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Chromatin Dynamics in Plants: At the Crossroad of Genetics and Epigenetics

Cristel Carles

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Chromatin Dynamics in Plants: At the Crossroad of Genetics and Epigenetics



Christel CARLES

Professor @ Grenoble Alpes University



Department of Biology & Chemistry
Chromatin Dynamics & Developmental Transitions team
Cell & Plant Physiology Lab



My curriculum in brief

1. PhD
ATER



Plant Genome and Development Laboratory (1997-2001)

- Embryogenesis and seed maturation



Bies et al, *J. Exp. Botany* 1998
Delseny et al, *J. Plant Physiology* 2001
Carles et al, *Plant Journal* 2002

2. Post-doc



Plant Gene Expression Center, UC Berkeley, USA (2001-2008)

- Post-embryonic development ... from genetics to epigenetics ...



Carles et al, *Genetics* 2004 ; *Development* 2005
Williams¹, Carles¹ et al, *PNAS* 2005
Carles & Fletcher, *Genes & Development* 2009
Monfared et al, *Mol Plant* 2013

3. Researcher



Institute for Research and Development (2008-2009)

- Viruses, reproductive development and epigenetics

Rodor et al, *Plant J.* 2011

4. Assoc. Professor
CNRS Chair



Cell and Plant Physiology Laboratory (2010 -)

- Chromatin dynamics and development



Smaczniak et al, *PNAS* 2012
Mandel et al, *Development* 2014, 2016
Engelhorn et al, *Annals Botany* 2014 *C
O'Maoiléidigh et al, *Plant J* 2015

5. Full Professor
Team Leader



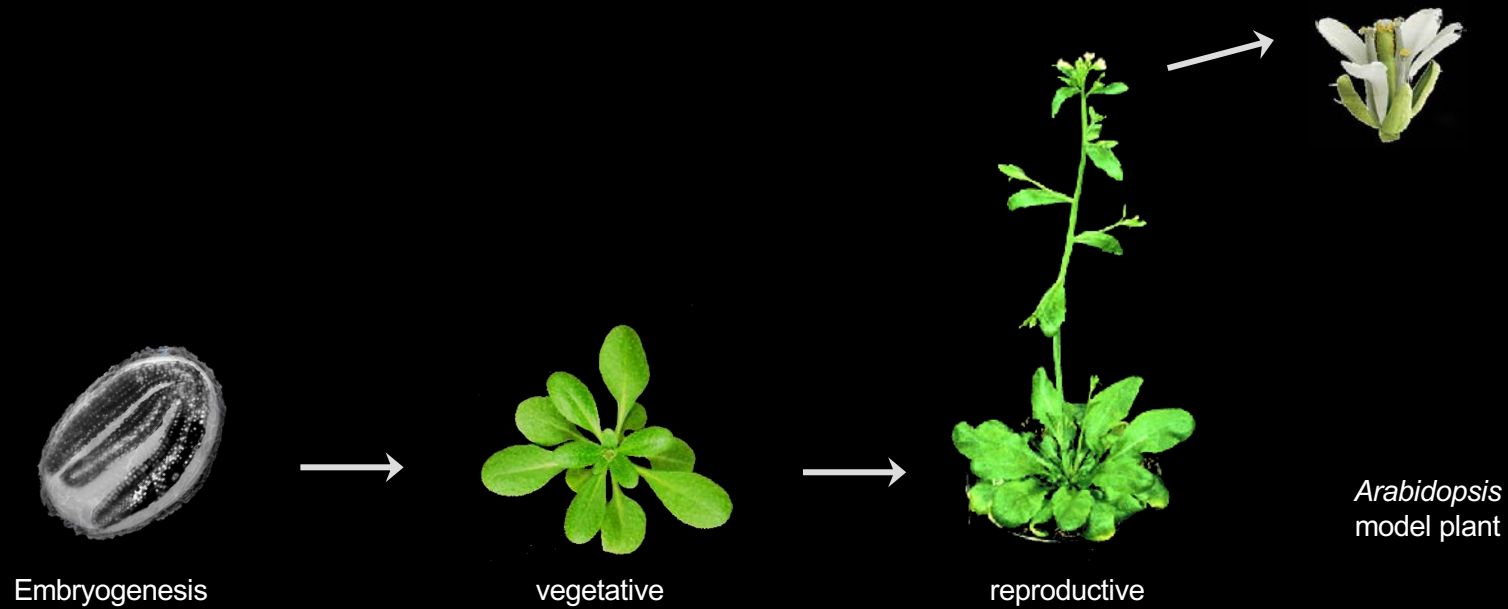
ChromDev Team (Chromatin Dynamics & Developmental Transitions)



Moreau et al, *Development* 2016 *C
Engelhorn et al, *Epigenomes* 2017 *C
Vachon et al, *J. Exp. Botany* 2018 *C
Yan et al, *Nature Plants* 2018; *Nature Com* 2019
Thouly et al, *Genes* 2020; Fal et al, *IJMS* 2021 *C
Fal et al, *New Phytol* 2023 *C; Fal & Carles, *MIMB* 2024 *C; Geshkovski et al, *MIMB* 2024 *C



My curriculum in brief



Guiding thread : The molecular basis of development [plant models]



OUTLINE

for our time together today

Introduction to EPIGENETICS

- General concepts and definitions
- The actors
- Zoom on Polycomb and trithorax complexes: key regulators of developmental genes

QUIZZ (on what you heard before)

Presentation of MY RESEARCH

Why it is exciting to study epigenetics & chromatin dynamics in plants

- The team
- The projects

Presentation of the PLANTA-international Master

Understanding how the genes that shape life are regulated



100% identical genes

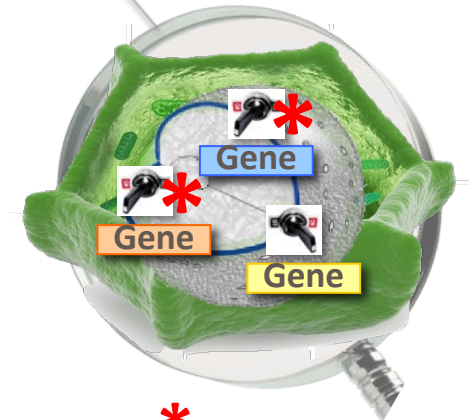
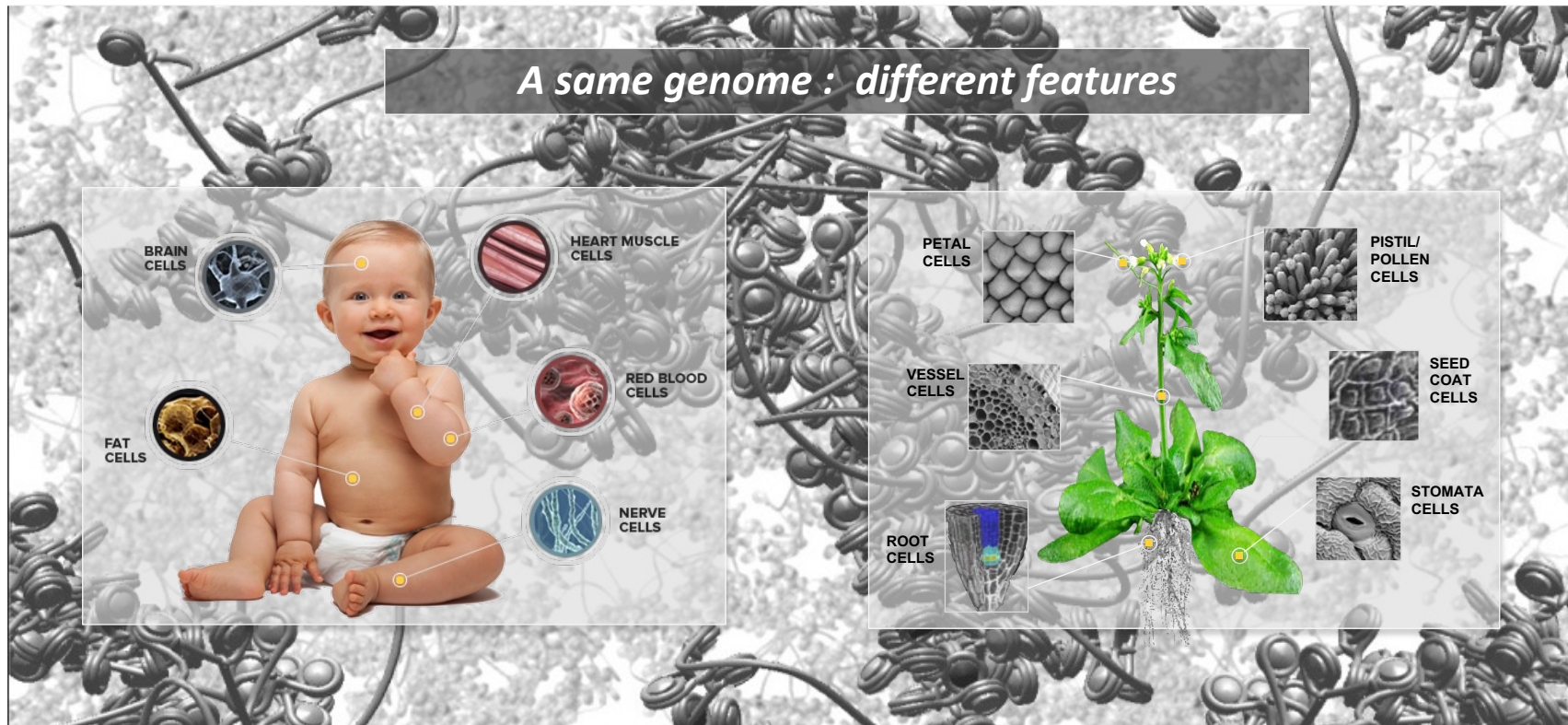
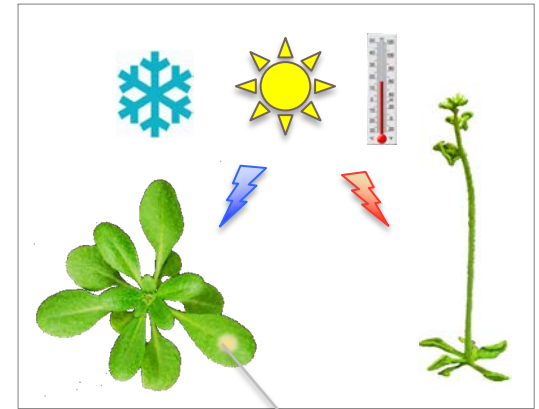


Epigenetics



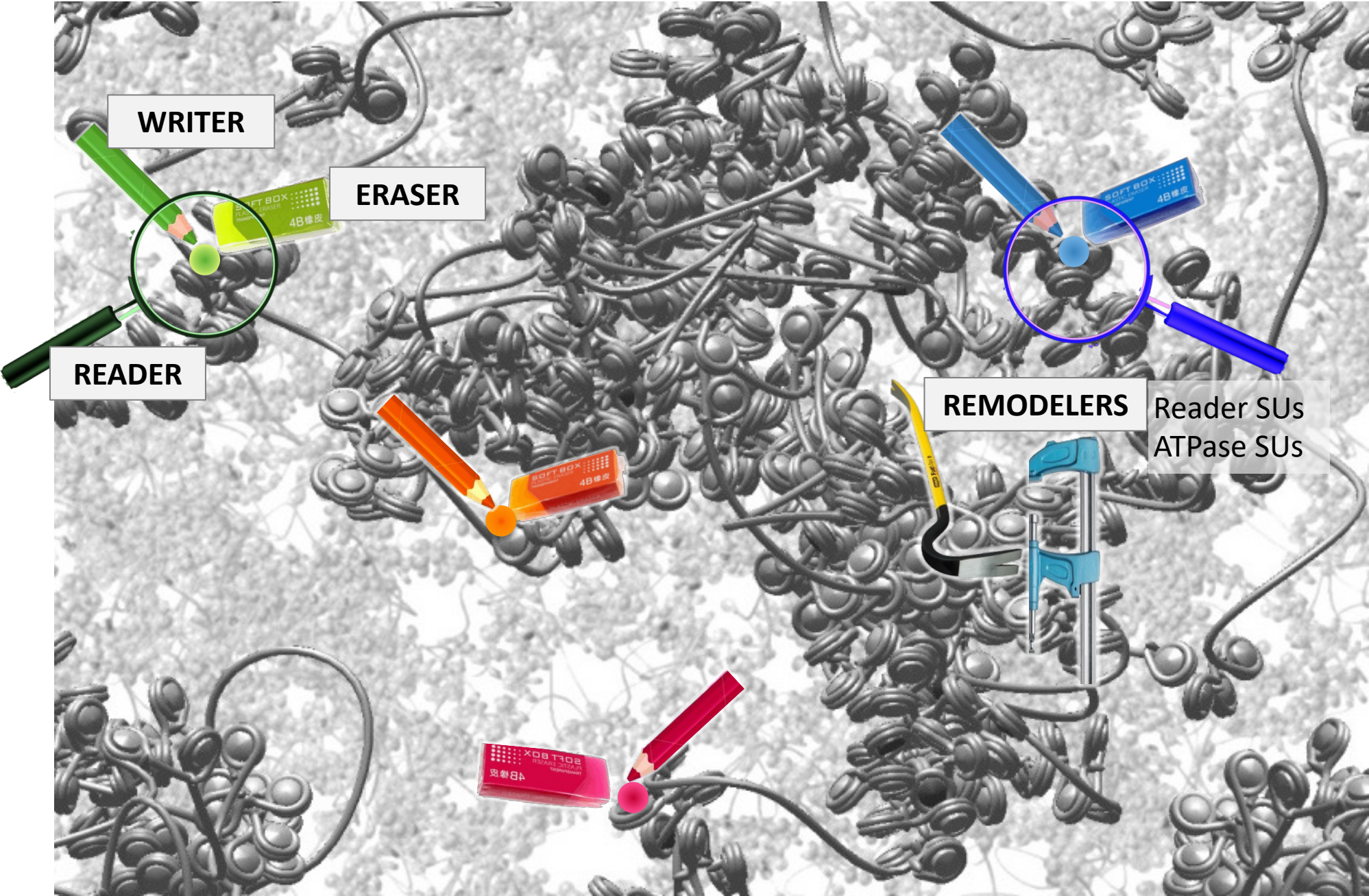
...

Different individuals

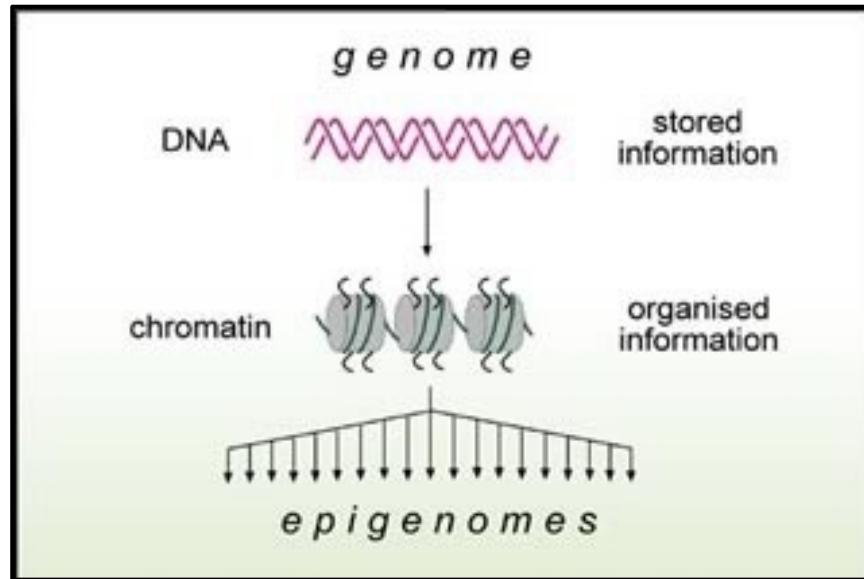


* epigenetic marks

Some key epigenetic actors



One genome, several epigenomes



Adapted from Allis *et al*, Epigenetics 2007, CSHL

Genetic alterations

- Mutations
- Changes to DNA sequence
- Not reversible

Epigenetic alterations

- **Heritable** and stable
- Changes in gene expression
- **Potentially reversible**

« The difference between **genetics** and **epigenetics** can probably be compared to the difference between **writing** and **reading** a book. Epigenetics would allow **different interpretations of a fixed template** and result in different read-outs, dependent upon the variable conditions under which the template is interrogated. »

Jonathan WEITZMAN, Université Paris Diderot

Another analogy: « **if the genome is the hardware, then the epigenome is the software** »

➔ Epigenetic regulation contributes to the selective readout of the genome



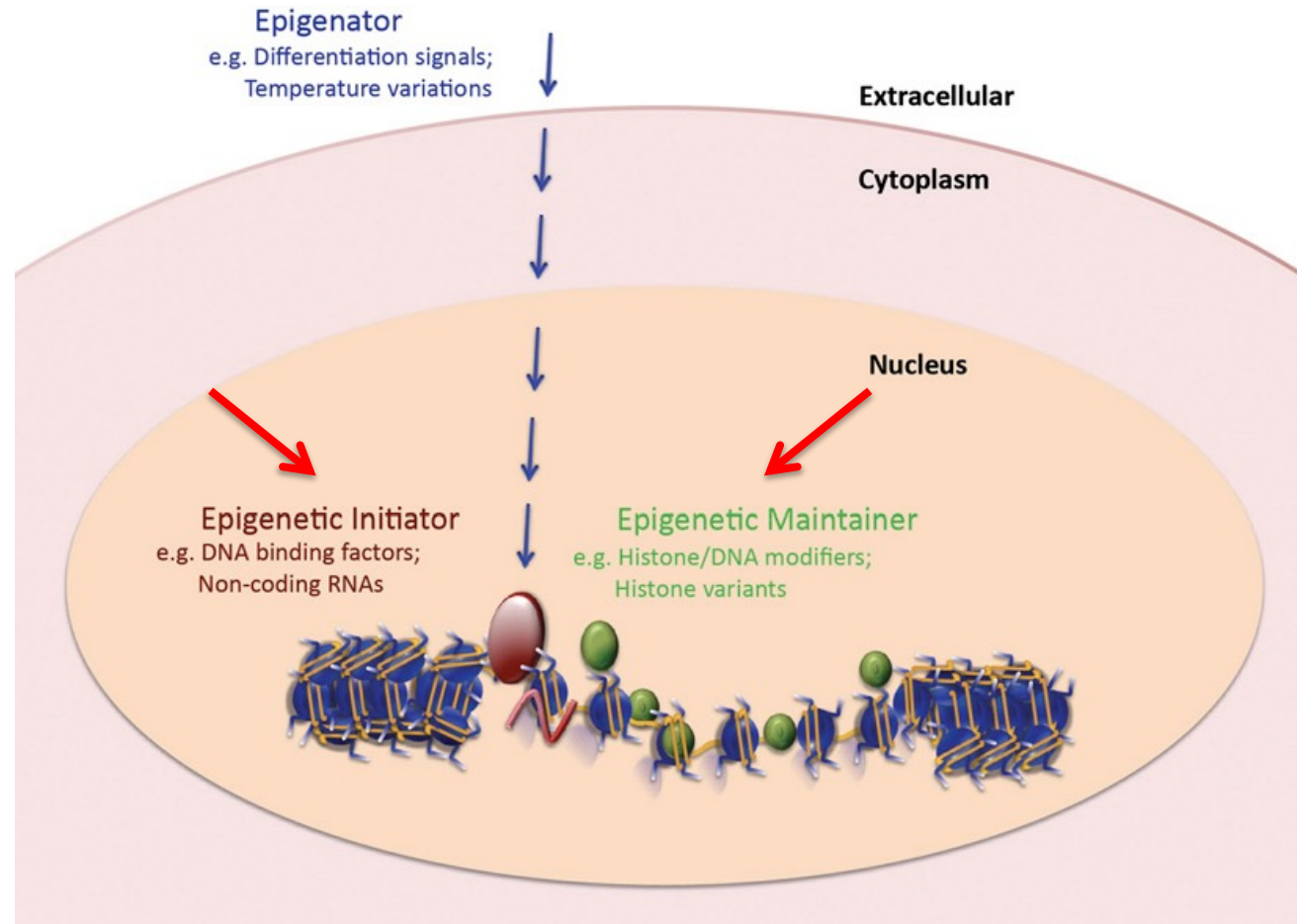
Epigenetics : the study of heritable changes in genome function that occur without a change in DNA sequence.

