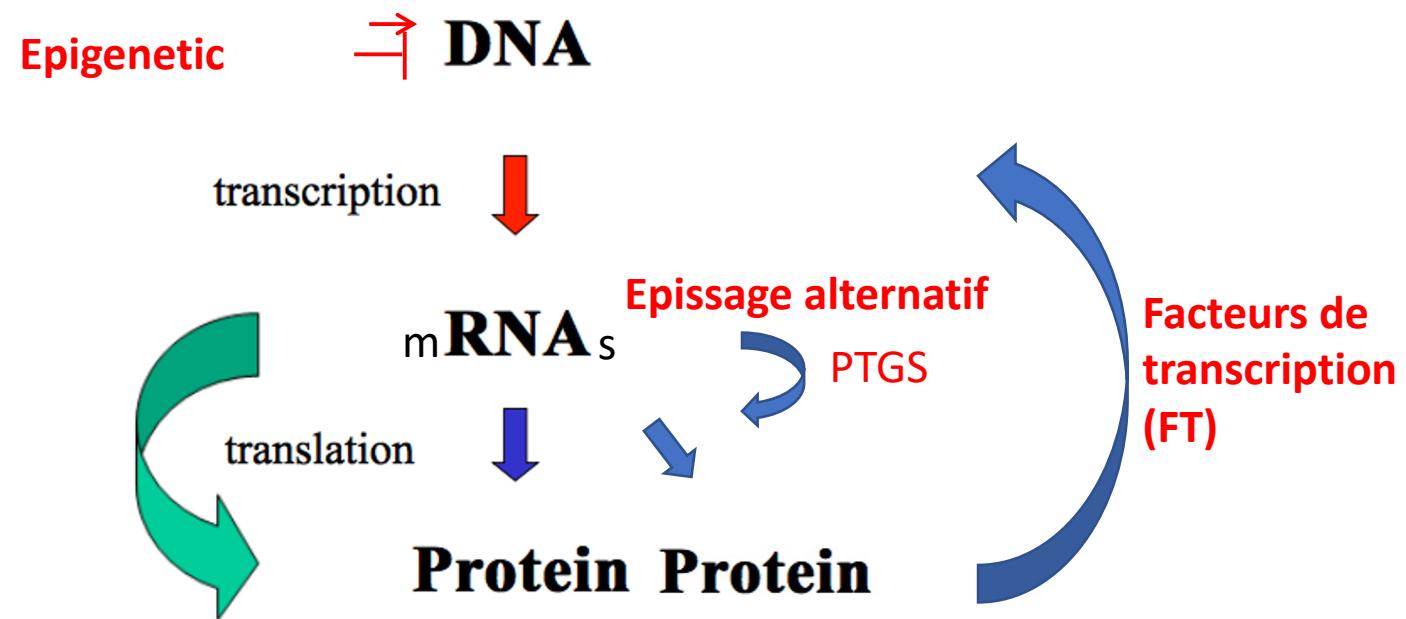
# Dynamique de la transcription

Dogme central:



# Dynamique de la transcription

Dogme central:

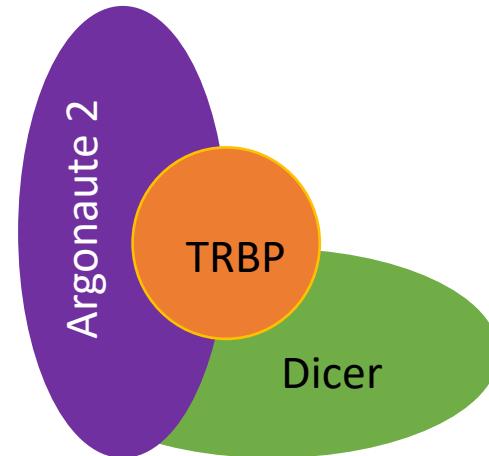


# Dynamique de la transcription

PTGS: Post Transcriptional Gene Silencing

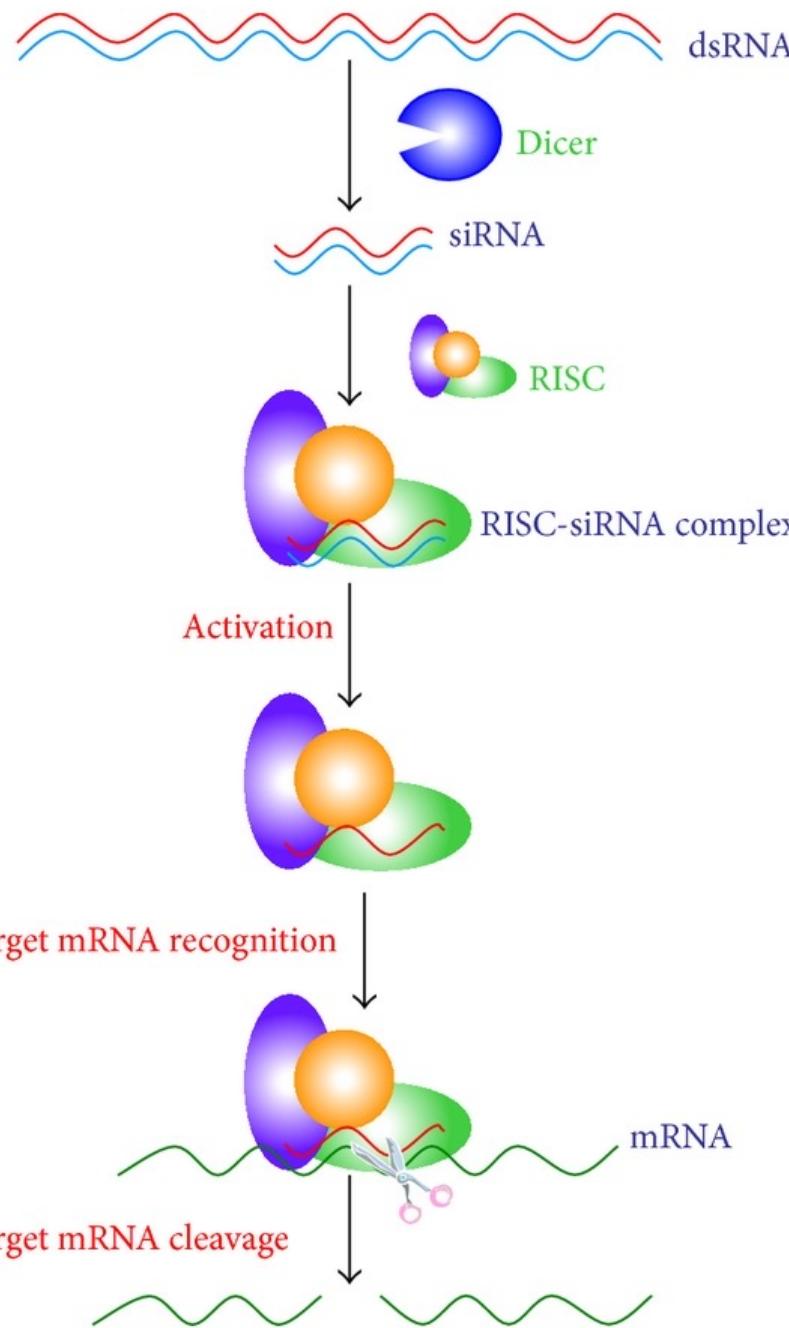
Ensemble des mécanismes affectant directement les molécules d'ARN produites lors de la transcription.  
Permet aux cellules de s'adapter rapidement aux changements de leur environnement.

Le mécanisme est basé sur l'action du complex RISC (RNA Induced Silencing Complex) qui joue un rôle central dans le phénomène d'interférence par ARN

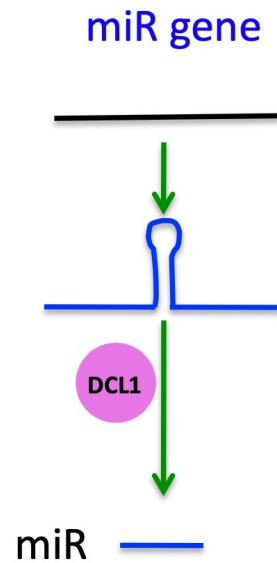


Principe:

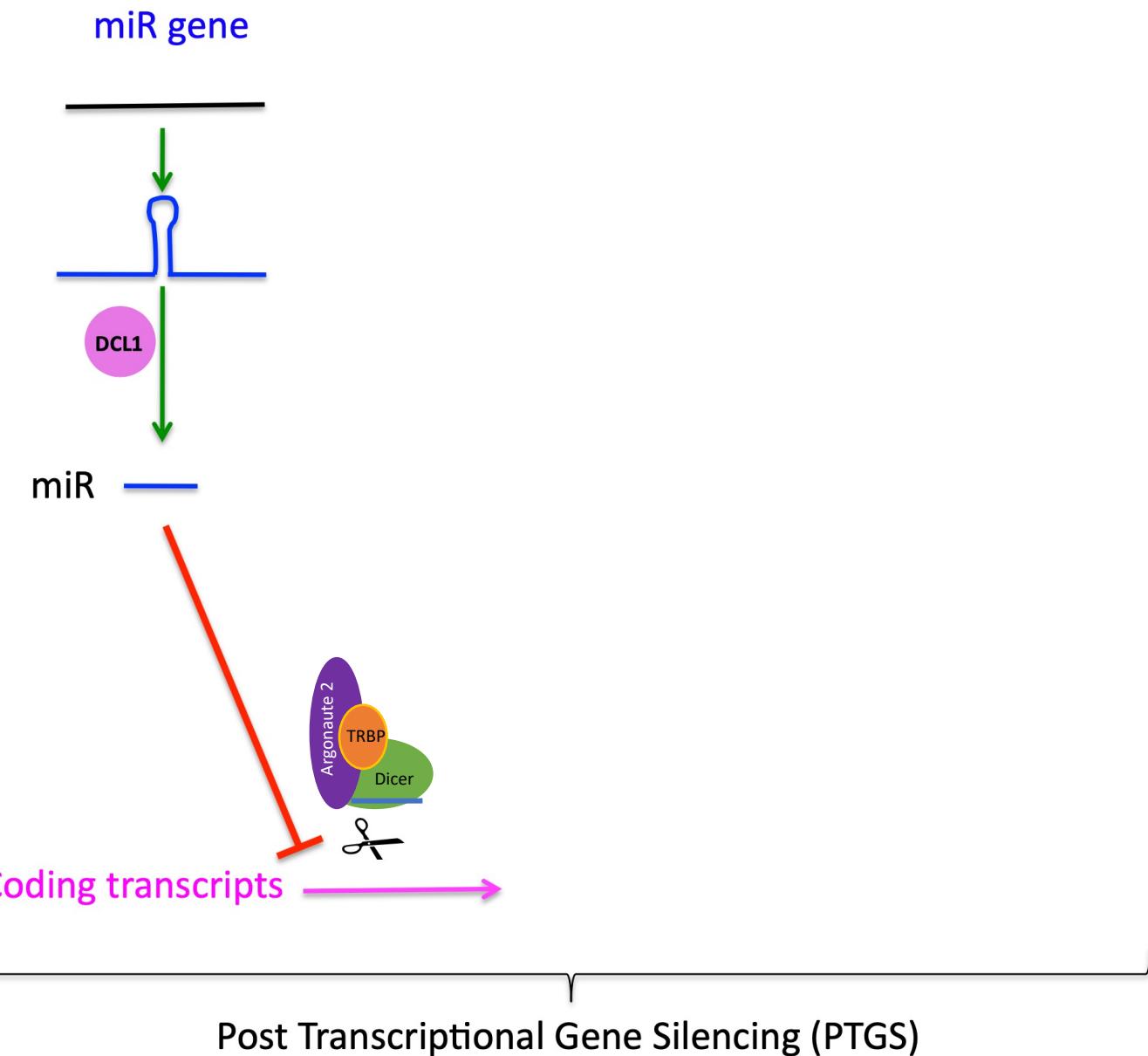
PTGS: Post Transcriptional Gene Silencing



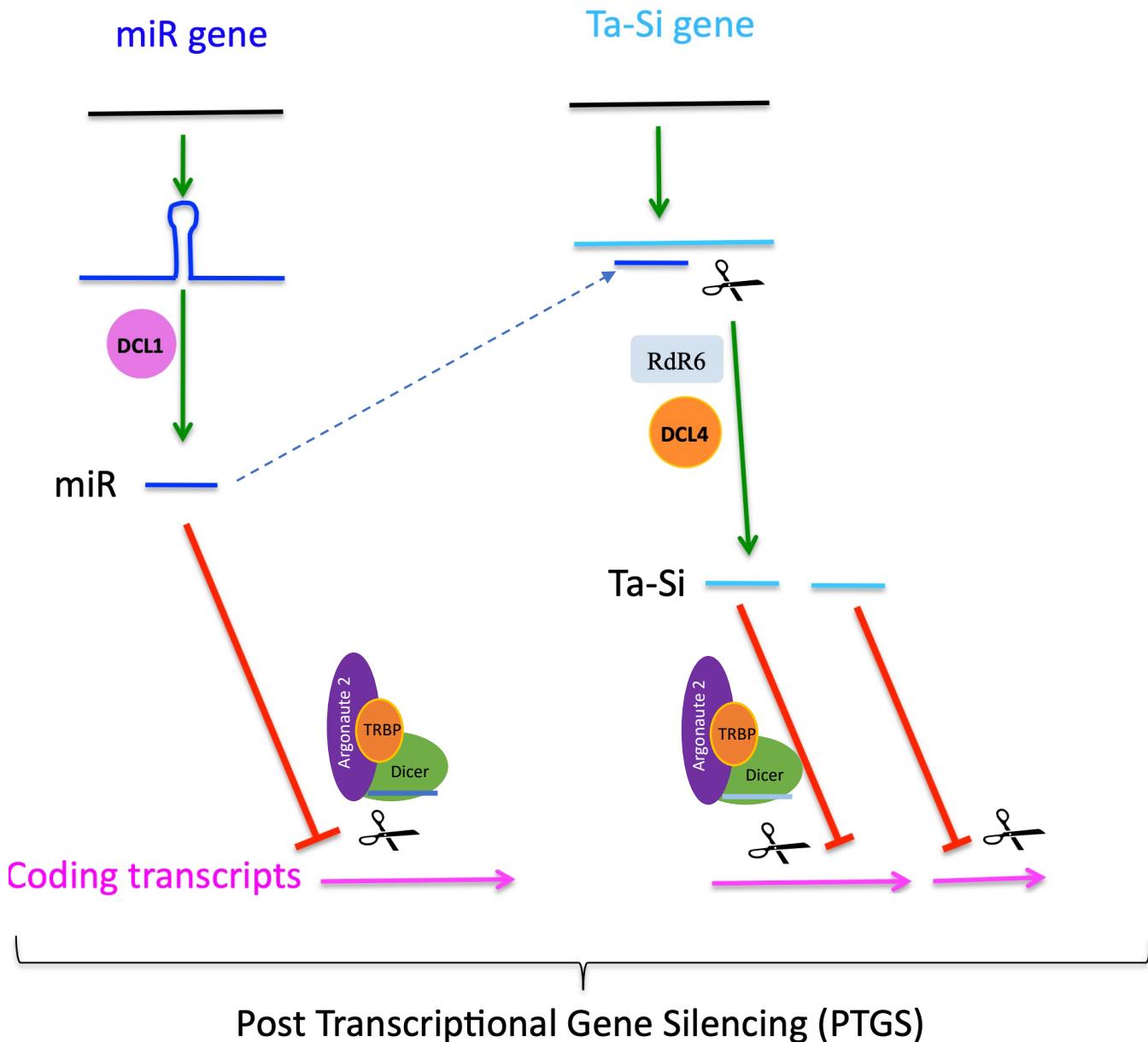
## PTGS: Post Transcriptional Gene Silencing



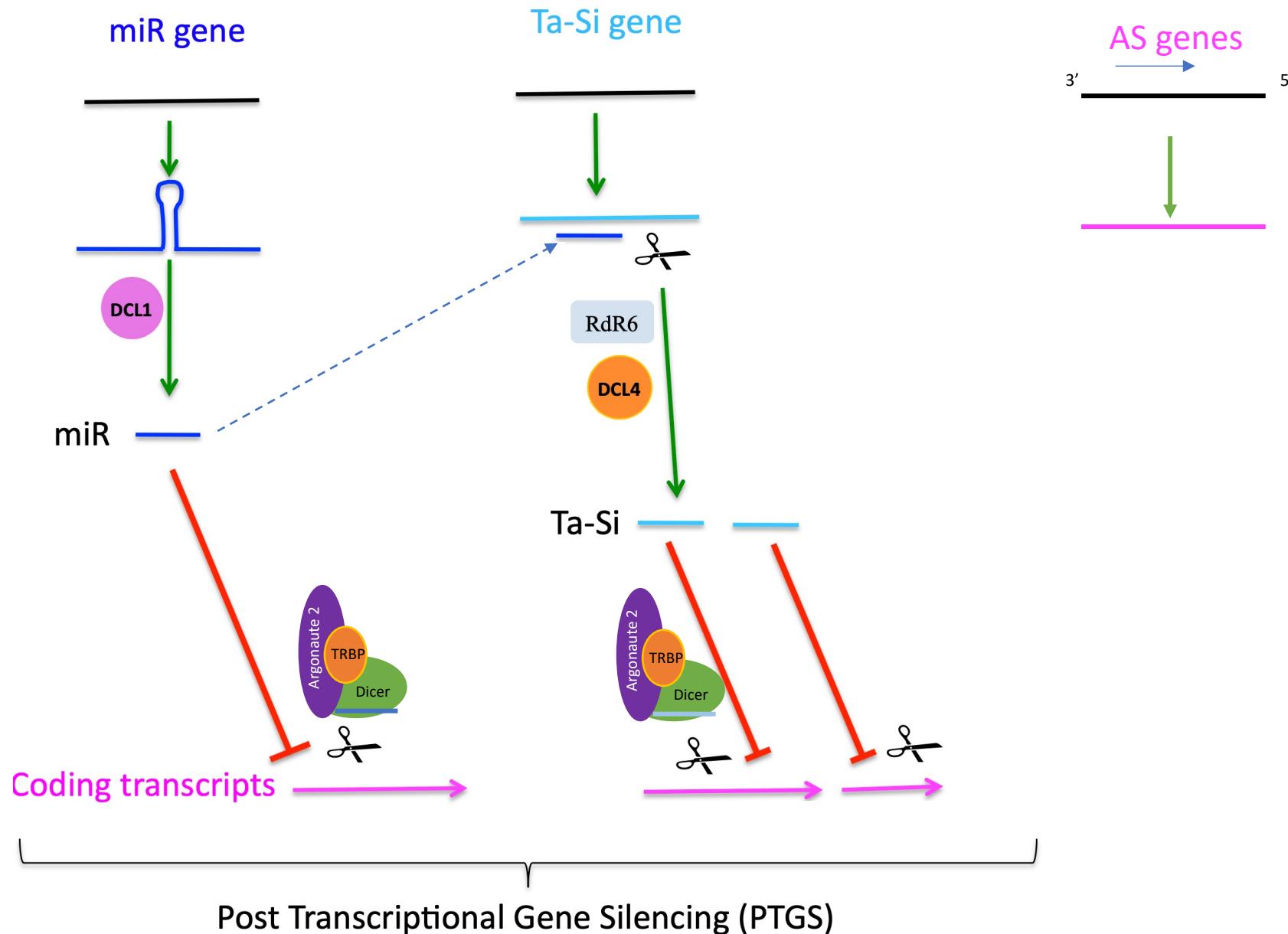
## PTGS: Post Transcriptional Gene Silencing