2004-2009 Epigenome Network of Excellence

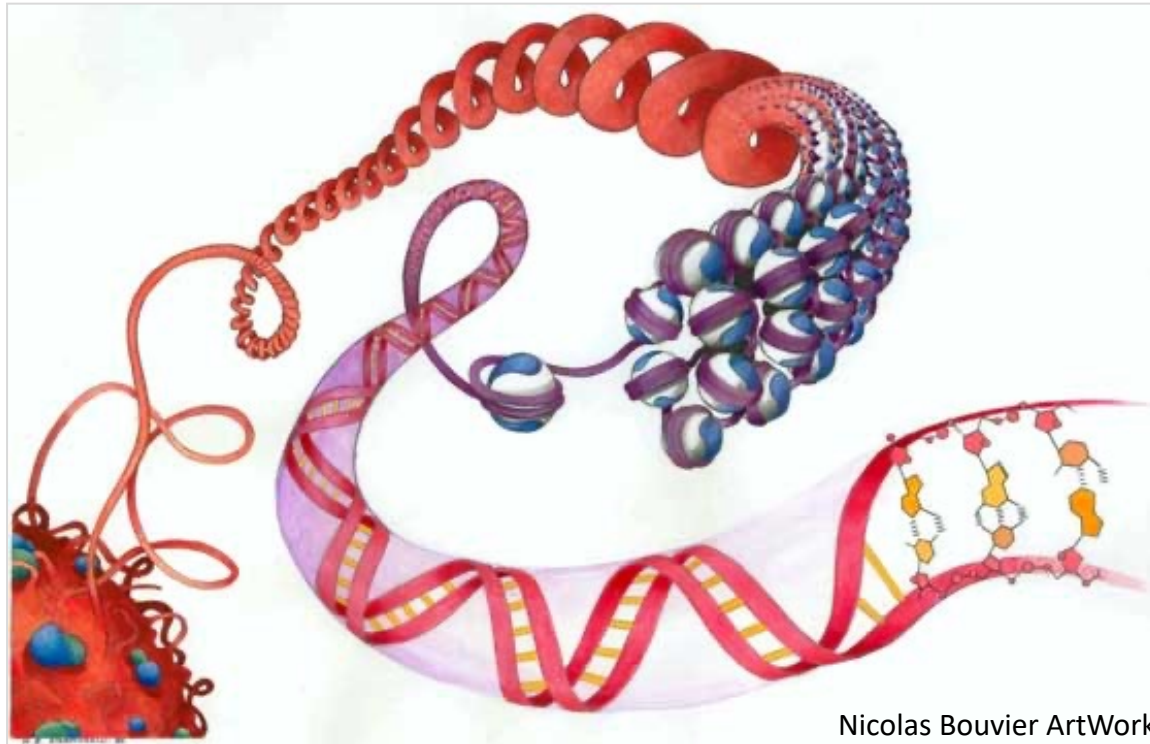
PERSPECTIVE

An operational definition of epigenetics

Shelley L. Berger,^{1,5} Tony Kouzarides,^{2,5} Ramin Shiekhattar,^{3,5} and Ali Shilatifard^{4,5}



Chromatin structure



Nucleus organization

Packaging of DNA

Nucleosomes

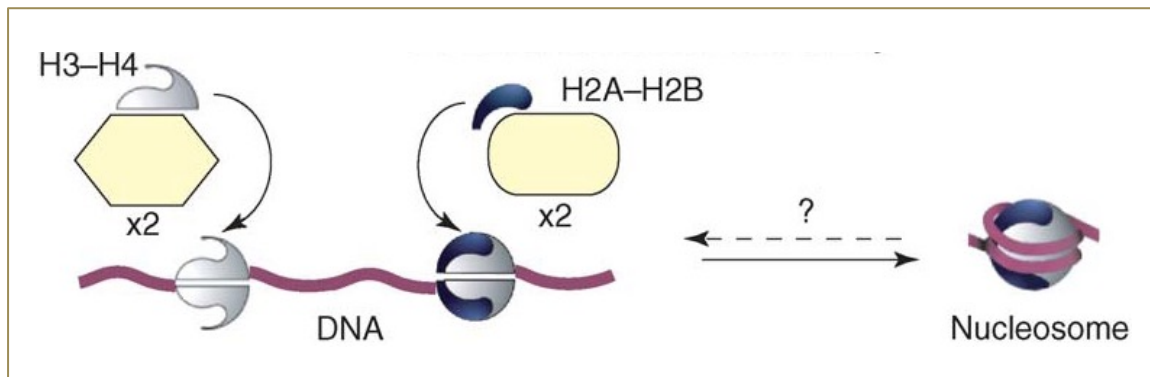
Assembly
Position & Density

Histones

Modifications
variants

DNA

methylation



A nucleosome = 8 histones
[2x (2A, 2B, 3, 4)] wrapped
with 147 bp of DNA (2 loops)

The « problems »

1- How does all that DNA get into the tiny nucleus?

Nearly 2m of human DNA into a nucleus that averages just 5 μ

« Imagine trying to stuff about 10,000 miles of spaghetti inside a basketball. Then, if that was not difficult enough, attempt to find a unique one inch segment of pasta from the middle of this mess, or try to duplicate, untangle and separate individual strings to opposite ends. »

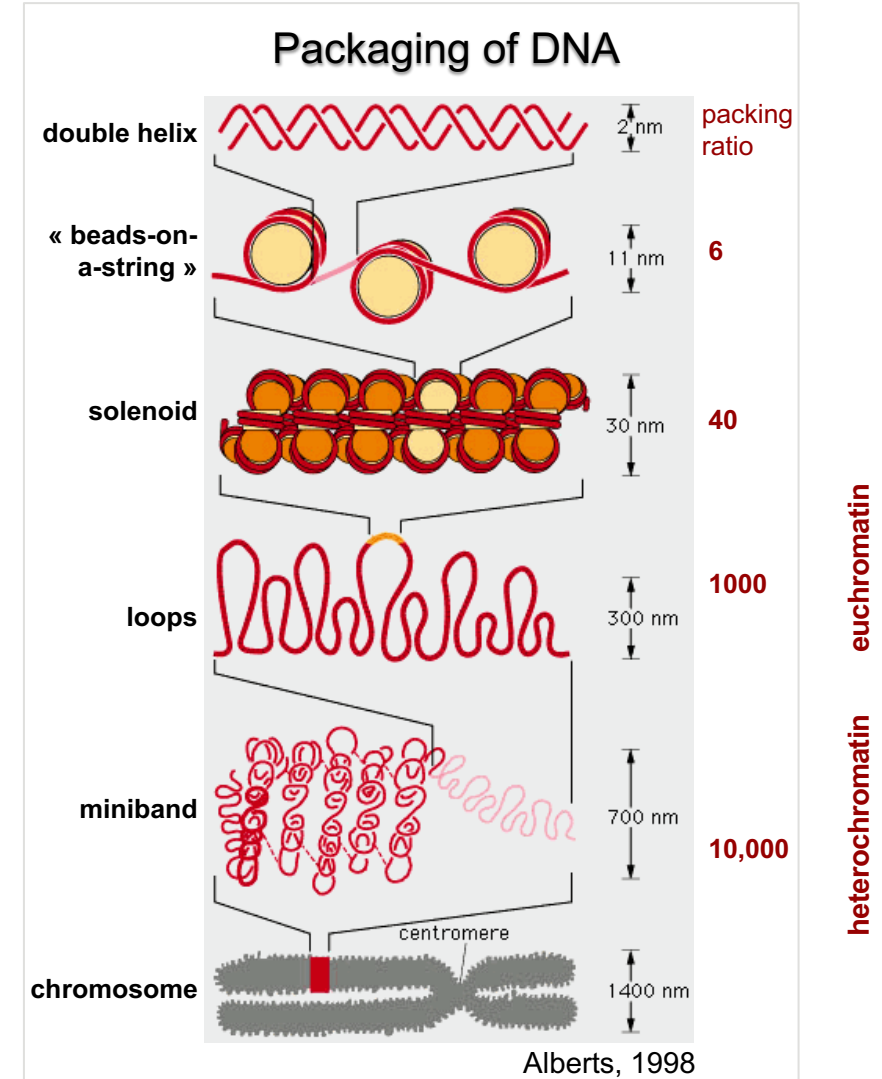
Peterson & Laniel, Curr Biol 2004

2- How can transcription factors access DNA that is packaged into the nucleus?

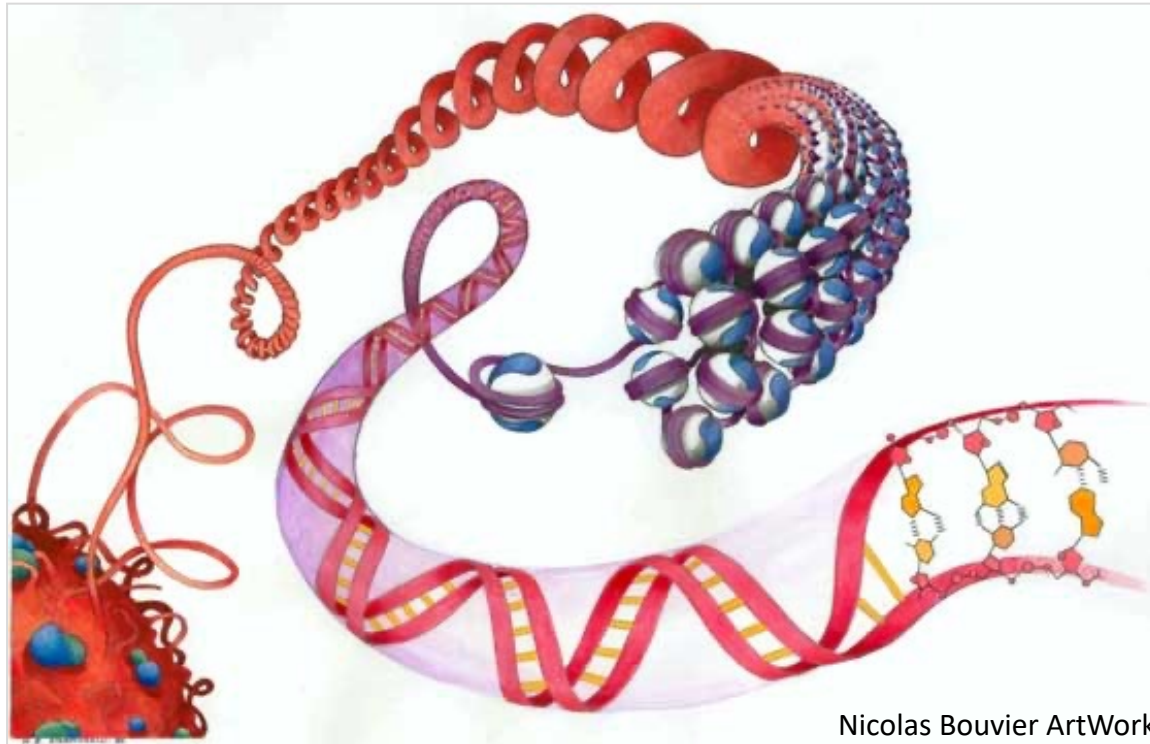
The solution: Assembly of eukaryotic genome into **CHROMATIN**

⇒ solves the basic packaging problem

⇒ provides a dynamic platform controlling all DNA-mediated processes within the nucleus



Chromatin structure



Nucleus organization

Nucleosomes

Assembly

Position & Density

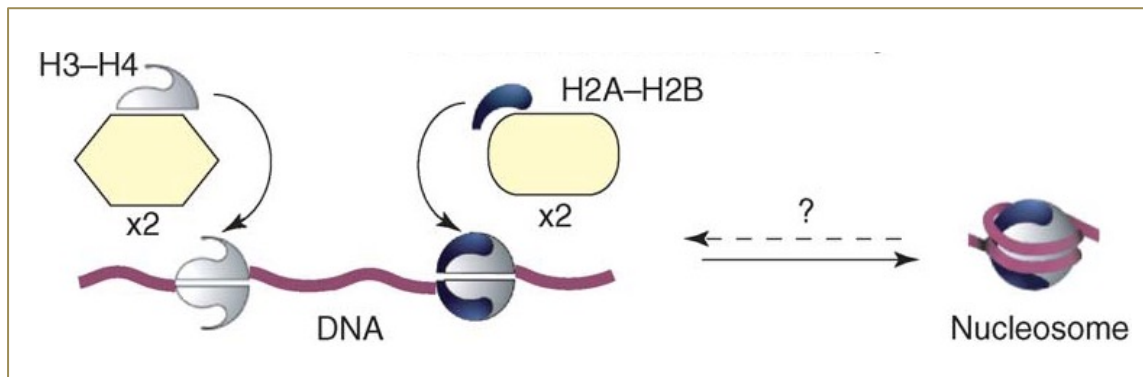
Histones

Modifications

variants

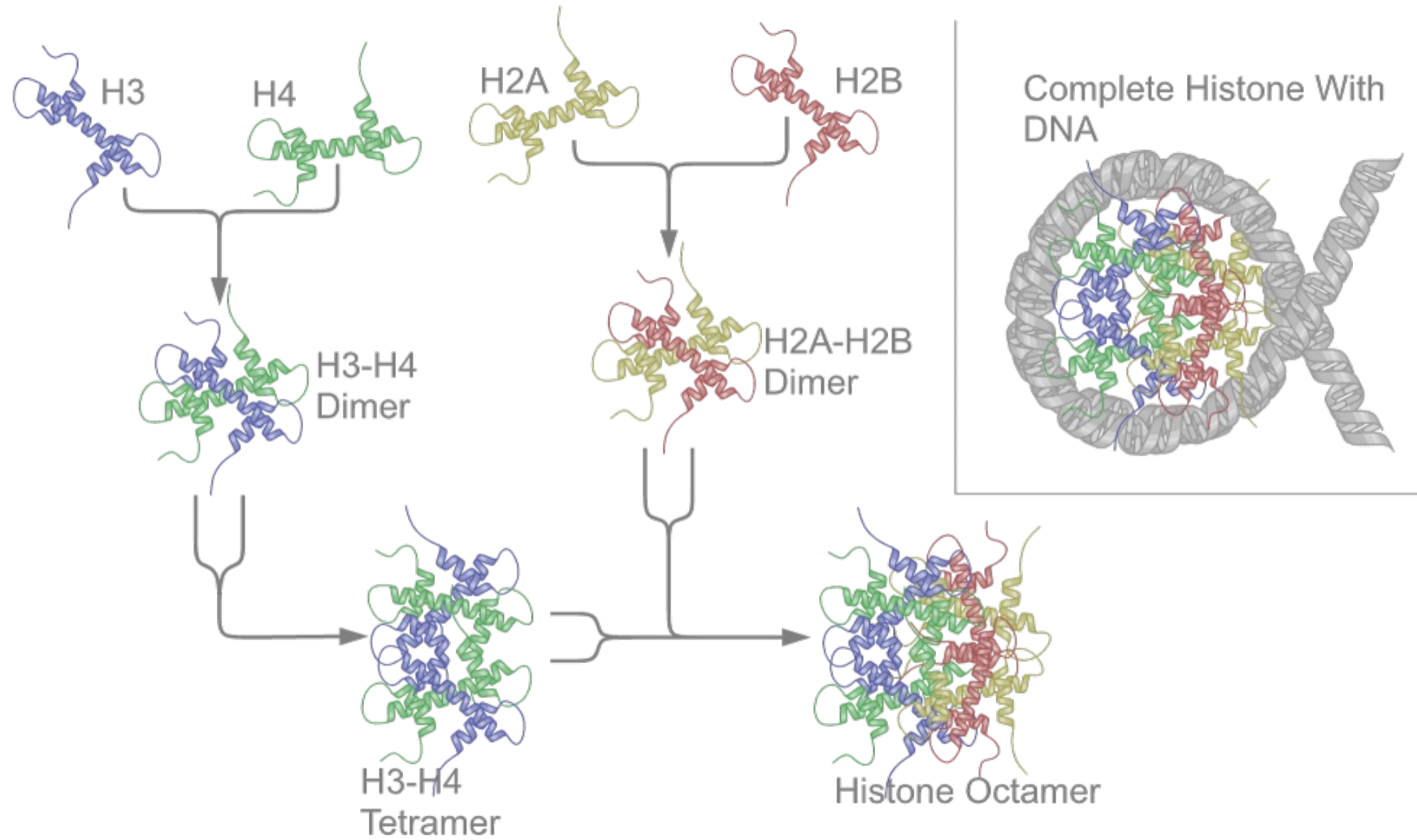
DNA

methylation

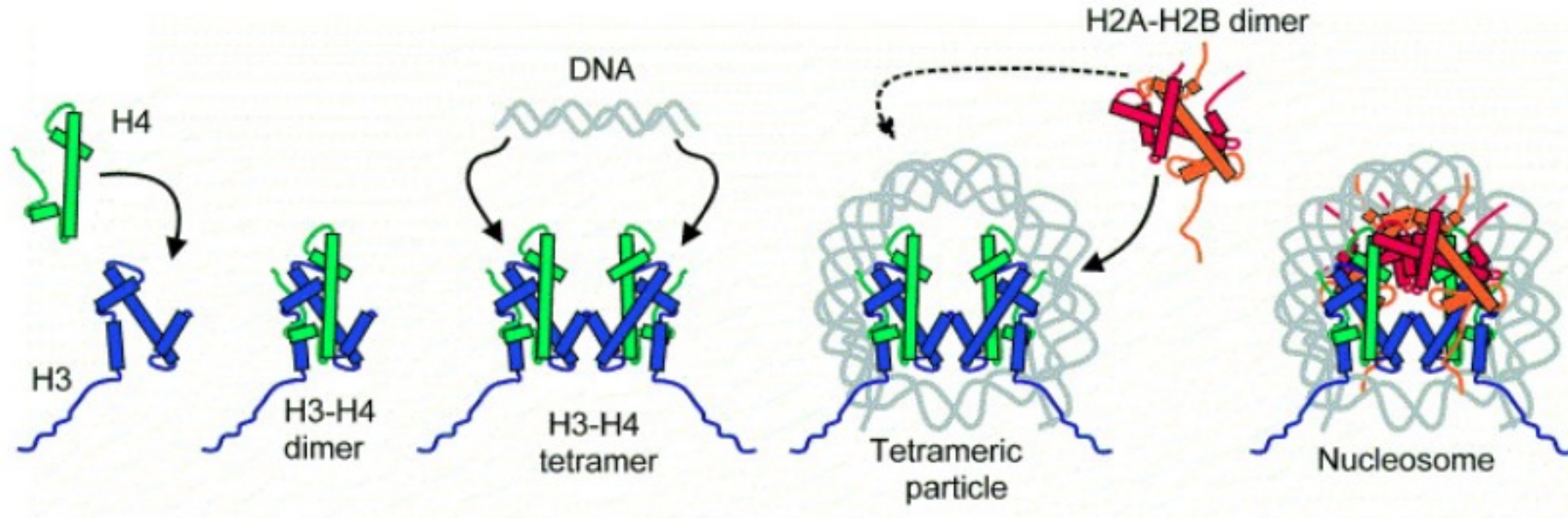


A nucleosome = 8 histones
[2x (2A, 2B, 3, 4)] wrapped
with 147 bp of DNA (2 loops)

Nucleosome assembly model



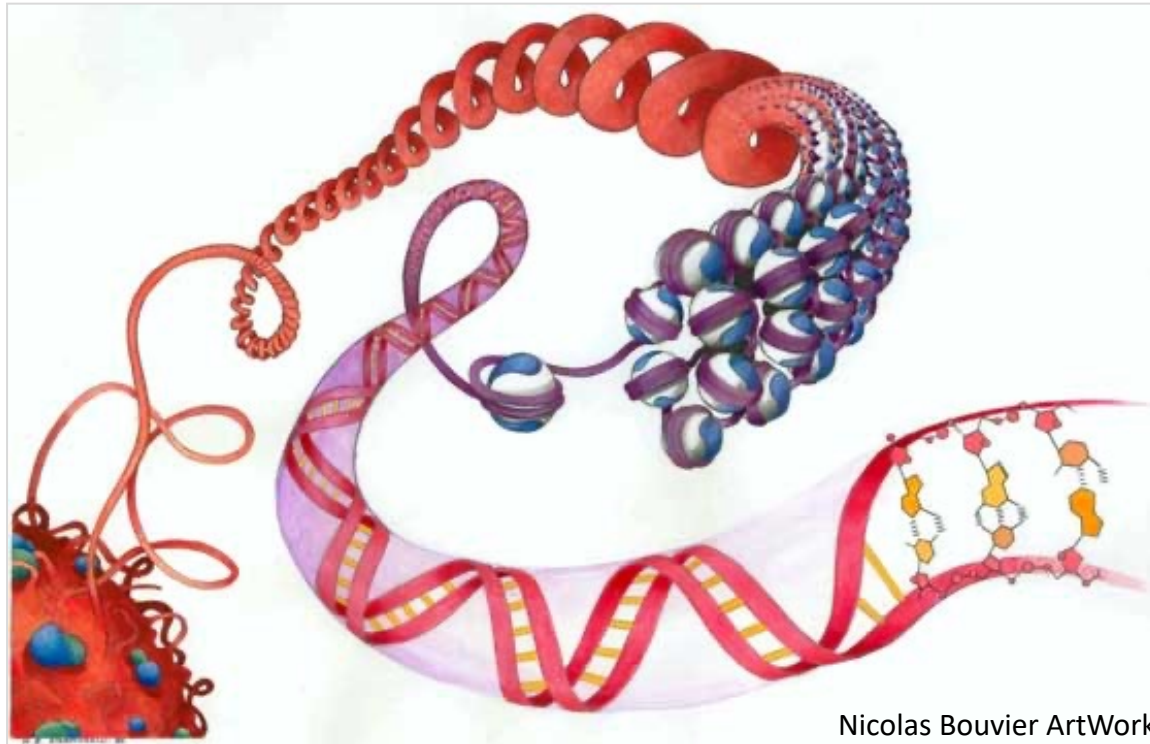
Mode of nucleosome assembly



Essential role of Histone chaperones

- **CAF-1** is a **replication-dependent** histone chaperone complex
- **HIR** histone chaperone complex is **replication-independent**
- ASF1 is actively involved in maintenance of chromatin states during DNA replication

Chromatin structure



Nucleus organization

Nucleosomes

Assembly

Position & Density

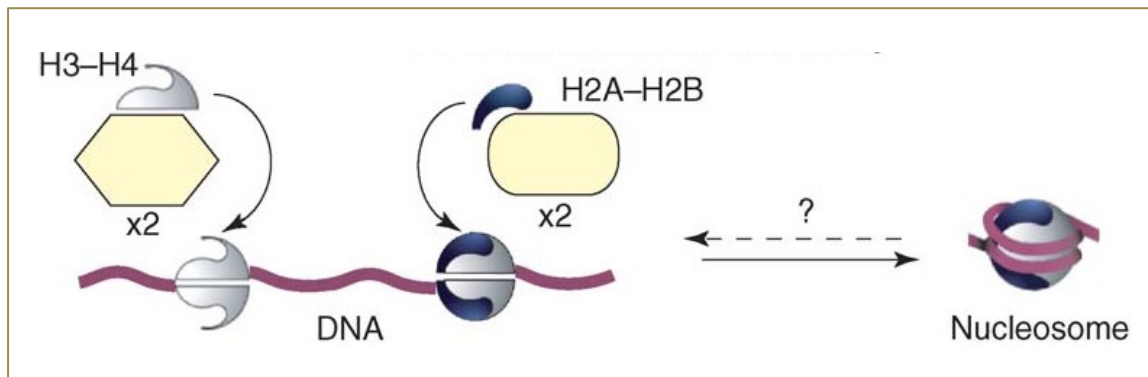
Histones

Modifications

Variants

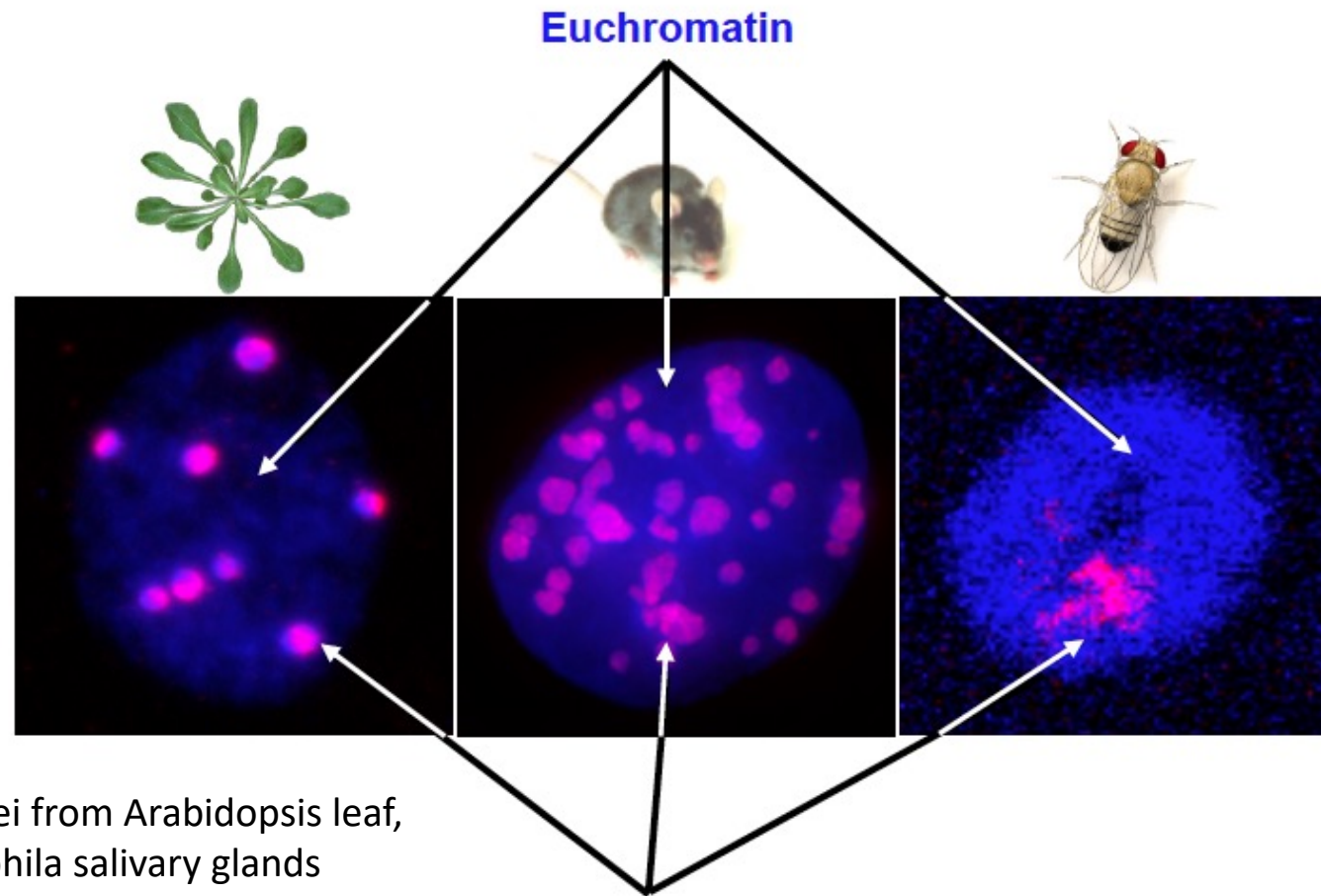
DNA

methylation



A nucleosome = 8 histones
[2x (2A, 2B, 3, 4)] wrapped
with 147 bp of DNA (2 loops)

Euchromatin and Heterochromatin define two distinct chromatin states in Eukaryotes

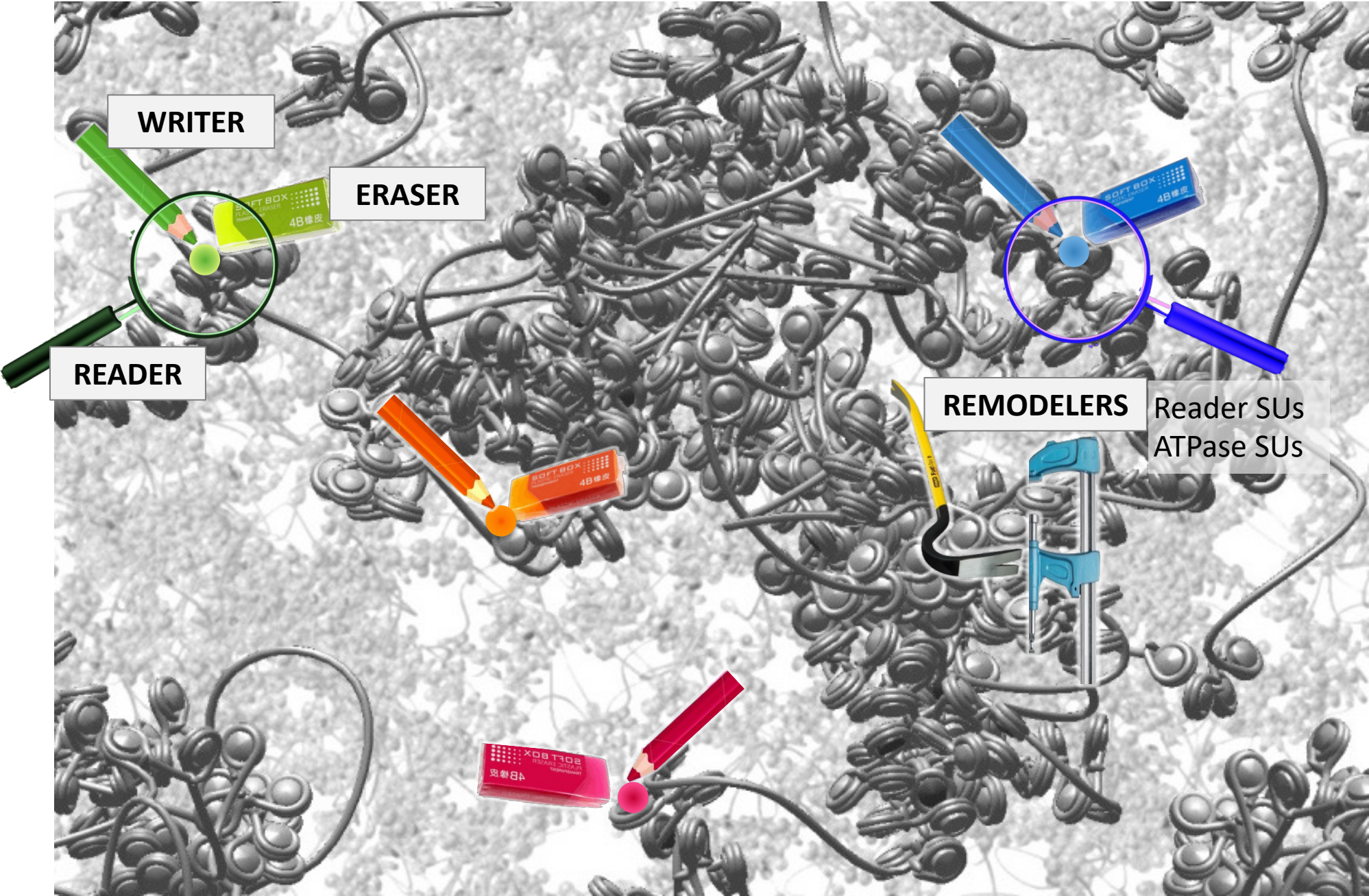


in blue : **DAPI** staining of nuclei from Arabidopsis leaf, mouse fibroblasts and Drosophila salivary glands

in pink : DNA fluorescence *in situ* hybridization of repetitive sequences

Heterochromatin remains condensed throughout the whole cell cycle, forms at repetitive sequences and transposable elements

Some key epigenetic actors



REMODELERS

Shared characteristics of chromatin remodeling complexes

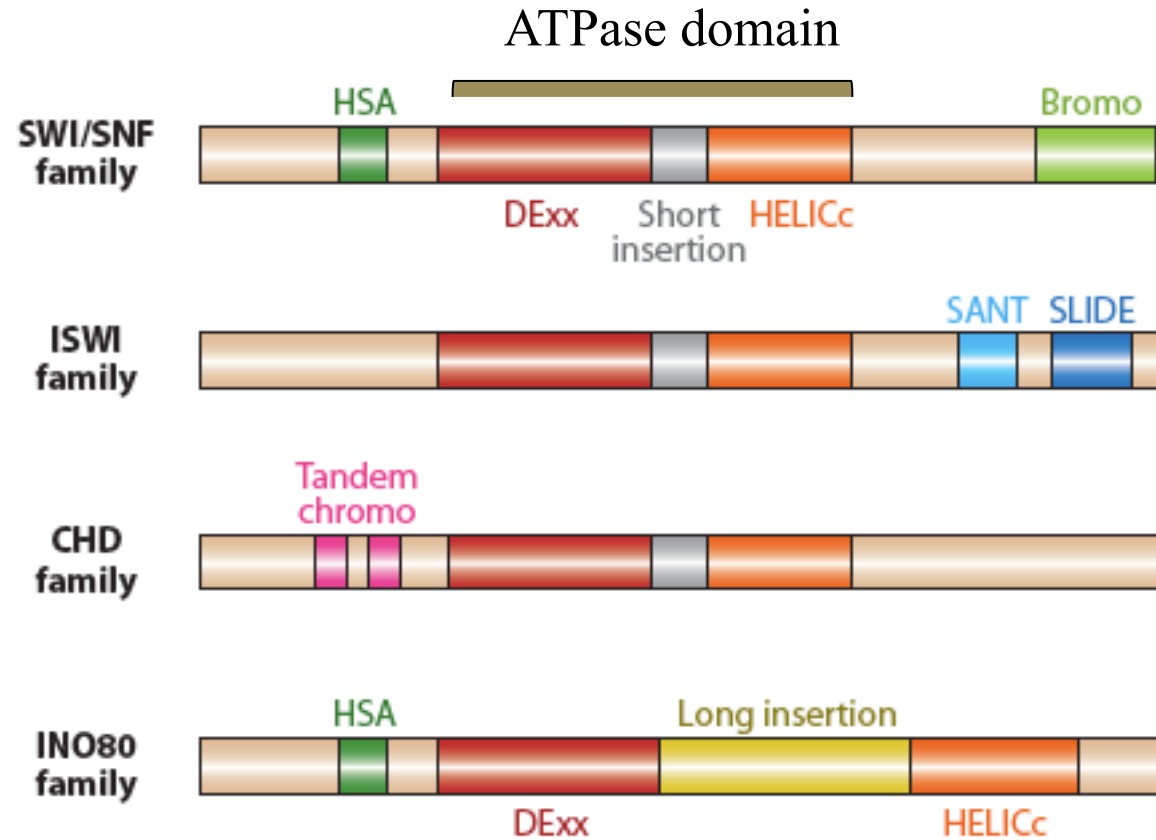
- bind nucleosomes
- are **DNA-dependent ATPases**
- **recognize histone modifications**
- ATPase activity can be regulated
- interact with other proteins