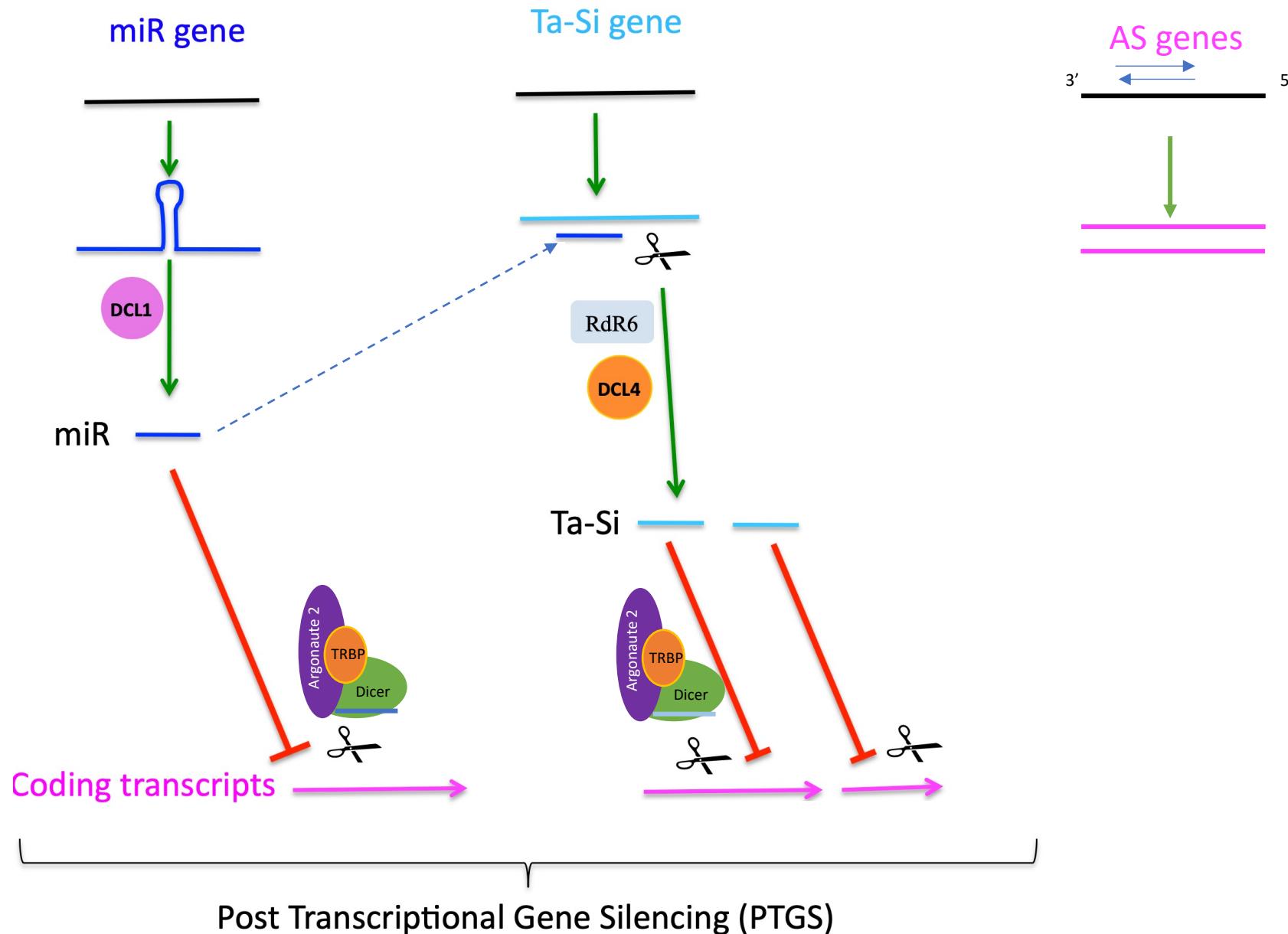
## PTGS: Post Transcriptional Gene Silencing



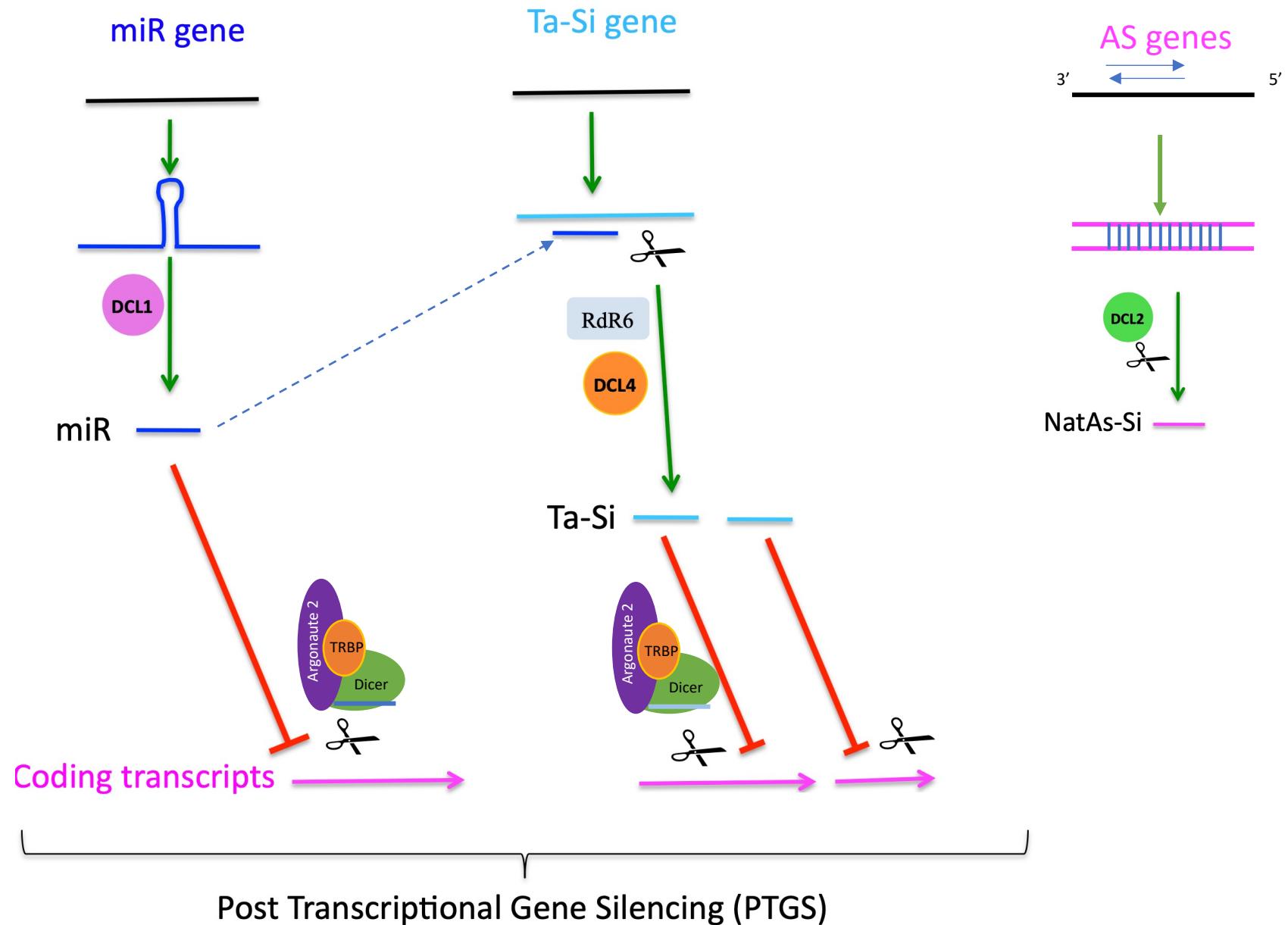
## PTGS: Post Transcriptional Gene Silencing