From Clapier and Cairns, Annu. Rev. Biochem. 2009

REMODELERS

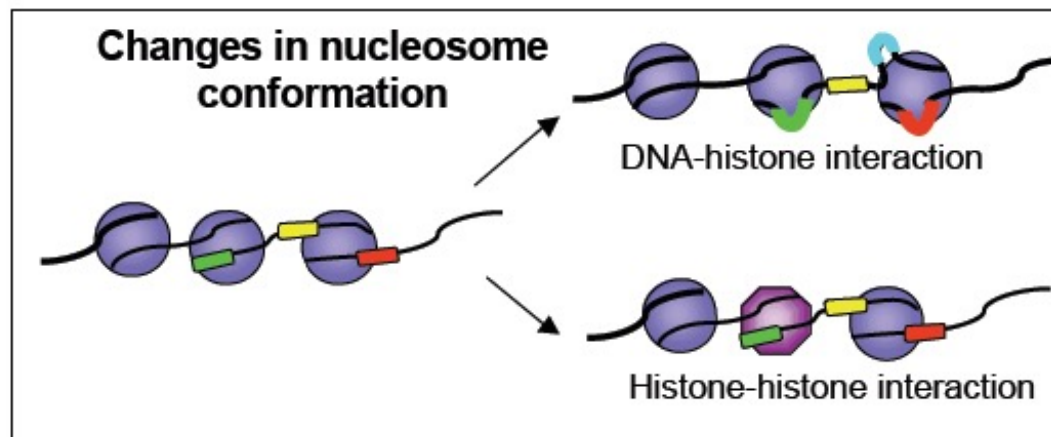
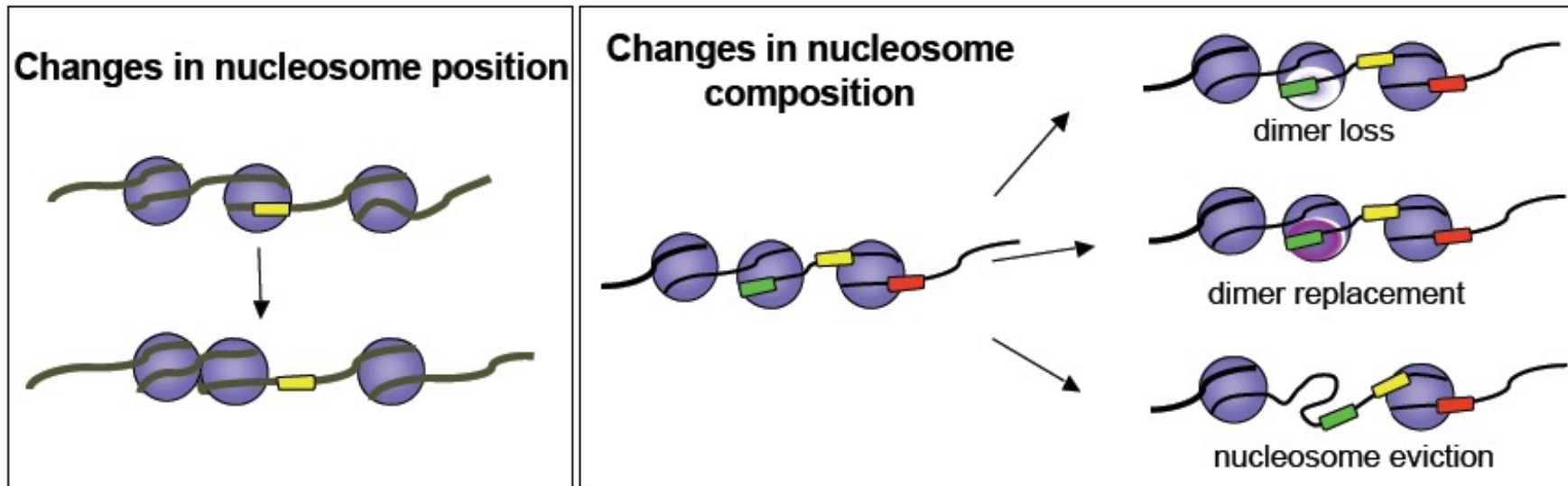


Families of chromatin remodeling ATPases



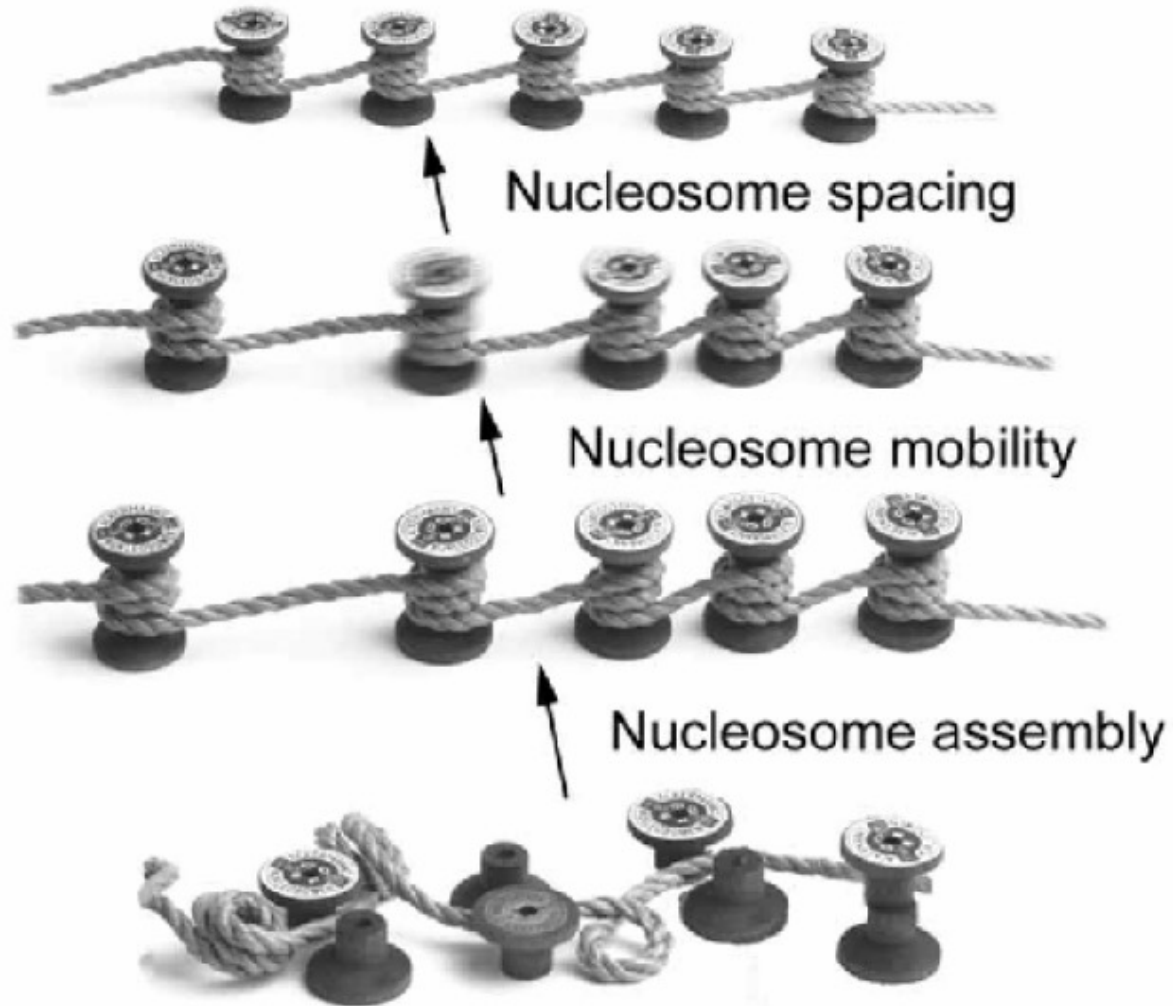
REMODELERS

Dynamic range of chromatin structure created by ATP-dependent chromatin remodeling



REMODELERS

Remodeling activities of ISWI subfamily



Langst, G. and P.B. Becker, *Nucleosome mobilization and positioning by ISWI-containing chromatin-remodeling factors*. J Cell Sci, 2001. **114**: p. 2561-8.

Chromatin structure



Nicolas Bouvier ArtWork

Nucleus organization

Nucleosomes

- Assembly
- Position & Density

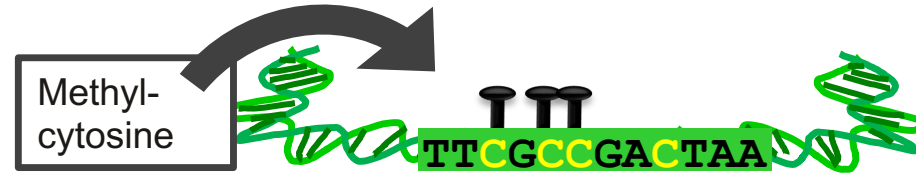
Histones

- Modifications
- Variants

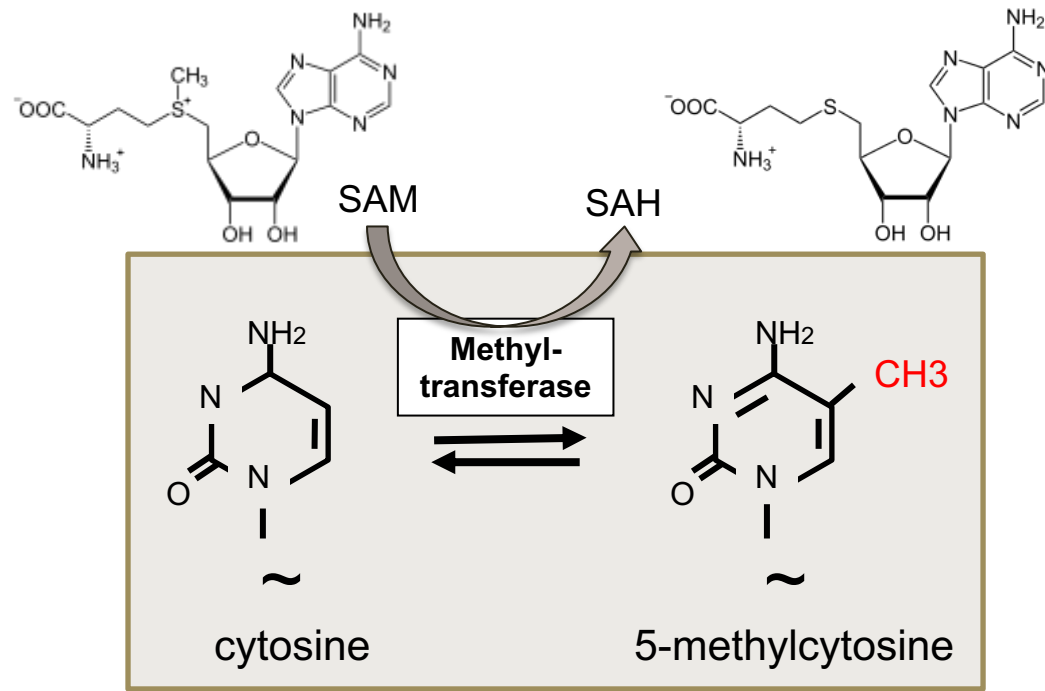
DNA

methylation

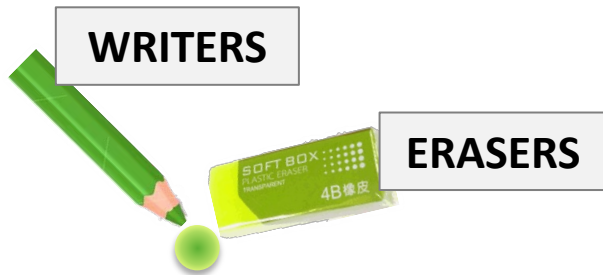
DNA methylation



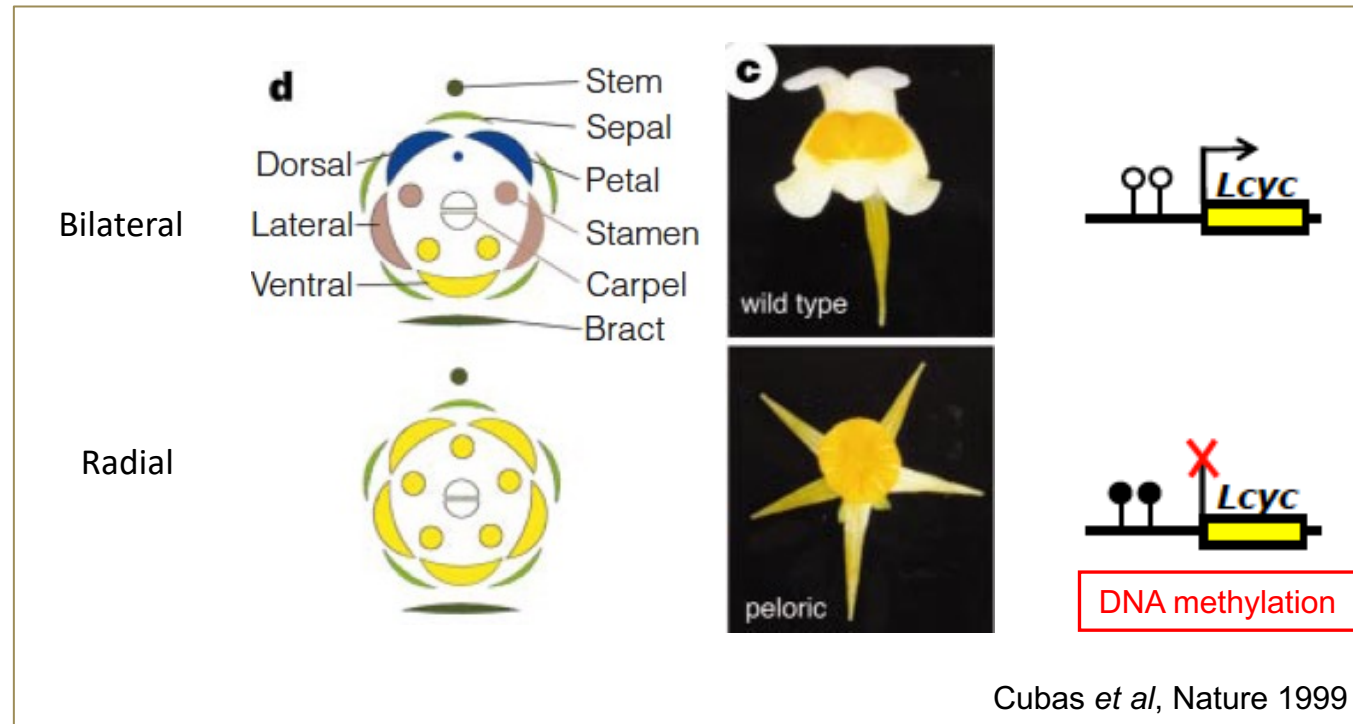
DNA can be covalently modified by cytosine methylation



SAM: S-adenosyl-L-methionine
SAH: S-Adenosyl-L-homocysteine



The peloric variant of *Linaria vulgaris* (toadflax): First recorded example of a spontaneous epimutation



DNA methylation

Methylation can affect Cytosines in different positions:

Pattern

propagated by

mCG

DNMT1 (animals) ; **MET1** (plants)

Plants also extensively methylate non-CGs:

mCNG

(N = any base)

CMT3

interacts with histone marks

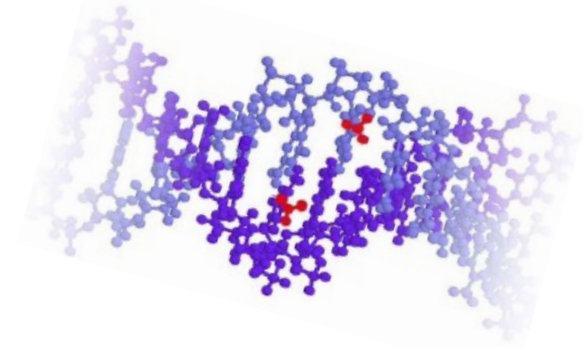
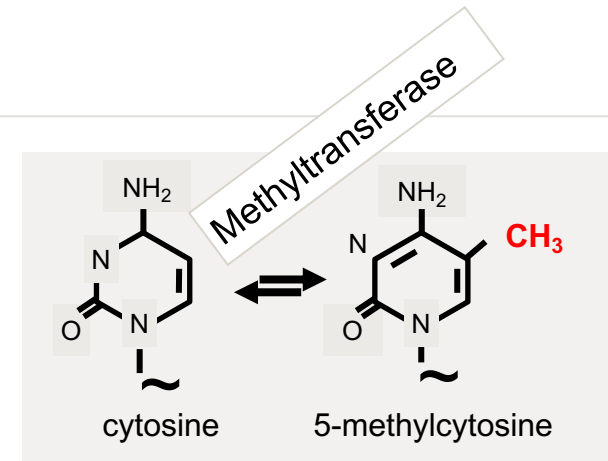
mCHH

(H = A, T, or C)

DRM1/2

preliminary targets repetitive elements

Asymmetric methylation maintained (and initiated) by information on **associated histones**, and **RNA-directed DNA Methylation**



CH₃ group exposed in major groove

represses transcription by

⇒ **blocking Transcription Factors** access

⇒ **recruiting proteins that compact chromatin**

Defects in DNA methylation trigger developmental defects and perturb stable trans-generational inheritance in plants

DNA methylation is **necessary to silence transposons**

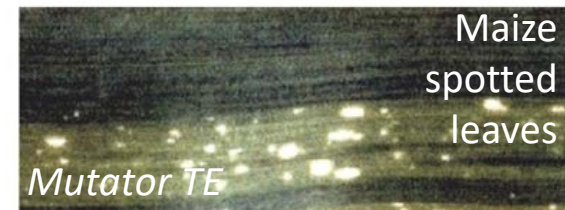
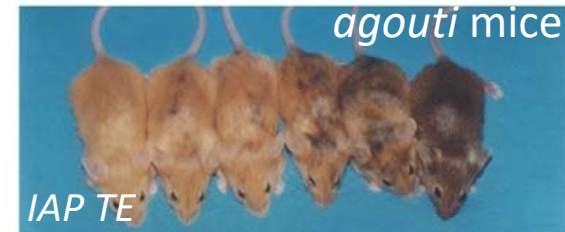
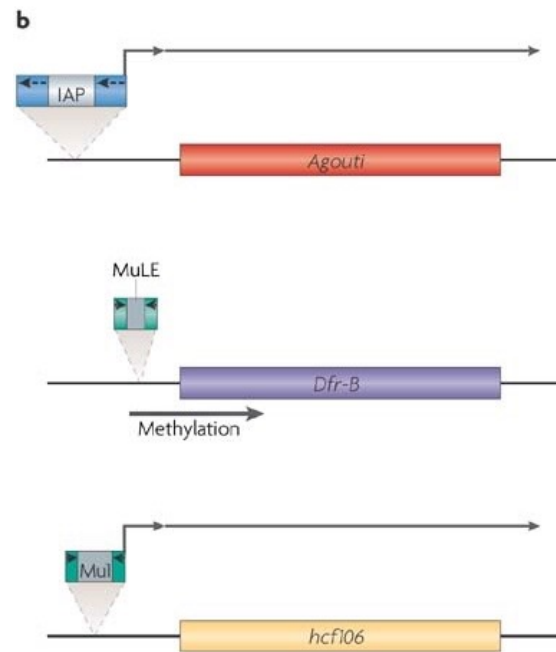
Transposons are DNA fragments capable of moving autonomously in the genome by a mechanism called transposition. Widely spread in all eukaryotes, they are powerful engines for evolution and diversity.

Transposable elements (TEs) were discovered in *Zea mays* by Barbara McClintock.



McClintock *et al*, Cold Spring Harb Symp. Quant. Biol. 1951

For her discovery, she was awarded the Nobel Prize in Physiology or Medicine in 1983.



Defects in DNA methylation trigger developmental defects and perturb stable trans-generational inheritance in plants

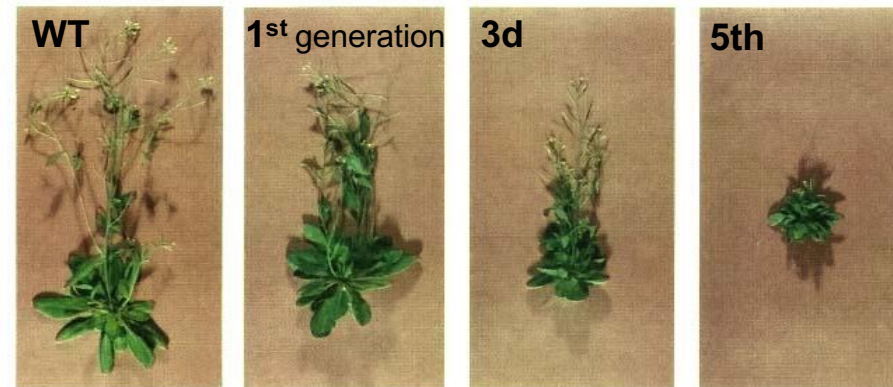
Loss of DNA methylation triggers developmental defects due to genome-wide, random deployment of aberrant DNA methylation

DDM1 = chromatin remodeling ATPase of the SNF2/SWI2 family
Required for mCG maintenance

ddm1 (decrease in DNA methylation1)



Mathieu et al, Cell 2007



Kakutani et al, PNAS 1996

6 generations after DNA methylation was reduced by *DDM1* inactivation, **newly inserted transposons were distributed throughout the genome.**

Miura et al, Nature 2001

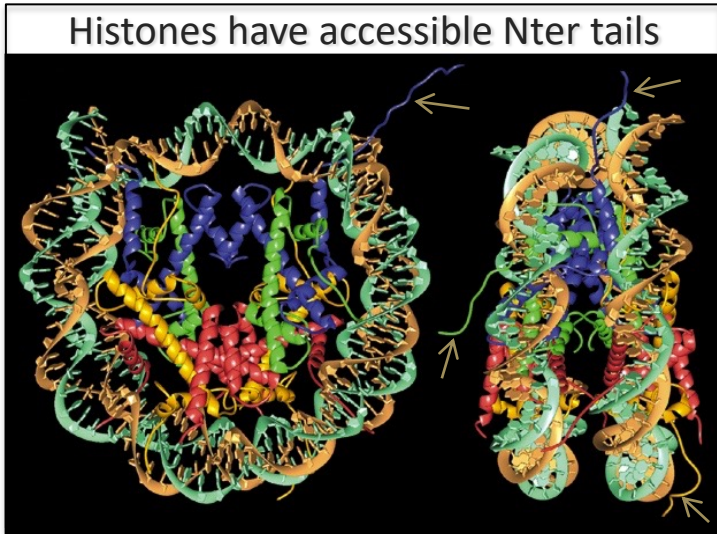
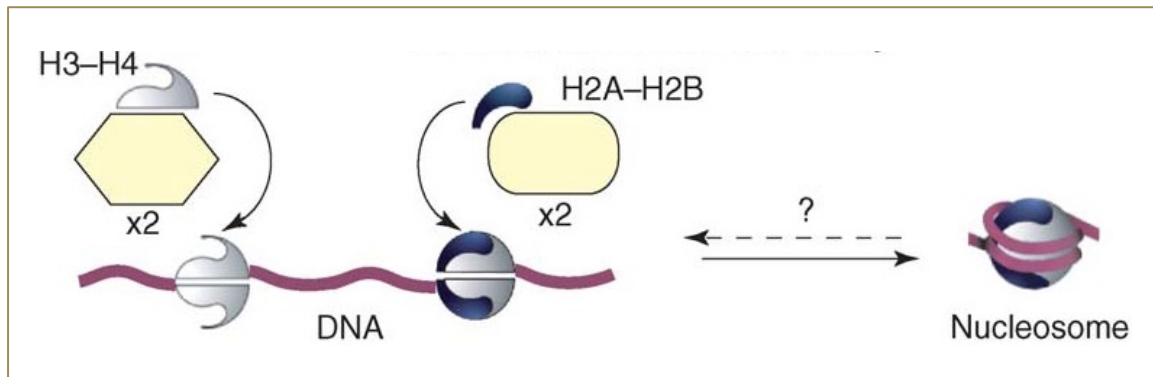
Chromatin structure



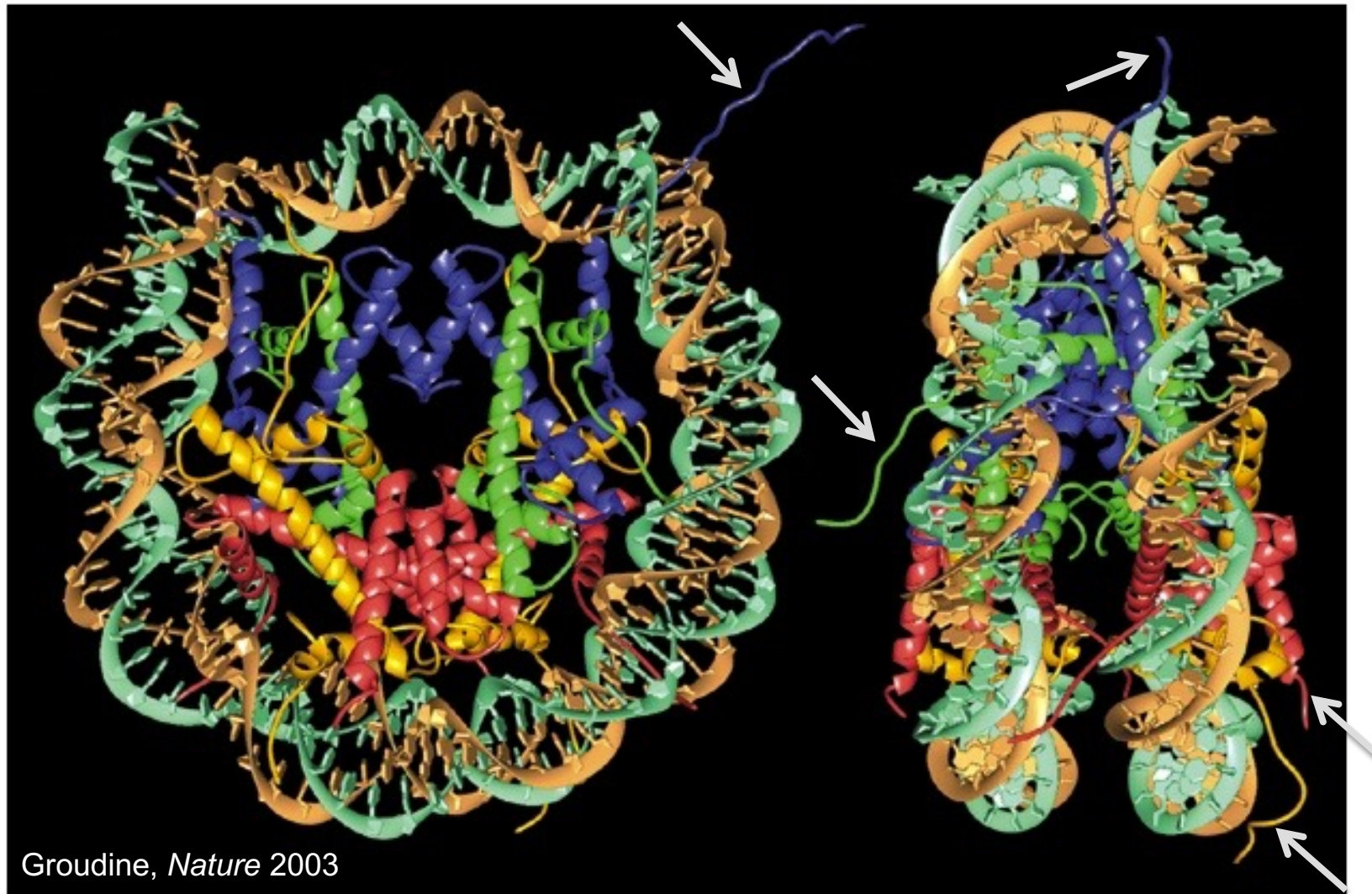
Nicolas Bouvier ArtWork

Nucleus organization

Nucleosomes	Assembly
	Position & Density
Histones	Modifications
	variants
DNA	methylation



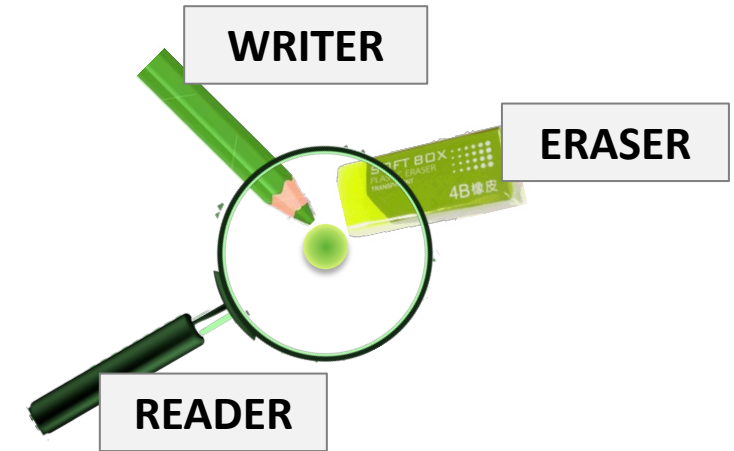
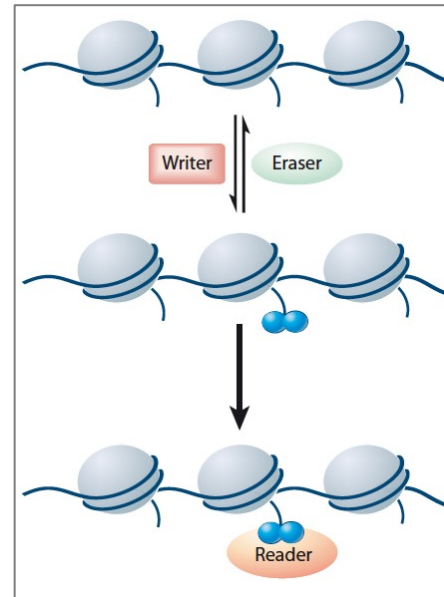
Nucleosome structure



The amino terminal regions of the histone monomers extend beyond the nucleosome and are accessible for modification

The non-exhaustive list of Histone marks

- Histones can be modified by:
 - Acetylation (Ac)
 - Ubiquitination (Ub)
 - Methylation (Me)
 - Phosphorylation (P)
 - Sumoylation (Su)
 -



Liu et al, *Annu Rev Plant Biol* 2010

- Based on their type and position, Histone marks contribute to transcriptional activation or inactivation

→ Histone code hypothesis:

Histone modifications regulate chromatin state and dynamic transitions between condensed heterochromatin and accessible euchromatin.

(Jenuwein & Allis, *Science* 2001)



WRITERS

ERASERS

Types of histone modifications and enzymes

<u>Residue</u>	<u>type of modification</u>	<u>modifying enzyme</u>
Lysine	acetylation deacetylation	HAT KAT HDAC
Lysine	methylation demethylation	HMT KMT HDM KDM
Lysine	ubiquitylation deubiquitylation	Ub ligase Ub protease
Serine/ Threonine	phosphorylation dephosphorylation	kinase phosphatase
Arginine	methylation demethylation	PRMT deiminase

- Others: Sumoylation (Lysine), ADP Ribosylation (Glutamate)
- One or up to 3 groups added per residue

Histone Modifications



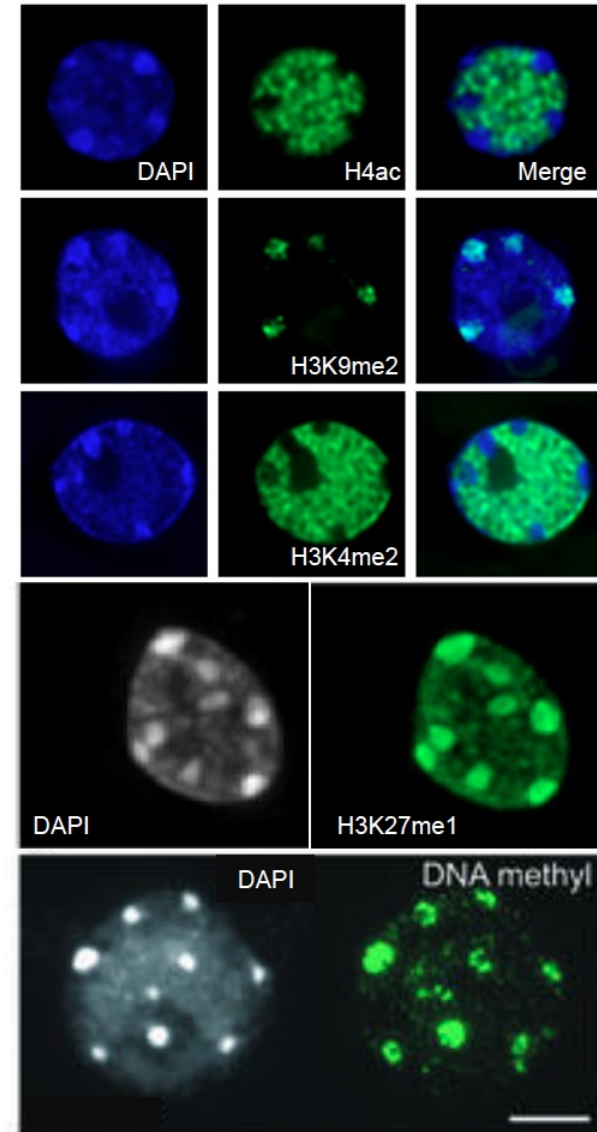
Portela & Esteller, *Nature Biotech* 2010

How are histone modifications studied?

- *in situ* immuno-localisation for global view

chromocenter : densely staining aggregation of heterochromatic regions in the nucleus of some cells.

Chromocenters are enriched in repressive chromatin marks, vs active chromatin marks



How are histone modifications studied?

- ***in situ* immuno-localisation** for global view
- **Chromatin immuno-precipitation (ChIP)**
followed by PCR (targeted) or by genome-wide approaches (ngs):
 - Targeted approach – ChIP-qPCR
 - Unbiased approach – ChIP-chip, ChIP-seq, other genome-wide techniques

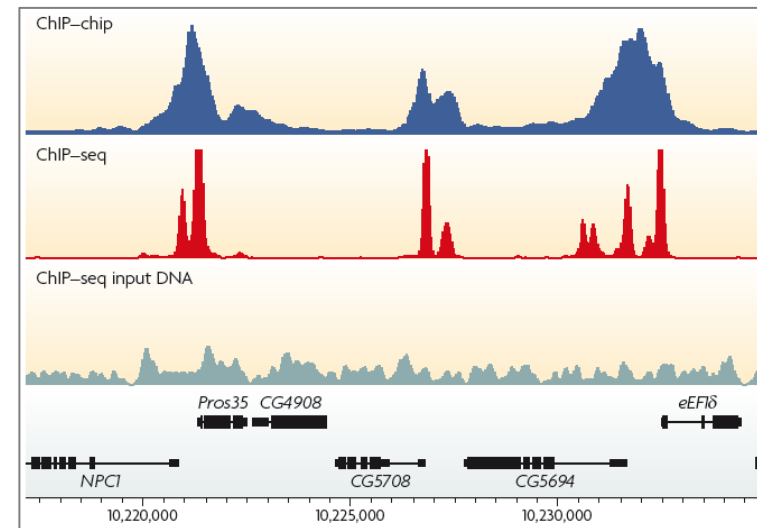
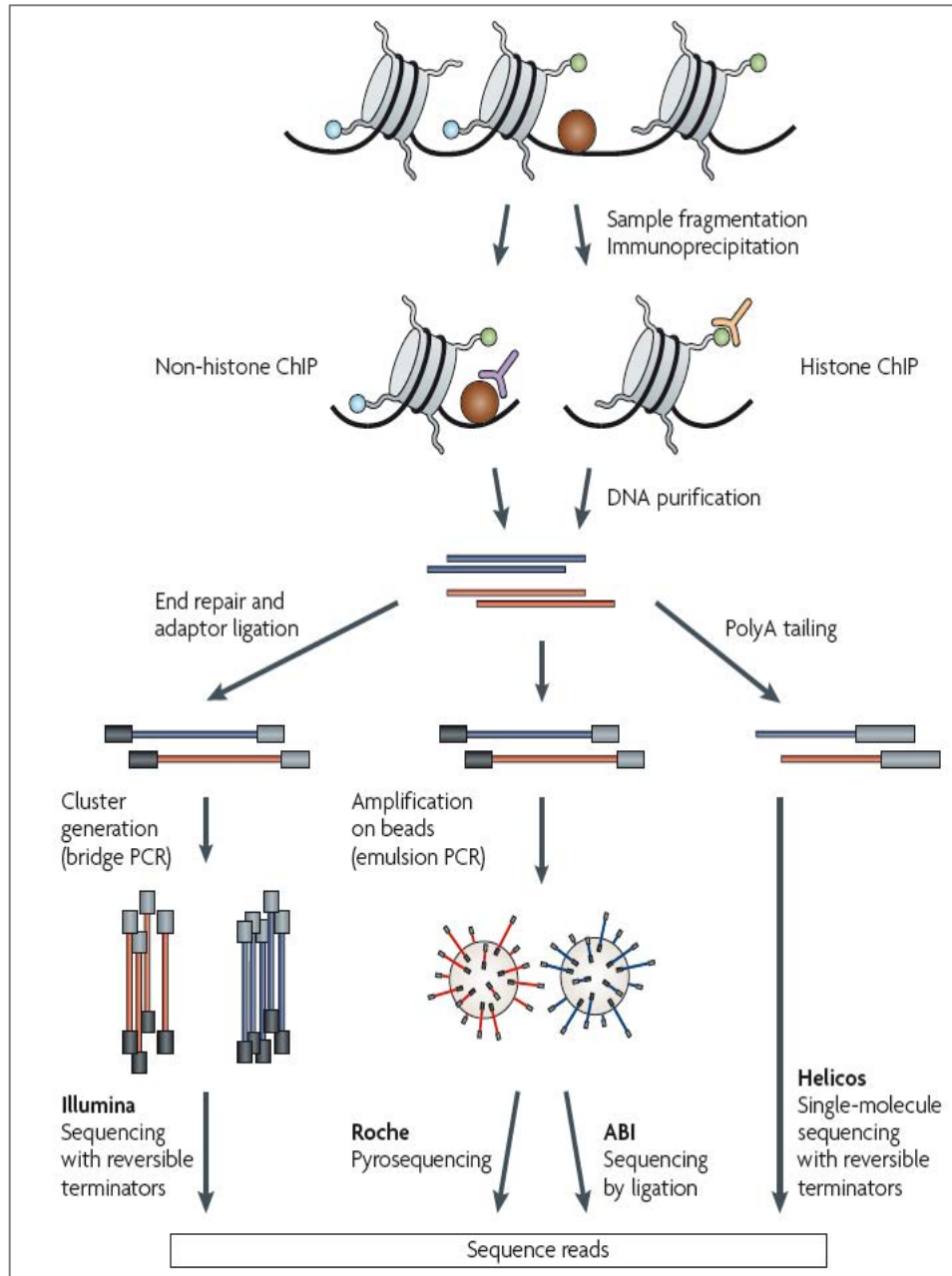
Limitations:

- Antibody specificity
- Inherent biases of localization methods

ChIP-chip ChIP-seq

« Every few years a new technology comes along that dramatically changes how fundamental questions in biology are addressed. »

Stanley Fields, *Science* 2007



Park, *Nature Rev* 2009

How are histone modifications studied?