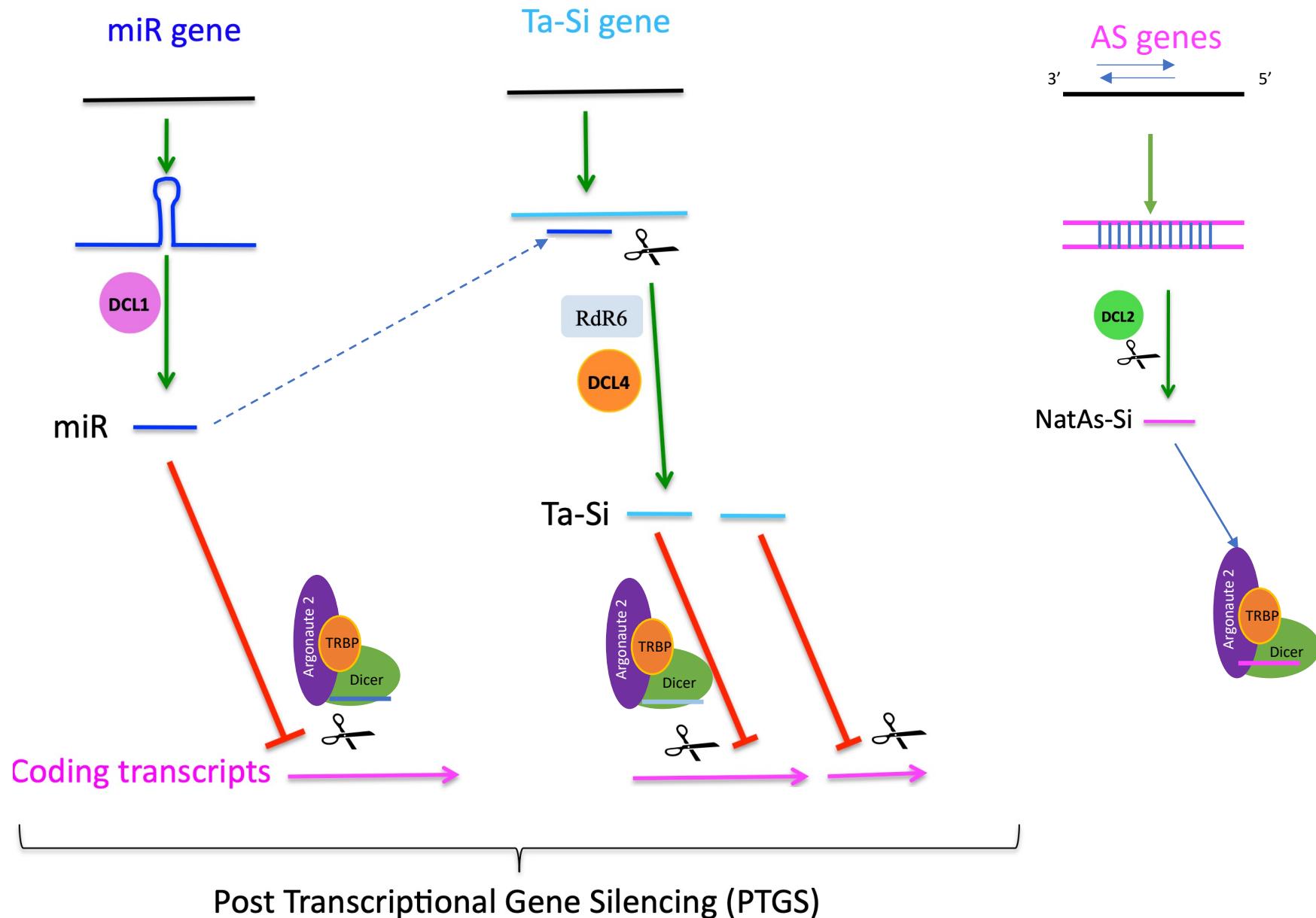
## PTGS: Post Transcriptional Gene Silencing



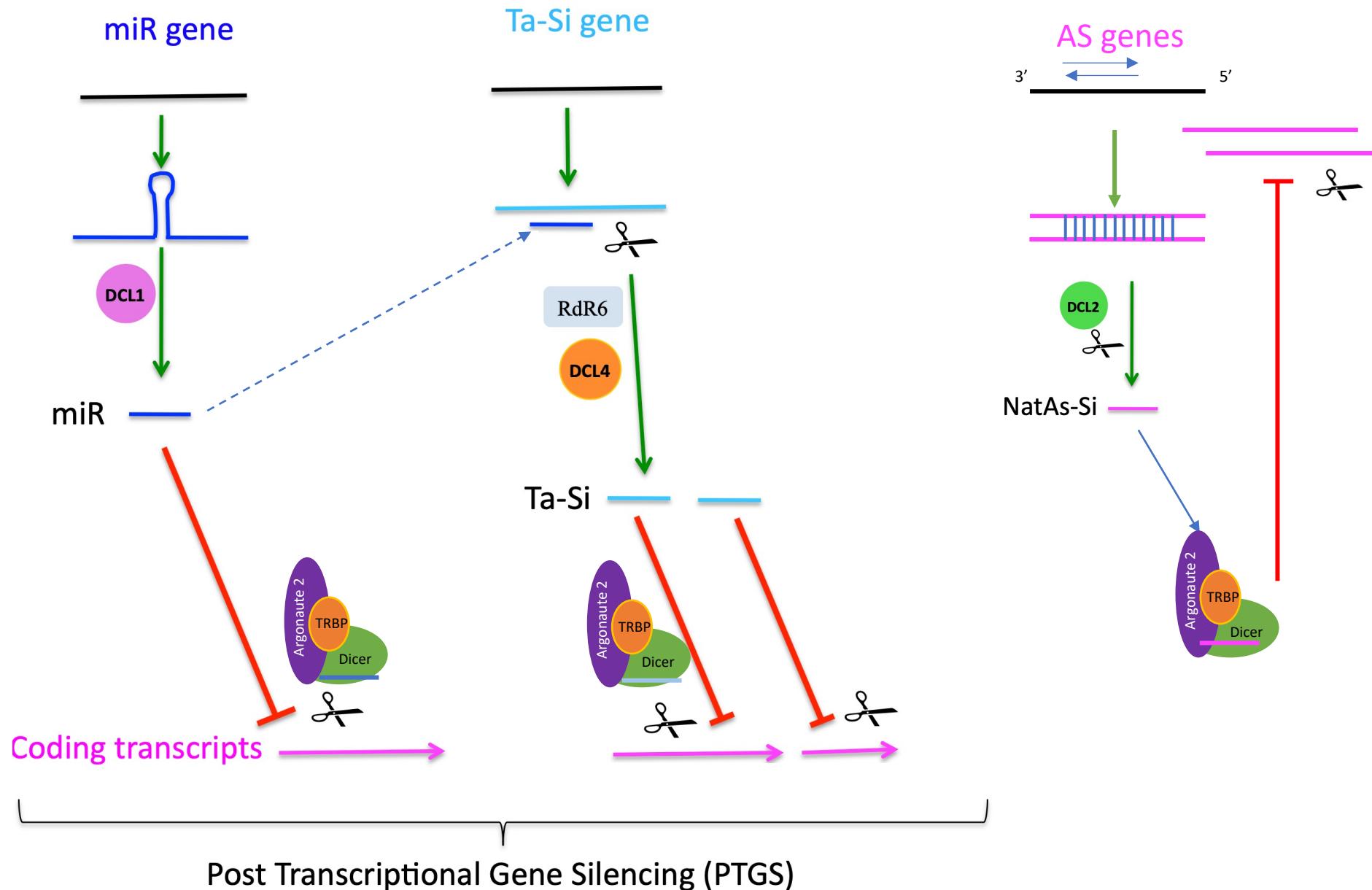
## PTGS: Post Transcriptional Gene Silencing



## PTGS: Post Transcriptional Gene Silencing



## PTGS: Post Transcriptional Gene Silencing



# Dynamique de la transcription

PTGS: Post Transcriptional Gene Silencing: importance de la transcription anti-sense

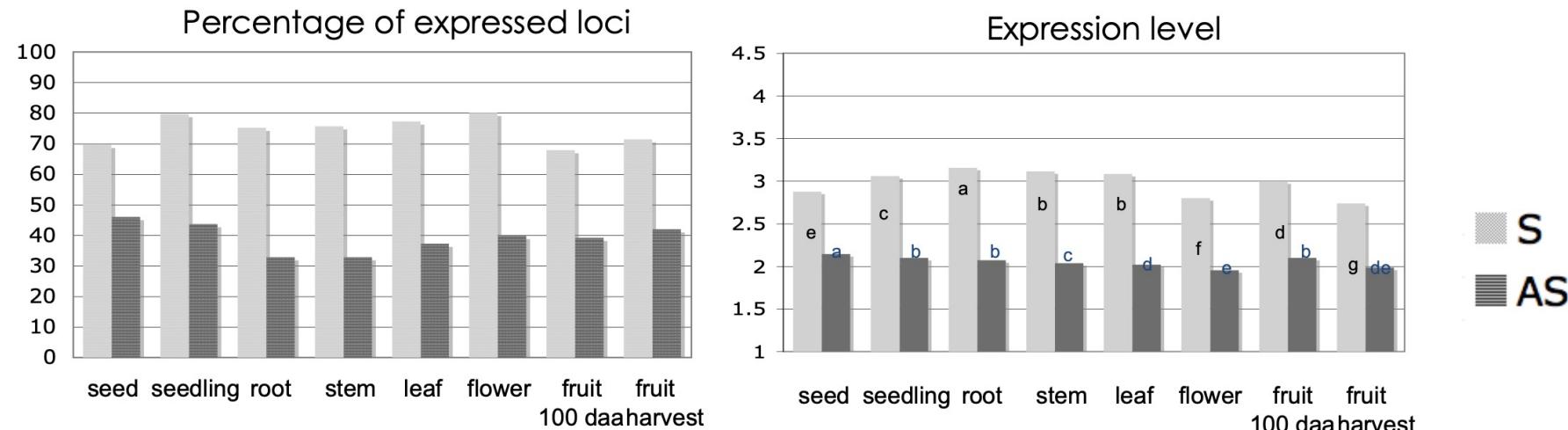
Développement d'un Atlas d'expression sur pommier à partir d'une puce microarray