- ***in situ* immuno-localisation** for global view
- **Chromatin immuno-precipitation (ChIP)**
followed by PCR (targeted) or by genome-wide approaches (ngs):
 - Targeted approach – ChIP-qPCR
 - Unbiased approach – ChIP-chip, ChIP-seq, other genome-wide techniques

Limitations:

- Antibody specificity
- Inherent biases of localization methods

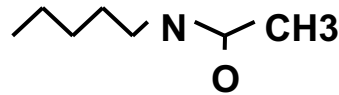
- **Mass Spectrometry**
Requires digestion of histones

Lysine can be acetylated, or mono, di- or tri-methylated



Lysine (K)

Acetylated lysine
(KAc)



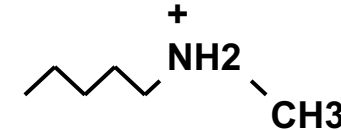
Lysine acetyltransferases: KAT

- Often multi-enzyme complexes
- Can modify multiple residues
- **Well correlated with transcriptional activation**

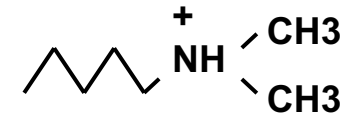
- Reduces the + charge on the histones (K: + charge)
→ **decreases the interaction of their N termini w/ the negatively charged phosphate groups of DNA**
→ Prevents chromatin compaction

Methylated lysine

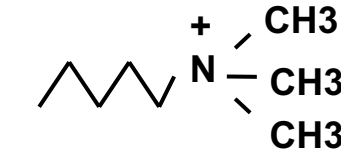
Mono (Kme1)



Di (Kme2)



Tri (Kme3)

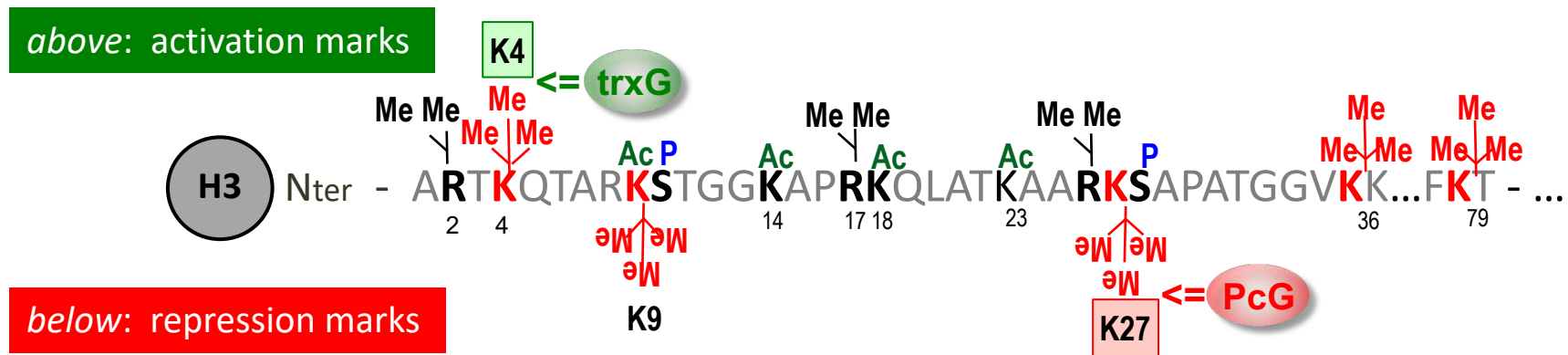


Lysine methyltransferases: KMT

- Very specific: target a certain lysine on a certain histone
- Put on mono, di, or tri me (me, me2, me3)
- Many contain SET domains (me-transferase)
- 'Readout' is very specific:
 - H3K4me1 vs. H3K4me3 (activating)
 - H3K27me2 vs. H3K27me3 (repressive)

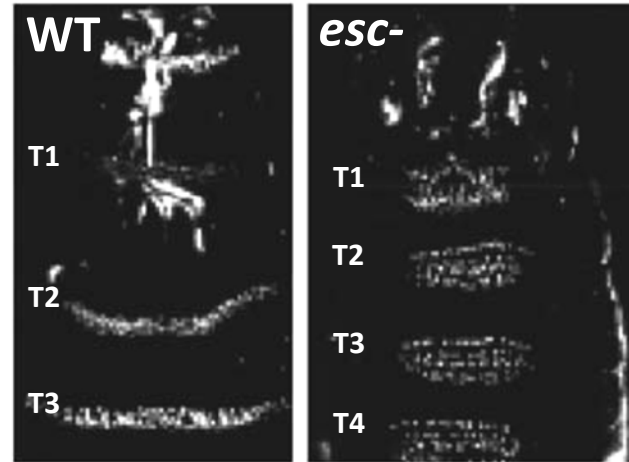
Histone Modifications brought by antagonist Polycomb (PcG) and trithorax (trxG) complexes

At thousands of developmental genes



PcG and trxG functions first identified in *Drosophila*

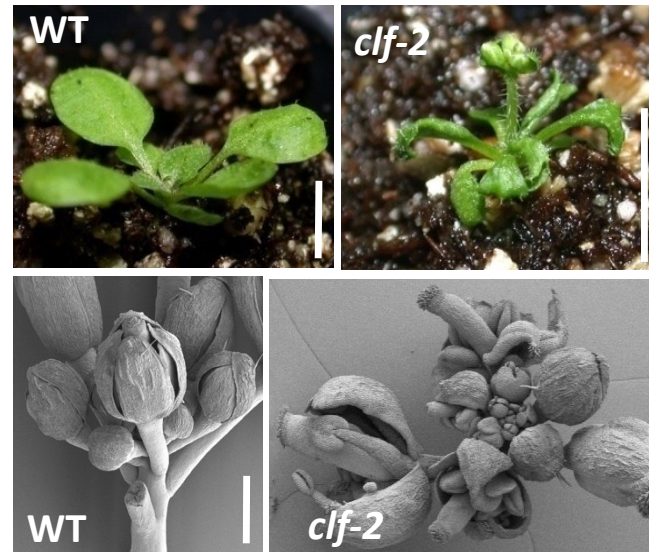
Drosophila PcG
and *Trx* mutants



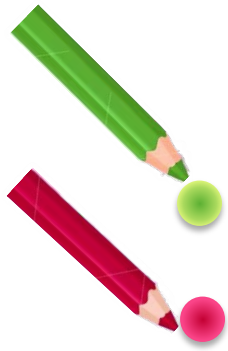
PcG mutant phenotypes due to mis-
expression of Hox genes

trxG mutations rescue
PcG mutant phenotypes

Arabidopsis PcG
and *Trx* mutants



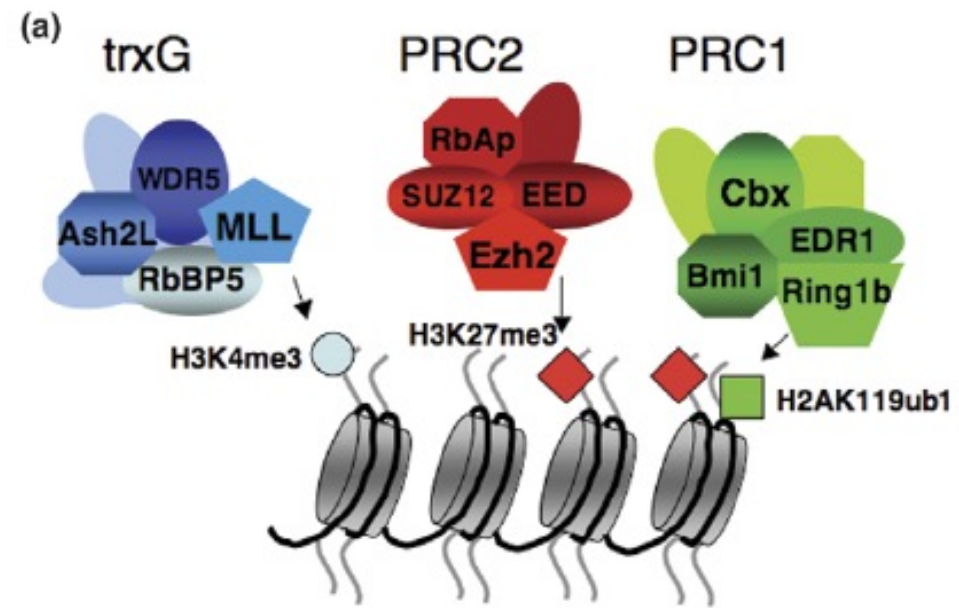
PcG mutant phenotypes due to mis-
expression of MADS-box genes



Opposing roles of TrxG and PcG

trxG → H3K4me3

PcG → PRC2 → H3K27me3
→ PRC1 → H2AK119ub1

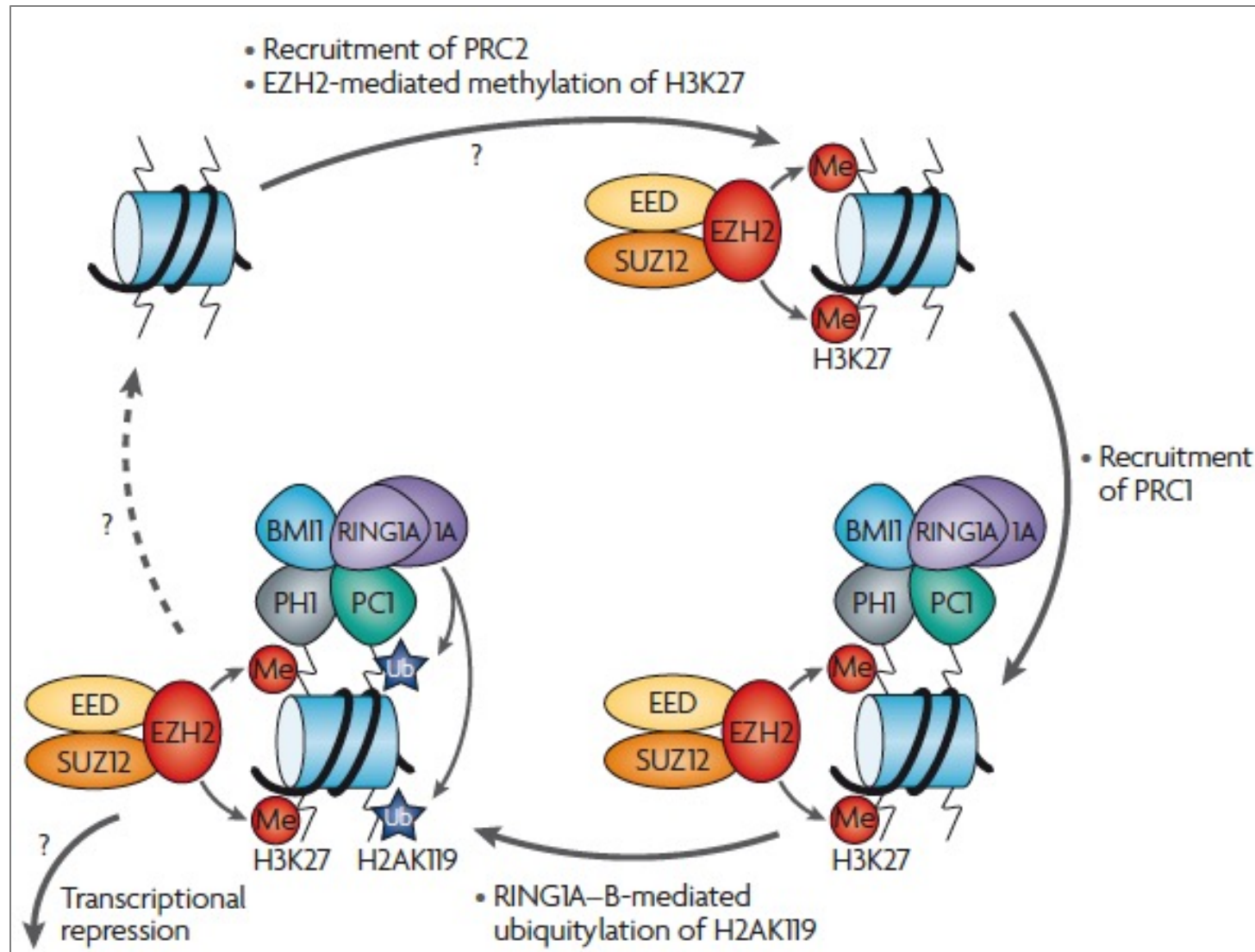


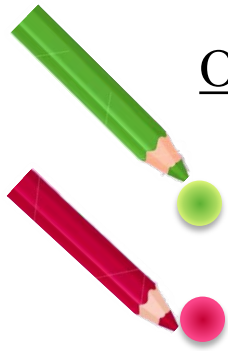
**Stem cell regulation by polycomb repressors:
postponing commitment**

Alexandra M Pietersen and Maarten van Lohuizen

Current Opinion in Cell Biology 2008, 20:201–207

Polycomb group function: PRC2 and PRC1 complexes

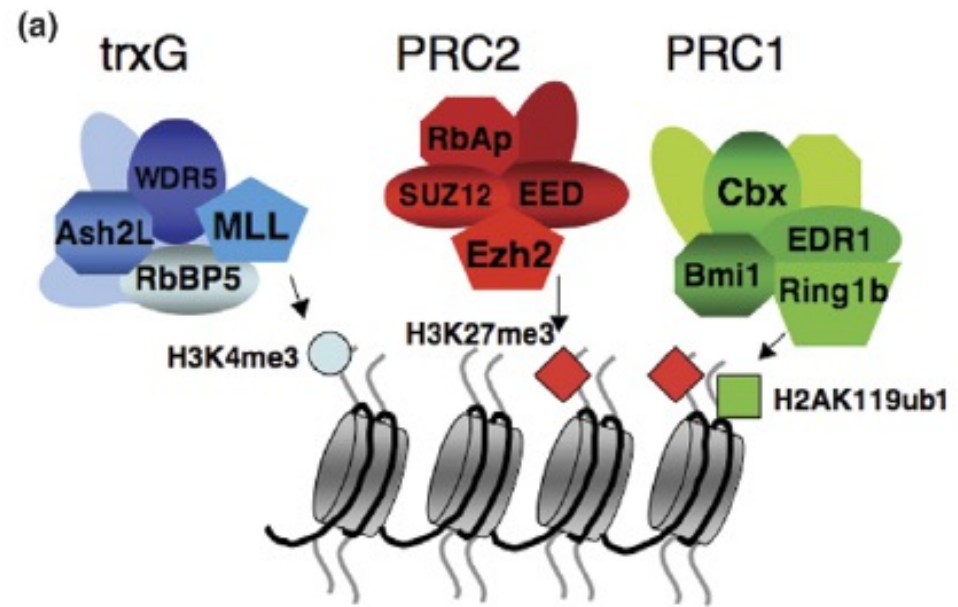




Opposing roles of TrxG and PcG

trxG → H3K4me3

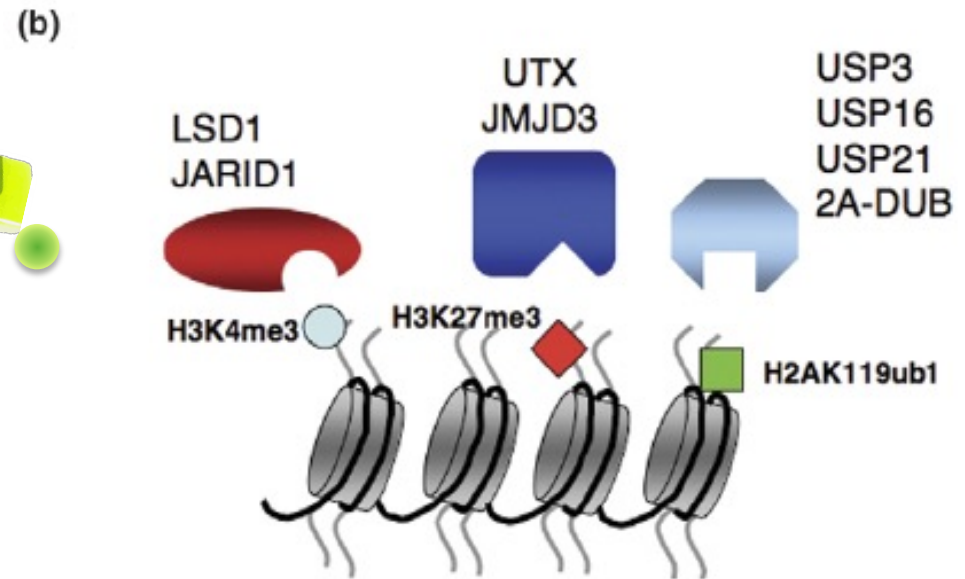
PcG → PRC2 → H3K27me3
 → PRC1 → H2AK119ub1



Reversibility of marks (demethylases)