## ➤ Global results:

➤ Sense transcript expression detected for 33,201 transcripts (69.1%)

➤ AS transcript expression detected for 21,774 transcripts

## ➤ Percentage and expression levels of S and AS varied depending on sample



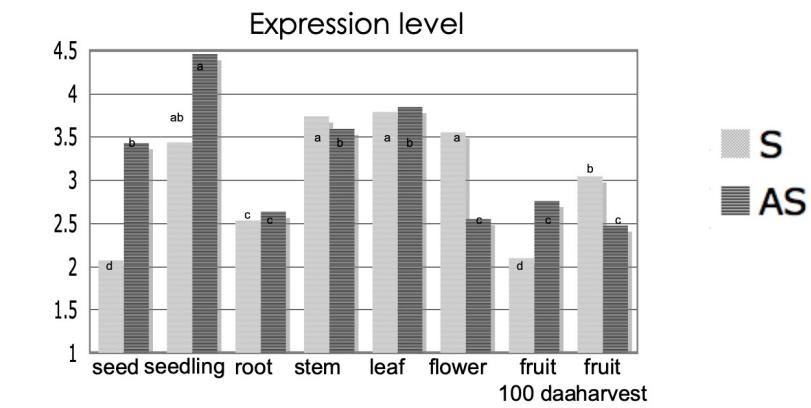
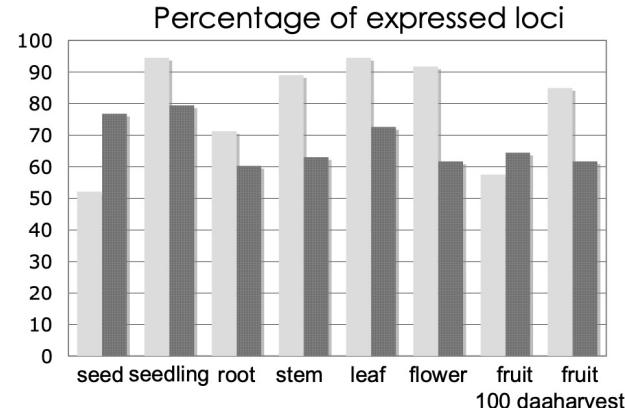
# Dynamique de la transcription

PTGS: Post Transcriptional Gene Silencing: importance de la transcription anti-sense

Développement d'un Atlas d'expression sur pommier à partir d'une puce microarray

➤Photosynthesis:

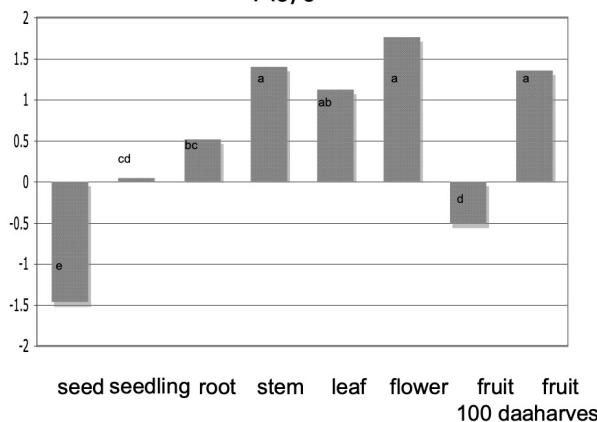
➤% and transcription levels of S and AS transcripts varied depending samples



S  
AS

Photosynthesis: 73 transcripts

AS/S

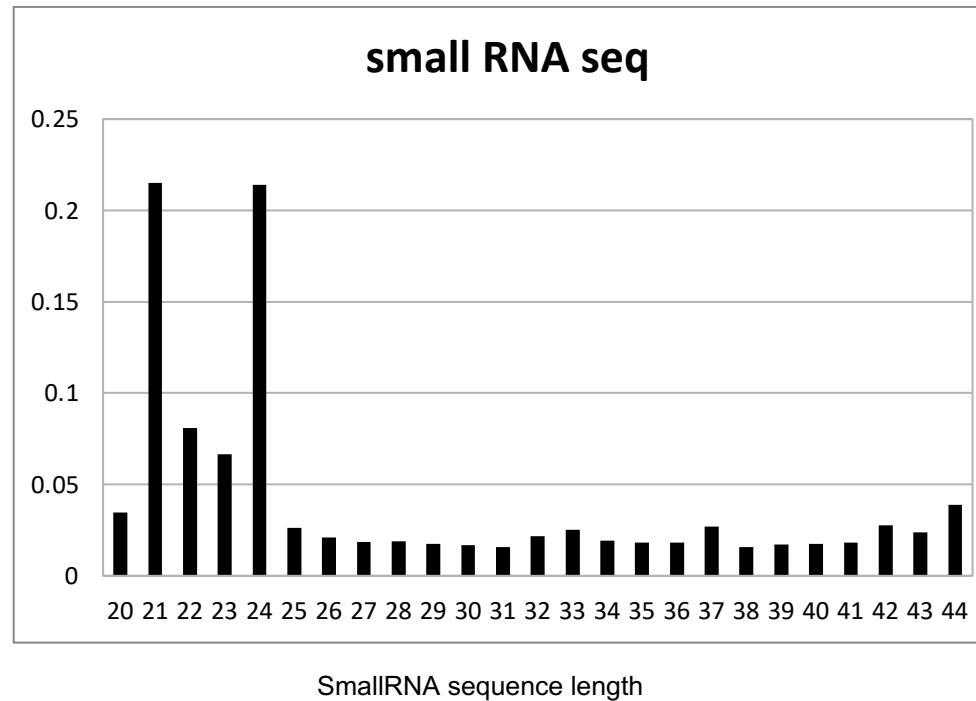


Regulation of S transcript expression by AS transcript?

# Dynamique de la transcription

PTGS: Post Transcriptional Gene Silencing: importance de la transcription anti-sense

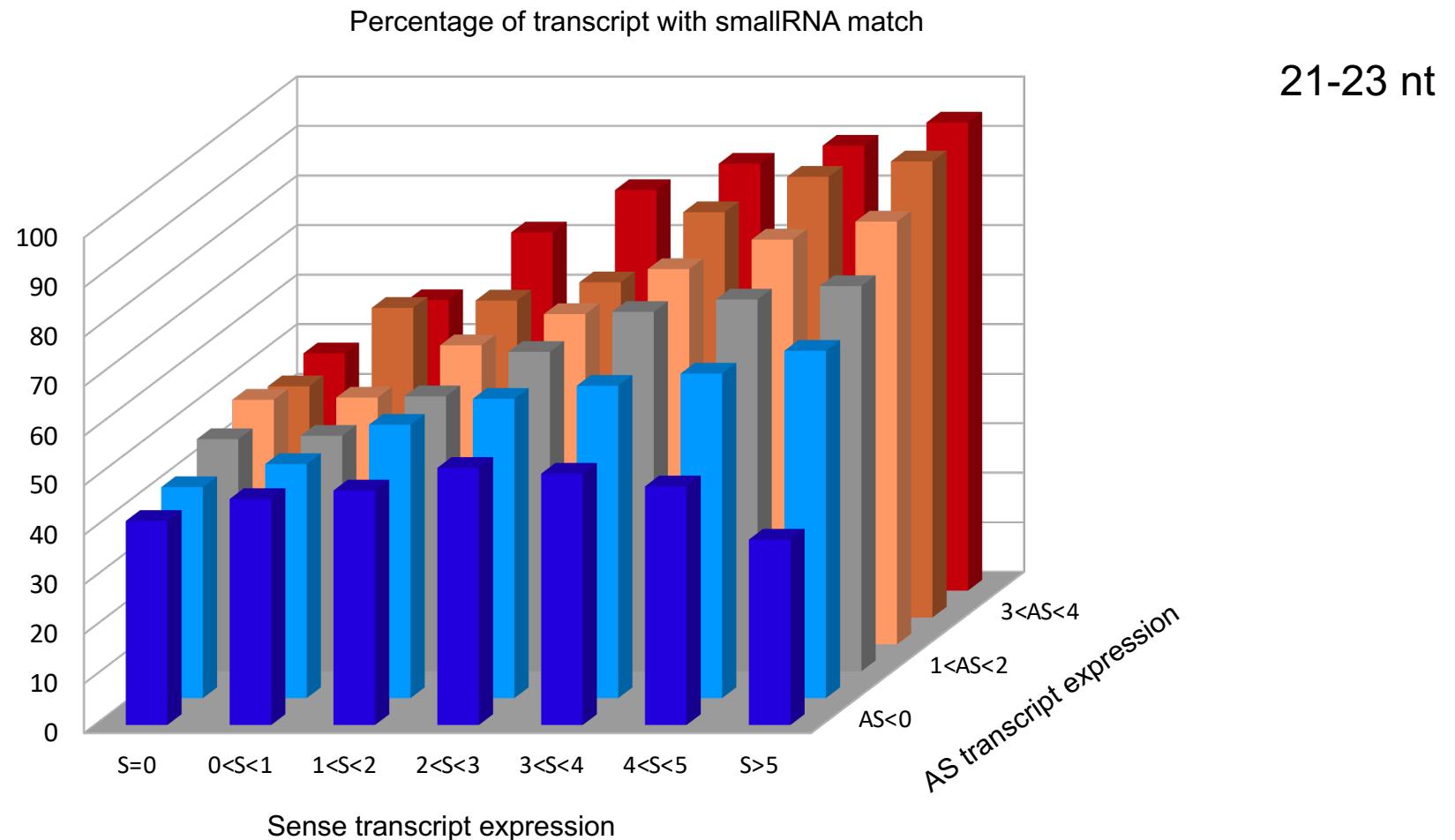
Séquençage de petits ARN chez le pommier:



# Dynamique de la transcription

PTGS: Post Transcriptional Gene Silencing: importance de la transcription anti-sense

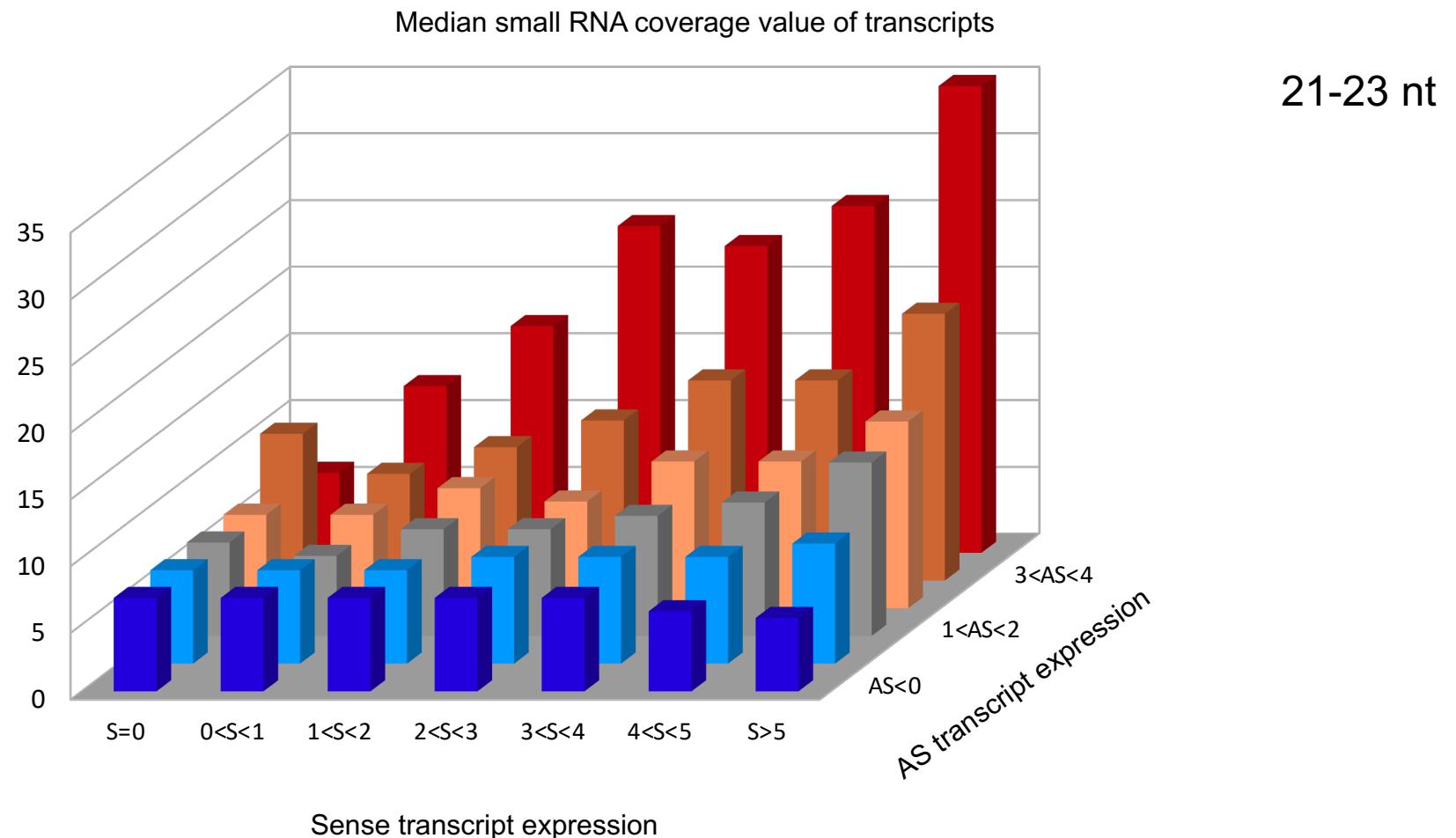
Alignment des petits ARN sur le transcriptome:



# Dynamique de la transcription

PTGS: Post Transcriptional Gene Silencing: importance de la transcription anti-sense

Alignement des petits ARN sur le transcriptome:



# Dynamique de la transcription



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Fungal Genomics & Biology

Mini-Review

Small RNAs at the Interface of the Plant-Fungal Interactions

Cole R. Sawyer<sup>1,2</sup>, Jessy L. Labbé<sup>1,2\*</sup>

REPORT



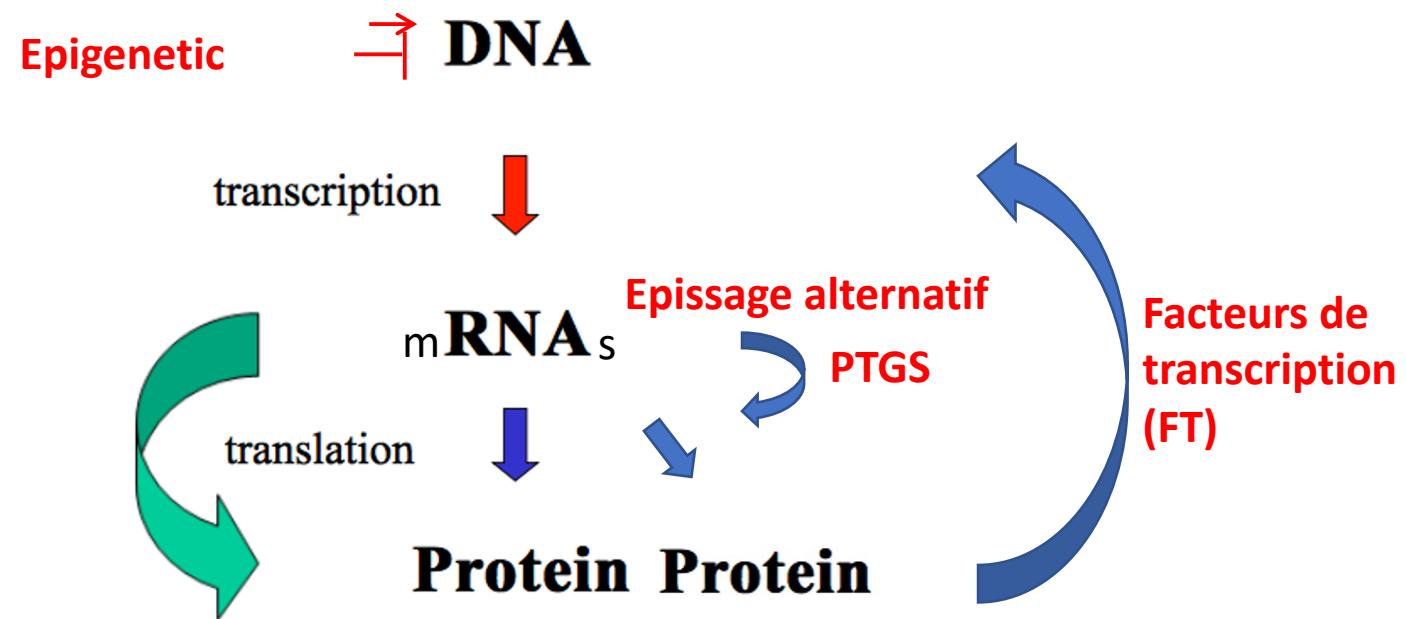
## Fungal Small RNAs Suppress Plant Immunity by Hijacking Host RNA Interference Pathways

ARNE WEIBERG, MING WANG, FENG-MAO LIN, HONGWEI ZHAO, ZHIHONG ZHANG, ISGOUHI KALOSHIAN, HSIEN-DA HUANG, AND HAILING JIN [Authors Info & Affiliations](#)

SCIENCE • 4 Oct 2013 • Vol 342, Issue 6154 • pp. 118-123 • DOI: 10.1126/science.1239705