UTX JMJD3 part of TrxG complex

LSD1 and JARID associate with PcG complex



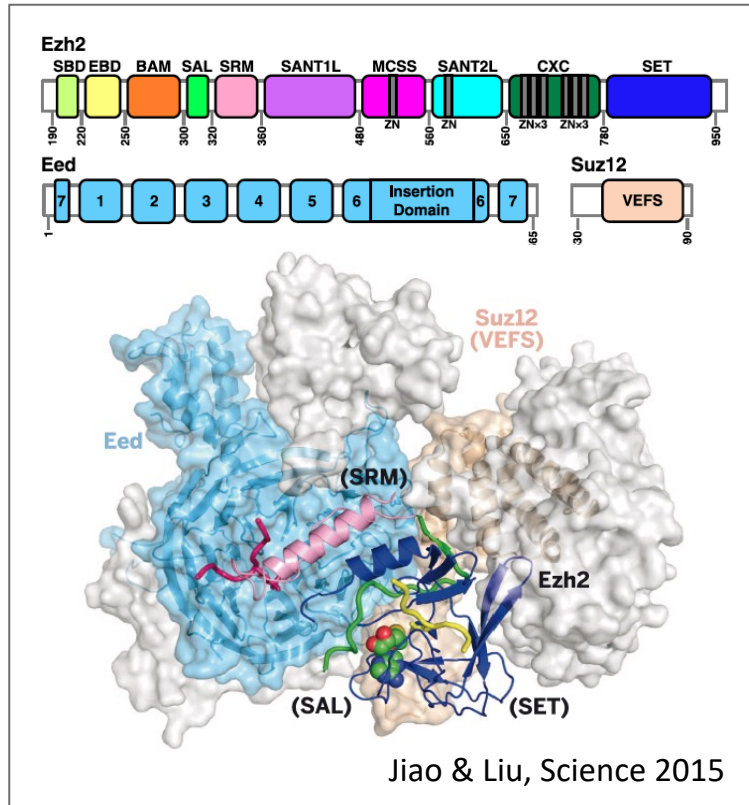
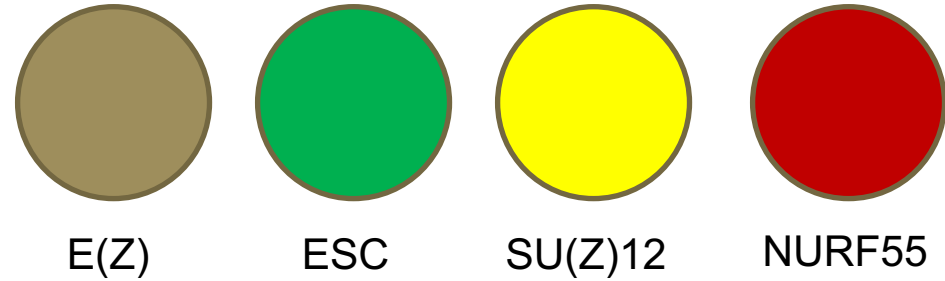
**Stem cell regulation by polycomb repressors:
 postponing commitment**

Alexandra M Pietersen and Maarten van Lohuizen

Current Opinion in Cell Biology 2008, 20:201-207

PRC2 core proteins in Drosophila

Drosophila PRC2 has a conserved core of four proteins



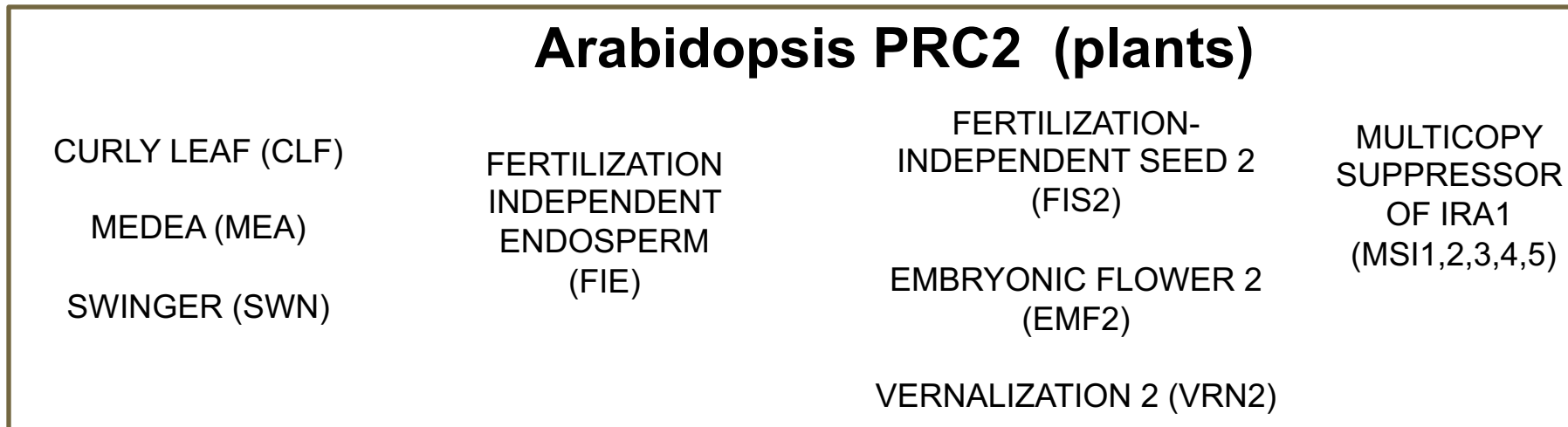
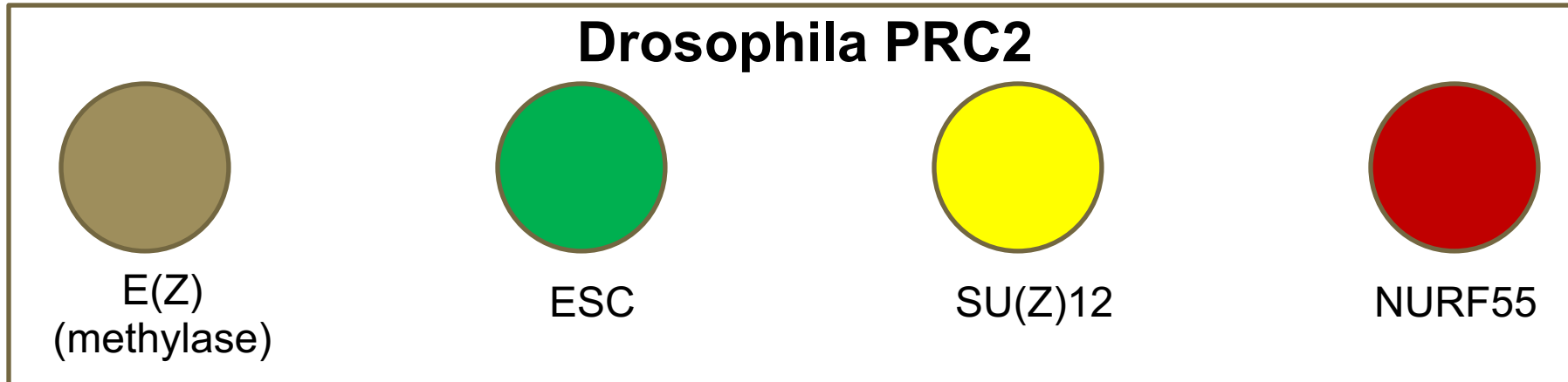
Enhancer of zeste (E(Z))
catalytic activity (SET domain methyl transferase)

Extra sex comb (ESC)
stimulates catalytic activity of E(Z)

Suppressor of zeste 12 (SU(Z)12)
complex association to nucleosomes

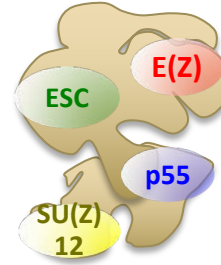
NURF55
complex association to nucleosomes