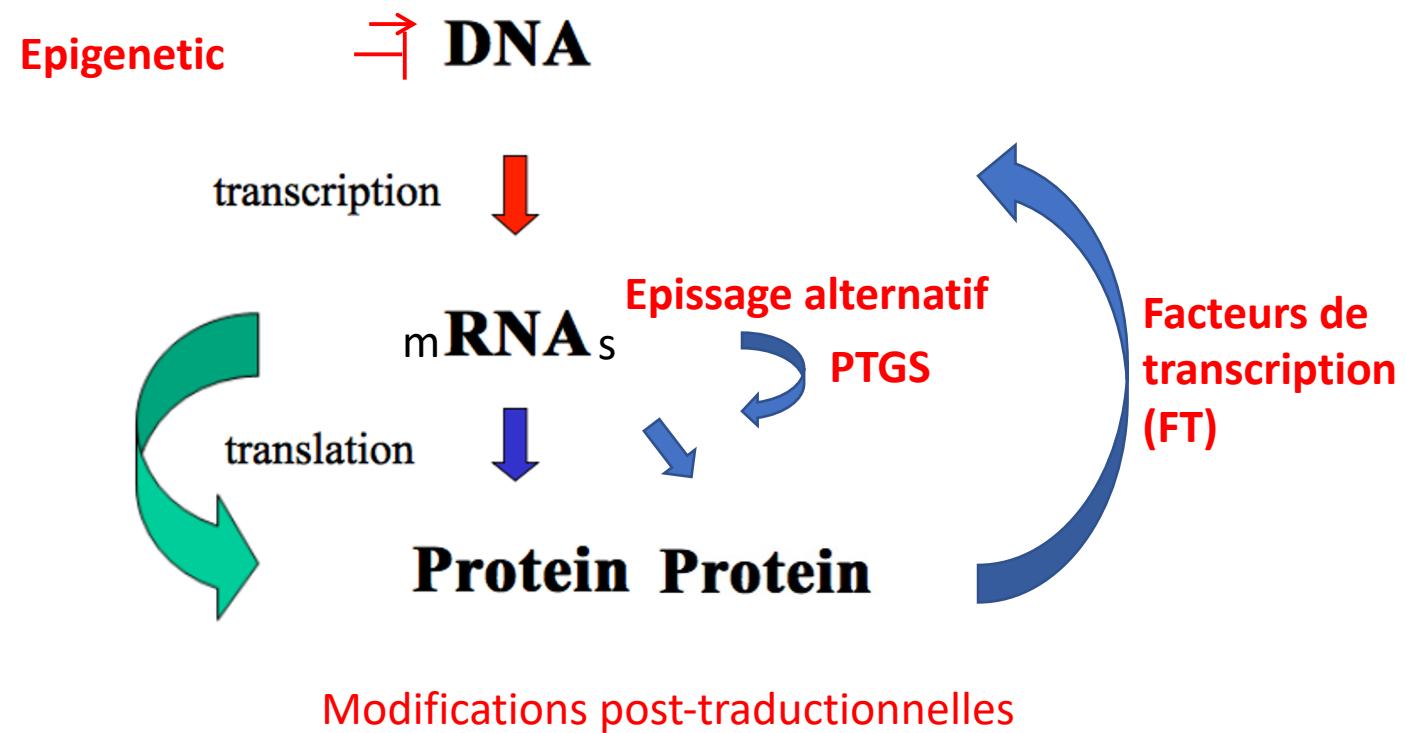
# Dynamique de la transcription

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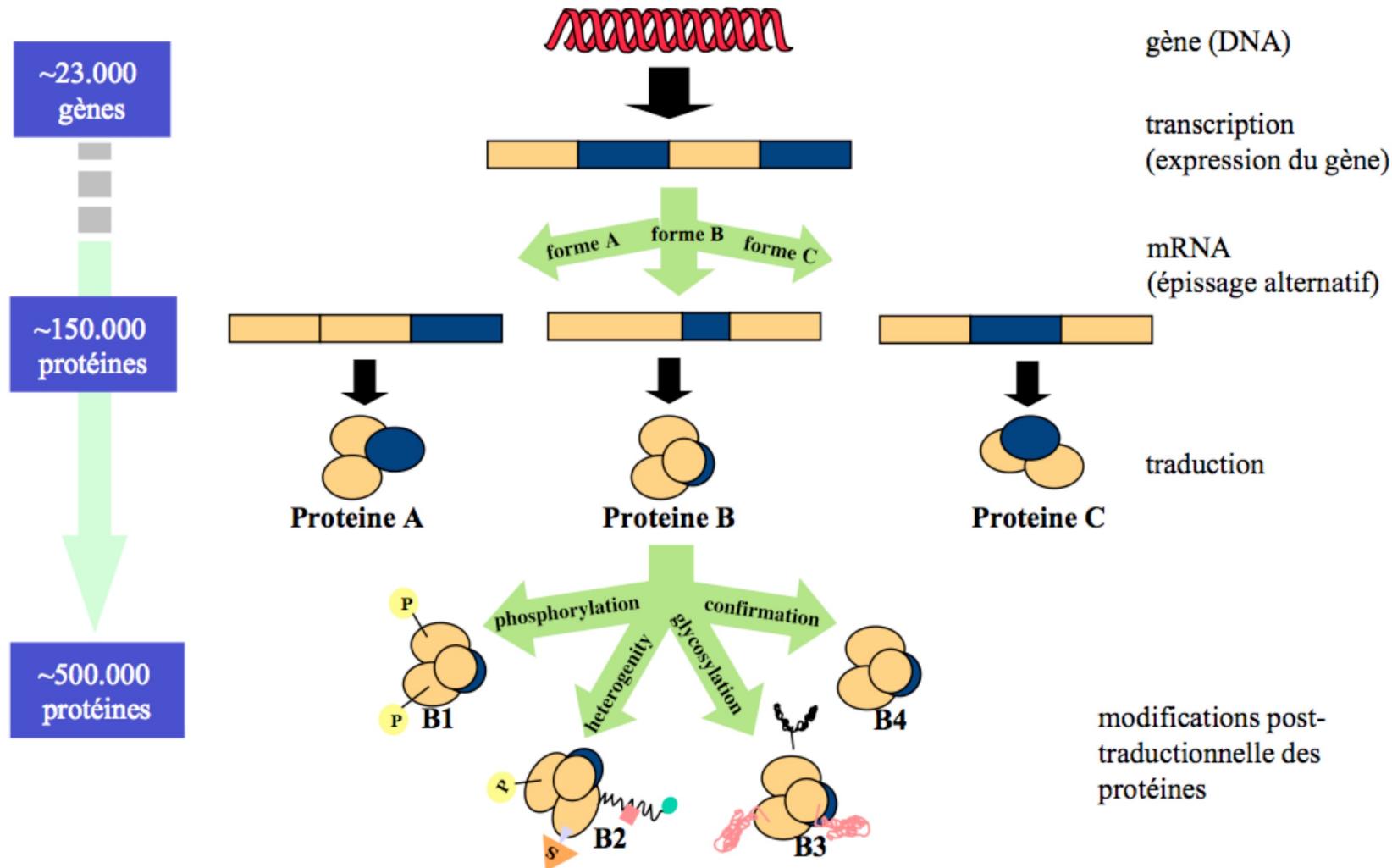
# Dynamique de la transcription

Dogme central:



# Modifications Post-traductionnelles

Contexte:



# Modifications Post-traductionnelles

Contexte:

**Locus: AT2G47240**

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**Representative Gene Model** [AT2G47240.1](#)

**Gene Model Type** protein\_coding

**Other names:** CER8, ECERIFERUM 8, LACS1, LONG-CHAIN ACYL-COA SYNTHASE 1

**Description** Encodes an acyl-CoA synthetase that acts on long-chain and very-long-chain fatty acids, involved in cuticular wax and cutin biosynthesis. The mRNA is cell-to-cell mobile.

**Other Gene Models** [AT2G47240.2](#) [AT2G47240.4](#) [AT2G47240.3](#)  
(splice variant) (splice variant) (splice variant)

[Center on AT2G47240](#) | [Full-screen view](#)

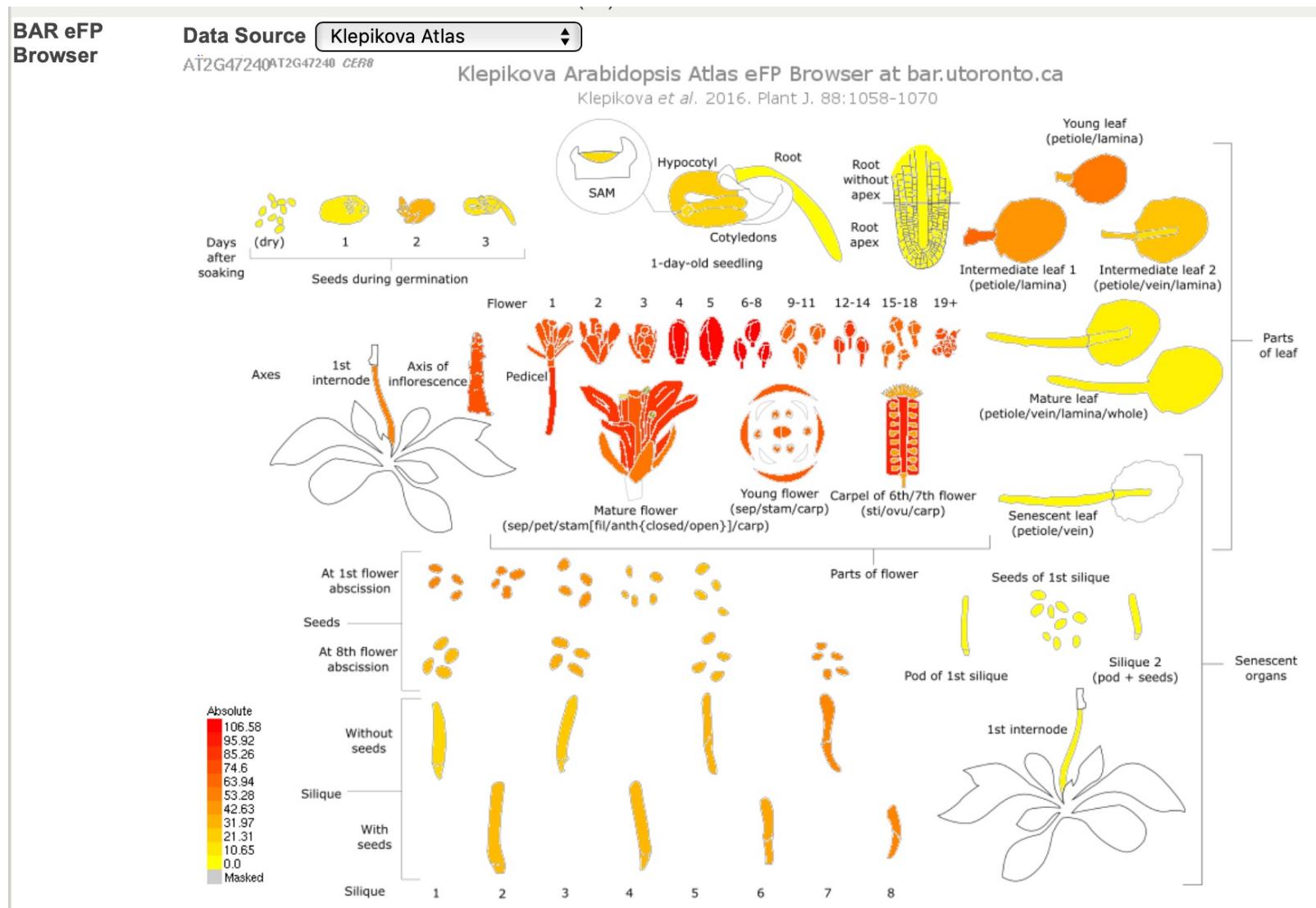
**Map Detail Image**

**Annotations**

category	relationship type	keyword
GO Biological Process	acts upstream of or within	cutin biosynthetic process, wax biosynthetic process
GO Biological Process	involved in	cutin biosynthetic process, fatty acid metabolic process, wax biosynthetic process

# Modifications Post-traductionnelles

Contexte:

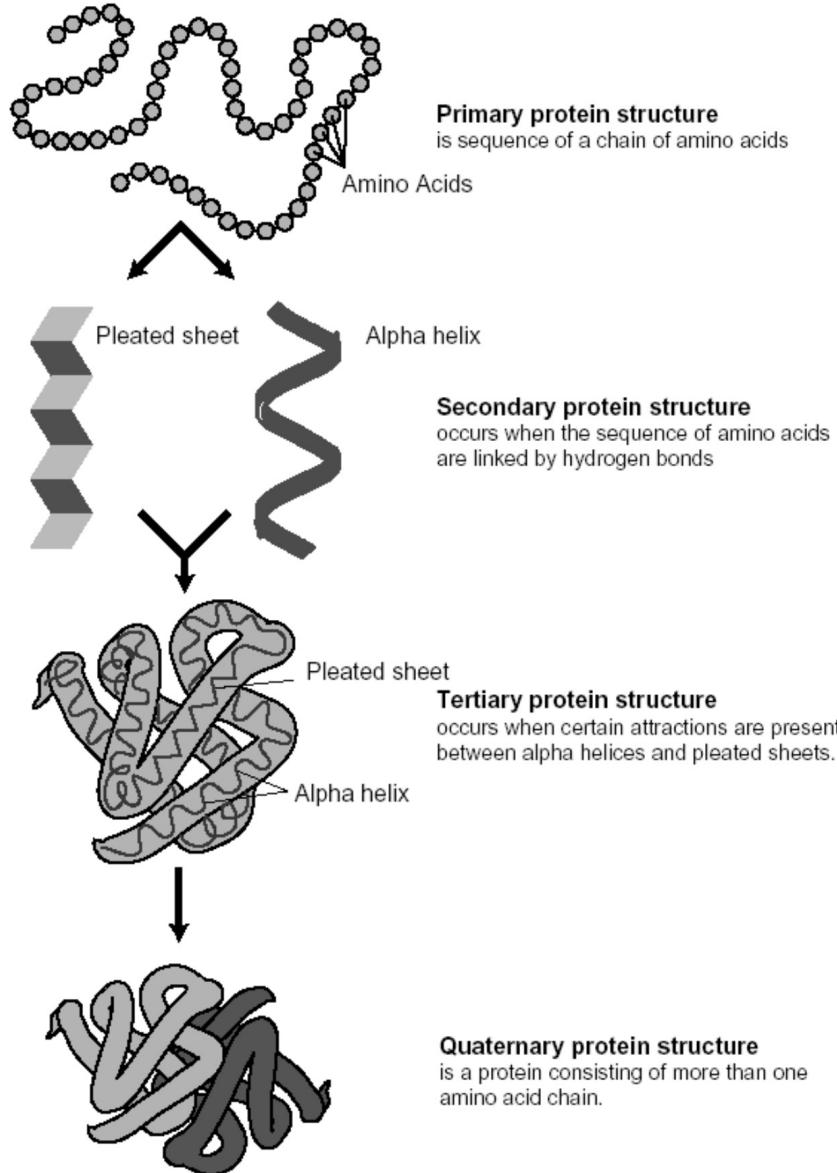


# Modifications Post-traductionnelles

Contexte:

External IDs <small>?</small>	UniProtKB O22898-1	GenPept 15226536	Similar Proteins in Genbank NCBI BLink		
Properties	Calculated MW <small>?</small> 74597.4	Calculated PI <small>?</small> 6.3	Length (aa) <small>?</small> 660		
Domains <small>?</small>	Database	Structural Class Type <small>?</small>	Accession	INTERPRO	Position
GENE3D	SSF56801		3.40.50.12780	null:IPR042099	27-367
	SUPERFAMILY				36-653
	HHMPFAM		PF00501	AMP-dep_Synth/Lig:IPR000873	50-522
	CDD		CD05927		72-653
	PATTERNSCAN		PS00455	AMP-binding_CS:IPR020845	225-236
	GENE3D		3.40.50.12780	null:IPR042099	368-518
	SEG		SEG		414-427
Sequence	<small>Send to BLAST</small>				
	1 MKSFAAKVEE GVKGIDGKPS VGPVYRNLLS EKGFPPIIDSE ITTAWDIFSK 51 SVEKFPDNMM LGWRRIVDEK VGPYMWKTYK EVYEEVLQIG SALRAAGAEP 101 GSRVGIYGWN CPQWIIAMEA CAAHTLICVP LYDTLGSGAV DYIVEHAEID 151 FVFVQDTKIK GLLEPDCKCA KRLKAIVSFT NVSDELSHKA SEIGVKTYSW 201 IDFLHMGREK PEDTNPPKAF NICTIMYTSG TSGDPKGVVV THQAVATFVV 251 GMDLYMDQFE DKMTHDDVYL SFLPLAHILD RMNEEYFFRK GASVGYYHGN 301 LNVLRDDIQE LKPTYLAGVP RVFERIHEGI QKALQELNPR RRFIFNALYK 351 HKLAWLNRGY SHSKASPMAD FIAFRKIRDK LGGRIRLLVS GGAPLSPEIE 401 EFLRVTCCCF VVQGYGLTET LGGTALGFDP EMCMLGTVGI PAVYNEIRLE 451 EVSEMGYDPL GENPAGEICI RGQCMFSGYY KNPELTEEVN KDGWFHTGDI 501 GEILPNGVLK IIDRKKNLIK LSQGEYVALE HLENIFGQNS VVQDIWVYGD 551 SFKSMVLAVV VPNPETVNRW AKDLGFTKPF EELCSFPELK EHIISELKST 601 AEKNKLKRKE YIKAVTVETK PFDVERDLVT ATLKNRRNNL LKYYQVQIDE 651 MYRKLASKKI				
Associated Genes	Gene Model <small>?</small>	Locus <small>?</small>	seqviewer link		
	AT2G47240.1	AT2G47240	Sequence Viewer		

# Modifications Post-traductionnelles



Repliement

Fonctionnalité de la macromolécule

# Modifications Post-traductionnelles

Locus: AT2G47240

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Representative Gene Model [AT2G47240.1](#)

Gene Model Type protein\_coding

Other names: CER8, ECERIFERUM 8, LACS1, LONG-CHAIN ACYL-COA SYNTHASE 1

## Structure<sup>i</sup>

### Model Confidence:

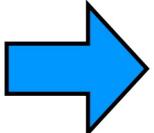
- █ Very high (pLDDT > 90)
- █ Confident (90 > pLDDT > 70)
- █ Low (70 > pLDDT > 50)
- █ Very low (pLDDT < 50)

AlphaFold produces a per-residue confidence score (pLDDT) between 0 and 100. Some regions with low pLDDT may be unstructured in isolation.



## Modifications Post-traductionnelles

- **Phosphorylation** : activation and inactivation of enzymes
- **Acetylation** : protein stability, used in histones
- **Methylation** : regulation of gene expression
- **Glycosylation** : cell–cell recognition, signaling
- **GPI anchor** : membrane tethering
- **Hydroxyproline** : protein stability, ligand interactions
- **Sulfation** : protein–protein and ligand interactions
- **Disulfide-bond formation** : protein stability
- **Deamidation** : protein–protein and ligand interactions
- **Ubiquitination** : destruction signal
- **Nitration of tyrosine** : inflammation



**Chaque profile de modifications post-traductionnelles correspond à une protéine.**

# THE END