Arabidopsis has multiple forms of three of the core PRC2 proteins



Diversification of PRC2 components in plants vs animals

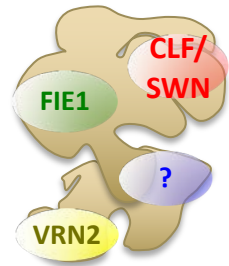
Drosophila
PRC2



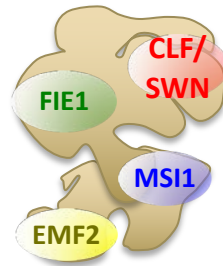
Arabidopsis
PRC2



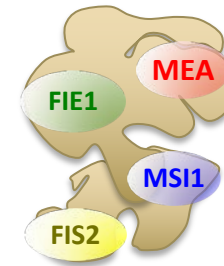
VRN2 complex



EMF2 complex



FIS complex



TARGET GENES

VEGETATIVE
DEVELOPMENT

FLORAL
TRANSITION

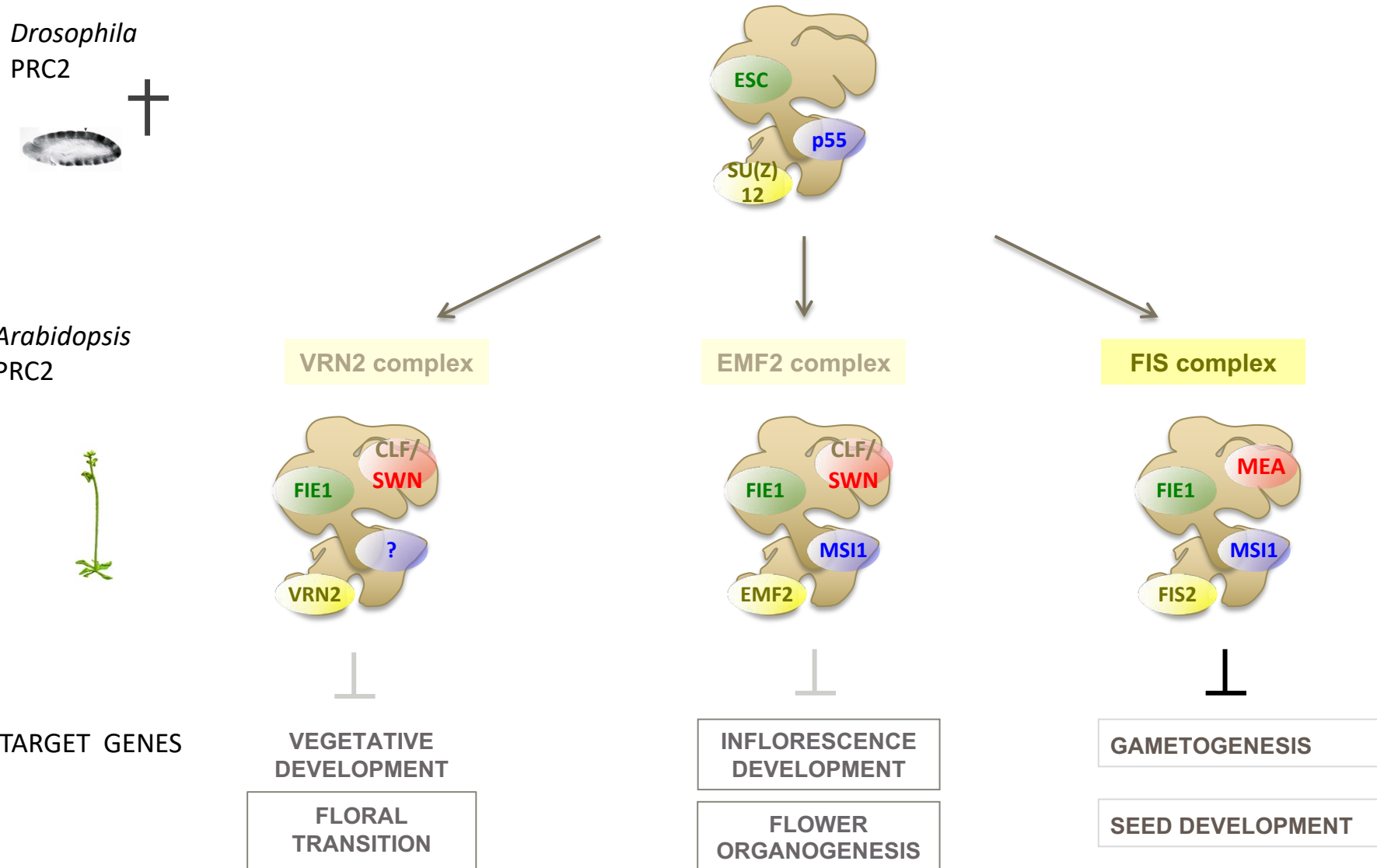
INFLORESCENCE
DEVELOPMENT

FLOWER
ORGANOGENESIS

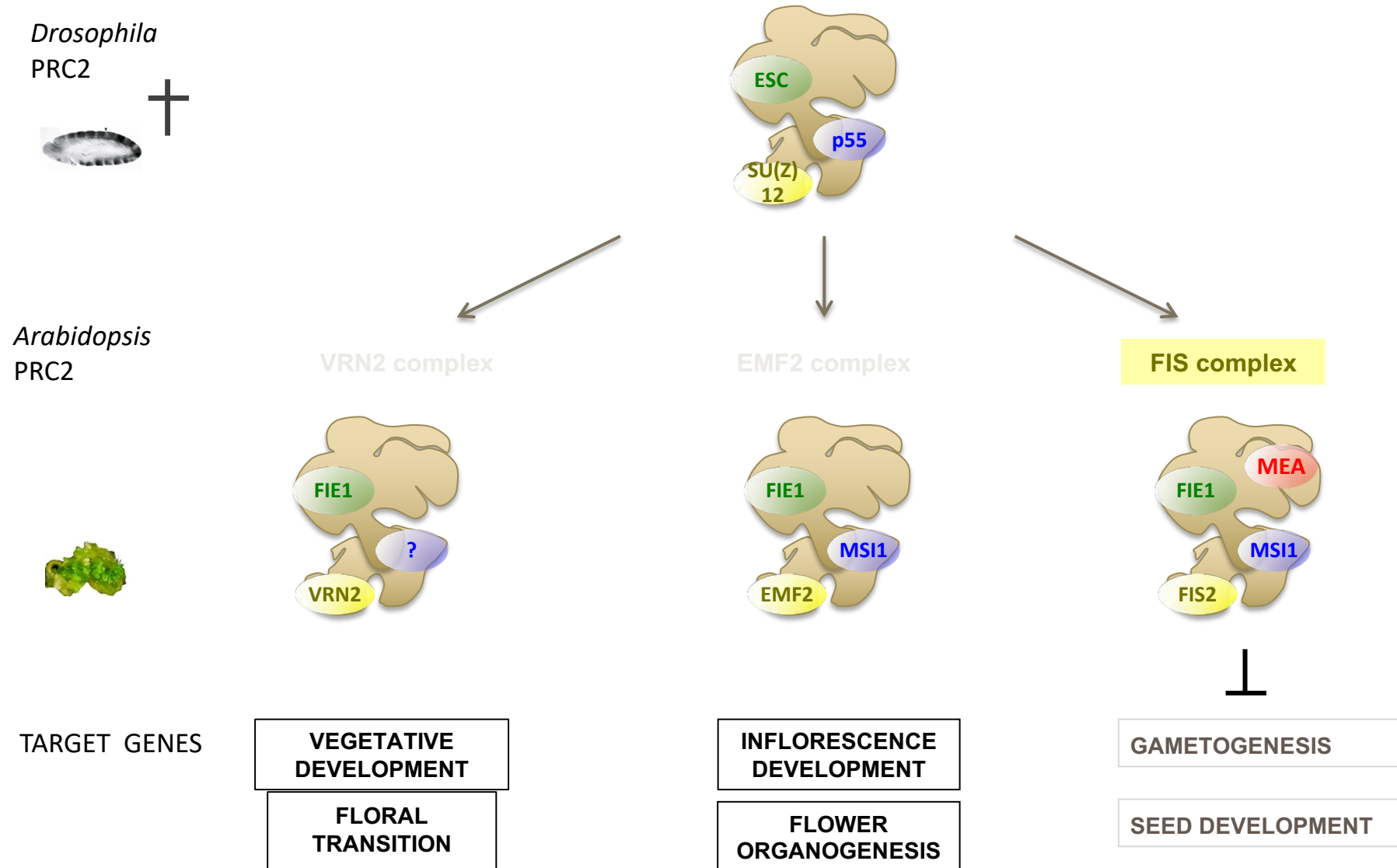
GAMETOGENESIS

SEED DEVELOPMENT

Diversification of PRC2 components in plants vs animals



Diversification of PRC2 components in plants vs animals



Chromatin structure



Nicolas Bouvier ArtWork

Nucleus organization

Nucleosomes

Assembly

Position & Density

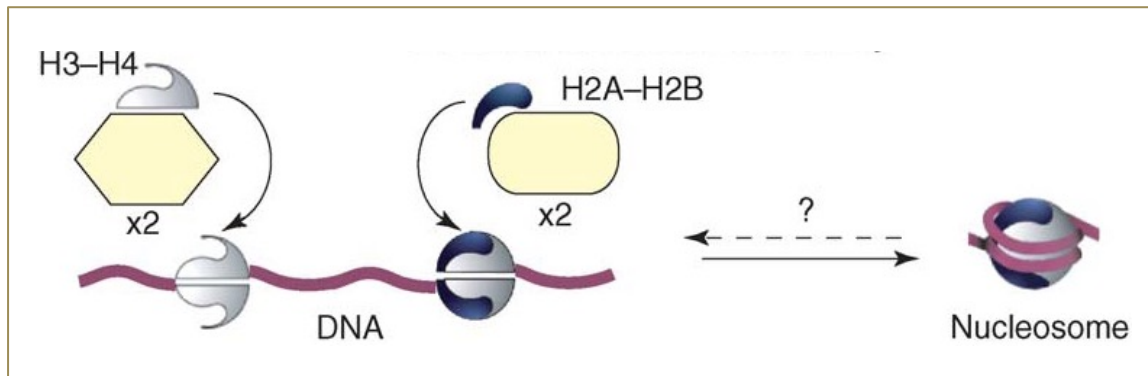
Histones

Modifications

variants

DNA

methylation

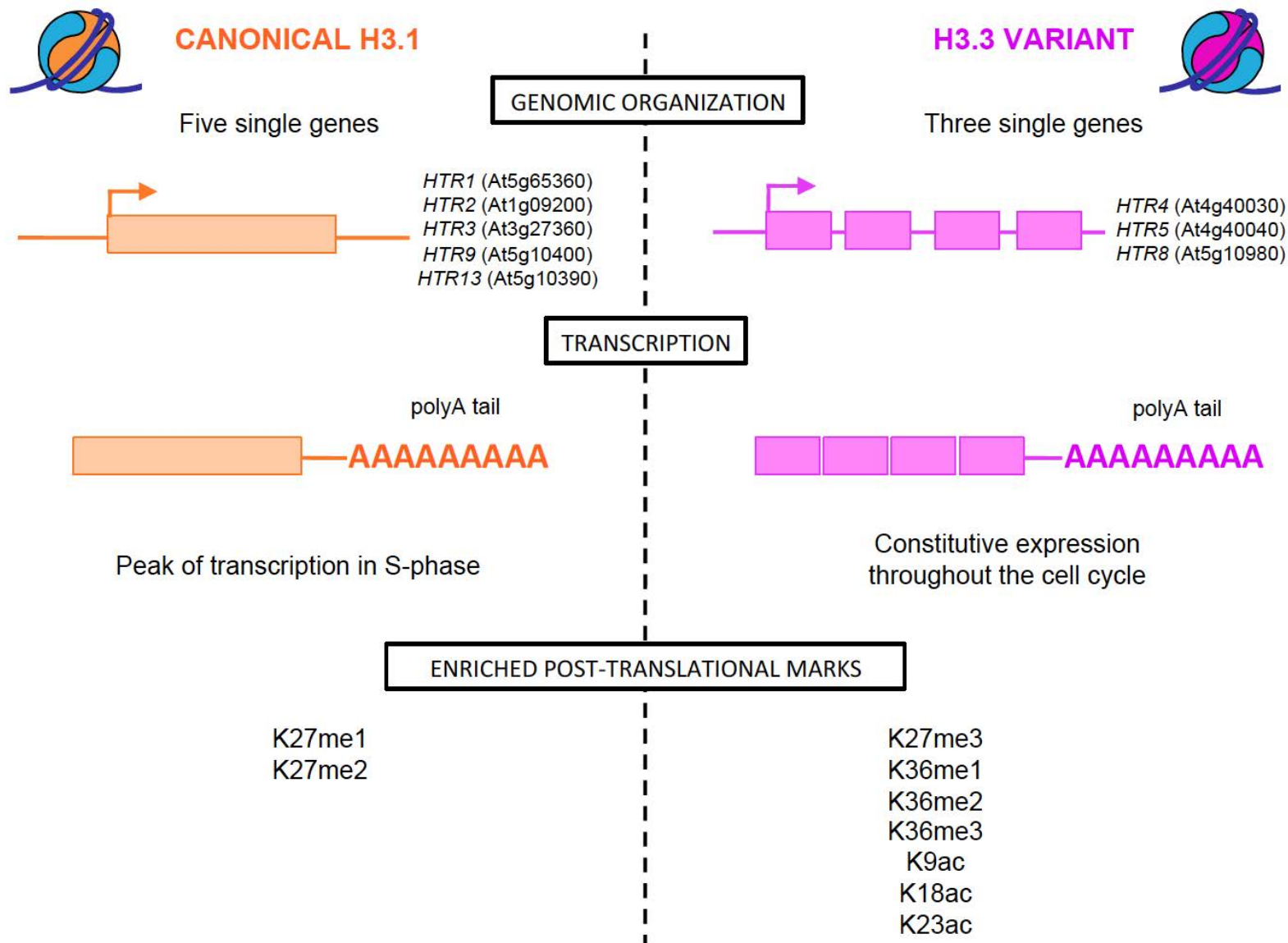


Histone VARIANTS:

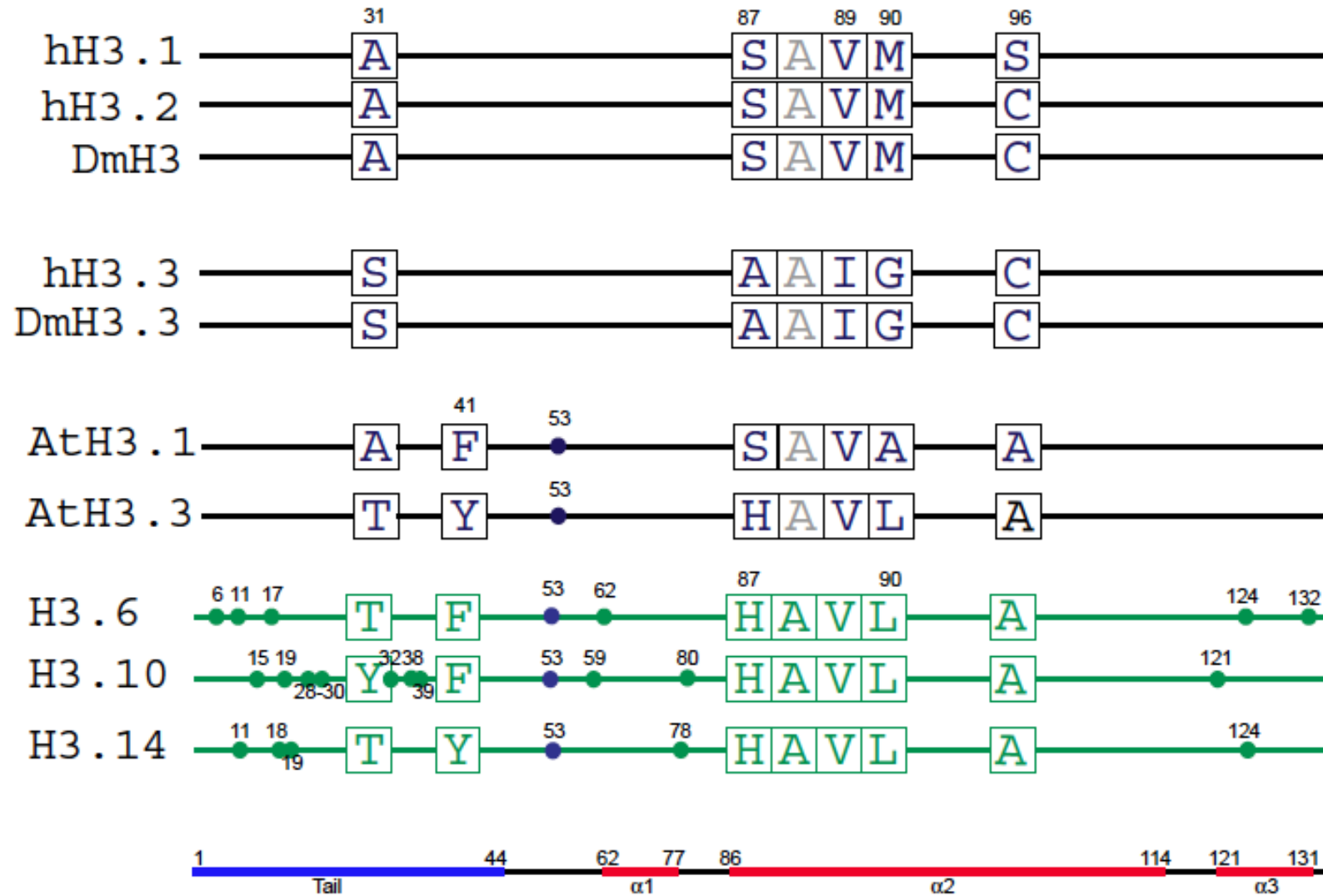
- for all, except H4
- **CENH3** : centromeric nucleosomes
- **H3.1** : at repressed *loci*
- **H3.3** : *loci* with active transcription, peak at 3' end of genes
- **H2A.Z** : heterochromatin boundaries and 5' start of active genes

1st Histone Variant EMBO meeting (Oct 2011)

Arabidopsis canonical H3.1 and replacement variant H3.3

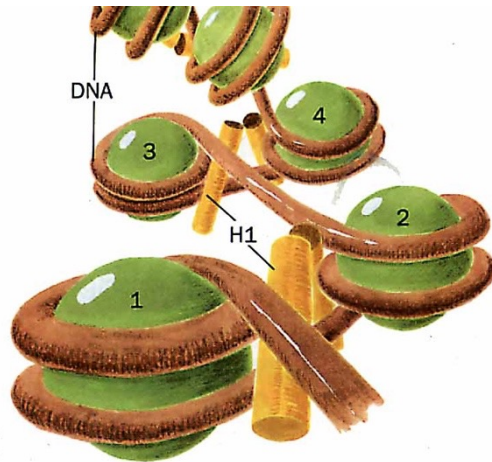


Divergences in aa sequences of canonical and variant H3

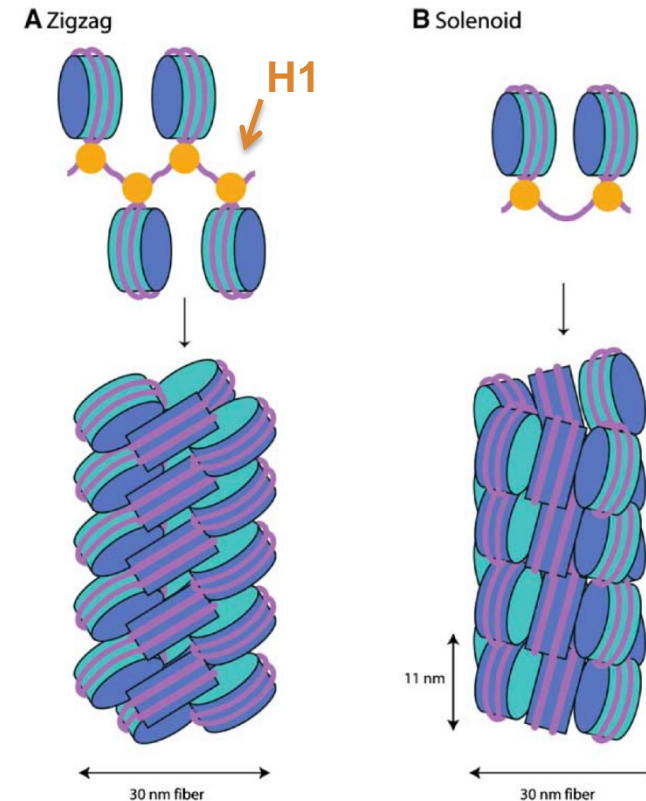


Another, non nucleosomic Histone: **Histone H1 = linker histone**

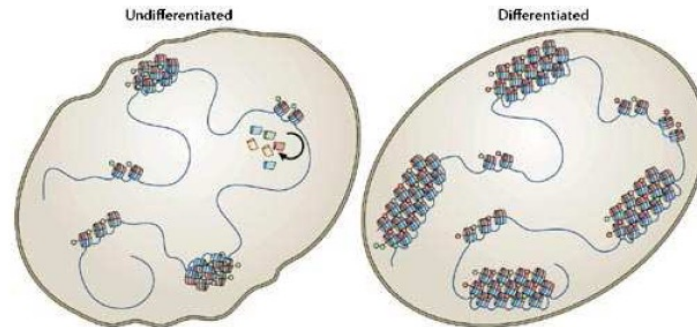
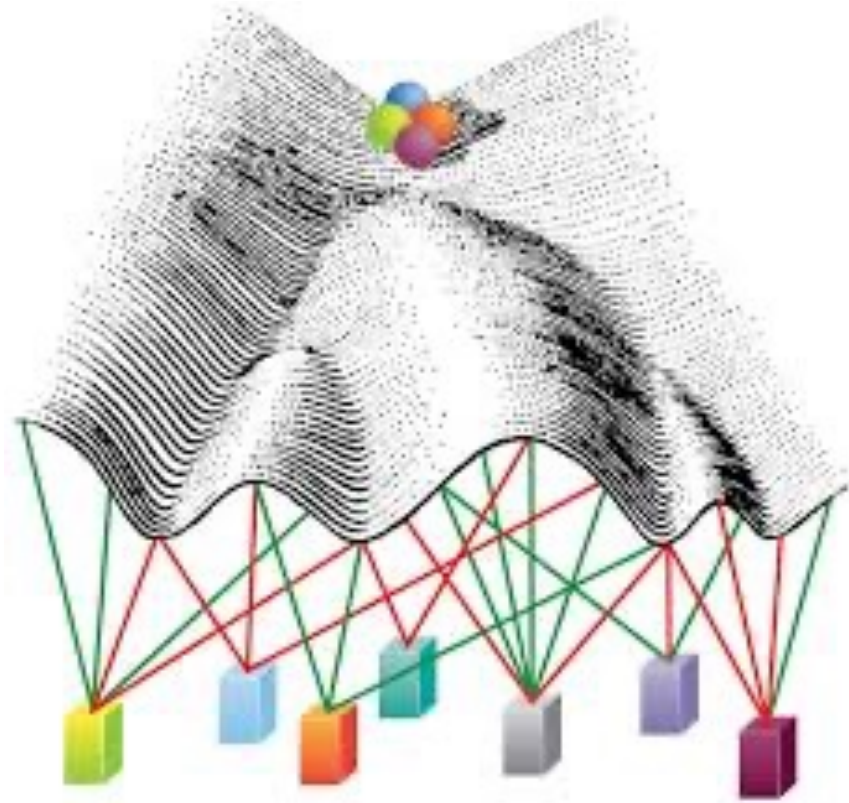
- associated with linker DNA between nucleosomes (about one H1 per nucleosome)
 - Binds DNA at entry/exit
 - stimulates folding 10 nm → 30 nm fiber
 - repressive effect on transcription
- H1 binds weaker to acetylated nucleosomes



- *Ordinary nuclear extracts contain high levels of H1*



The Epigenetic Landscape



Conrad Waddington, 1950s

Take-Home message

Actors in Chromatin dynamics are:

- Part of large complexes
- Made of several modules
 - recognition domain (reader: Bromo, PHD...)
 - enzymatic (modifier= writer or eraser: HMT, HAT, HDAC...)
- Involved in cross-talking pathways
 - e.g. DNA me → Histone PMT → nucleosome remodeling
- Largely conserved between kingdoms, but with some variations
 - in function
 - in number (more in plants)
- Key to control of gene expression => read-out of the genome

Questions ?

QUIZZ !!

Question 1:

“**Epigenetics** is the study of heritable changes in genome function that occur without a change in

- A) Histone sequence
- B) DNA sequence
- C) RNA sequence
- D) Epigenator

Answer: B

Question 2:

All the following names correspond to **enzymes that modify epigenetic marks**, but one. Which one isn't such an enzyme?

- A) writer
- B) eraser
- C) DNA methyl transferase
- D) ATPase remodeler

Answer: D

Question 3:

Which of the following propositions is **false**?

- A) A nucleosome is made of 8 histones, each present in two copies (2 H2A, 2 H2B, 2 H3, 2 H4), wrapped with 147 bp of DNA
- B) A nucleosome is a tetramer of histones (H2A, H2B, H3, H4), wrapped with 2 loops of DNA
- C) Nucleosomes can slide, assemble or disassemble, during DNA replication or transcription
- D) Chromatin structure is highly dynamic, contributing to gene expression dynamics

Answer: B

Question 4:

Among epigenetic marks that can be deposited at the chromatin (find the **false proposition**):

- A) Methylation marks on histones are always activating marks for transcription
- B) Acetylation marks are always activating marks for transcription
- C) DNA methylation can prevent the binding of transcription factor to target DNA
- D) All correspond to covalent modifications

Answer: A

Question 5:

The **Polycomb** and **trithorax chromatin complexes** display **functions** that **are**, in regard to their effect on gene expression (find the right answer):

- A) Epistatic
- B) Bivalent
- C) Antagonistic
- D) Cooperative

Answer: C



CHROMDEV team

Exploring molecular regulators of gene expression for developmental transitions

Permanent



Robert Blanvillain
Ass Prof UGA



Gilles Vachon
CNRS Scientist



Cristel Carles
Prof UGA

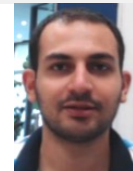


Marie Le Masson
CNRS Eng.

Non permanent



Vangeli Geshkovski
PhD 3^d year



Salim El Khoury
PhD 1st year



Laura Turchi
Post-Doc



Veronica-Astrid Morlacchi
M2 PLANT-Int



Ivan Cubillas
M2 NanoSc

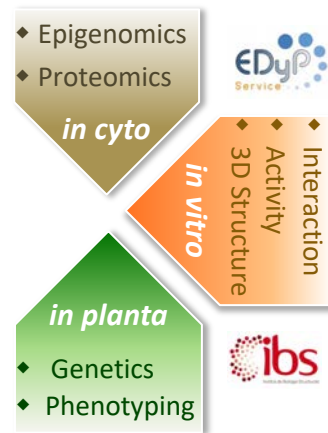
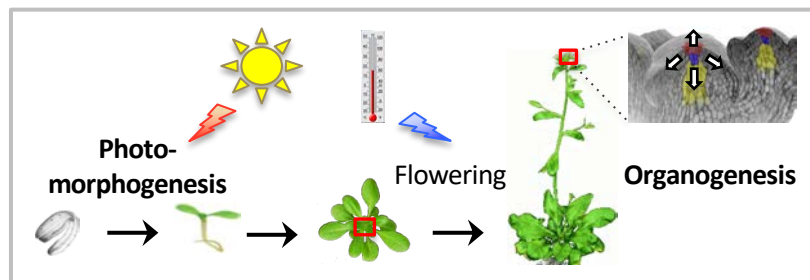
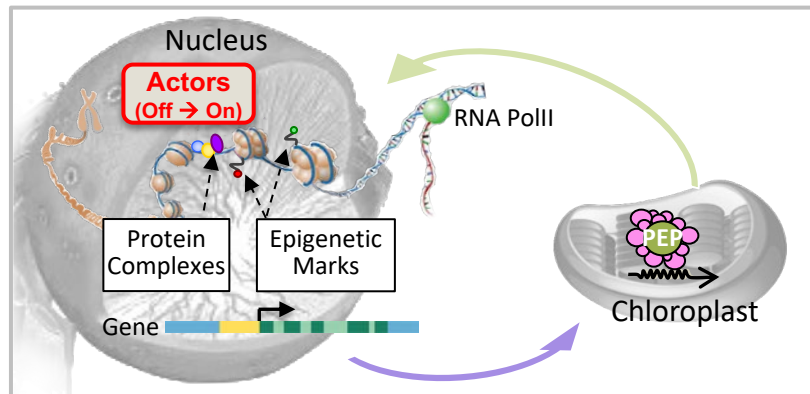


Leonard Calistru
M1 PhEDC

Soon ...

TBA
Post-doc

TBA
Engineer



Two paradigms : **Photo morphogenesis** and **core organogenesis**

* **PAPs : nucleus – chloroplast communications**
Chloroplast biogenesis, photomorphogenesis

* **ULTRAPETALA : chromatin-TF scaffold**
Flowering transition, flower morphogenesis

REWIRE : Epigenome editing

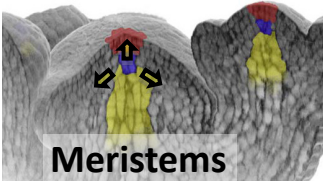
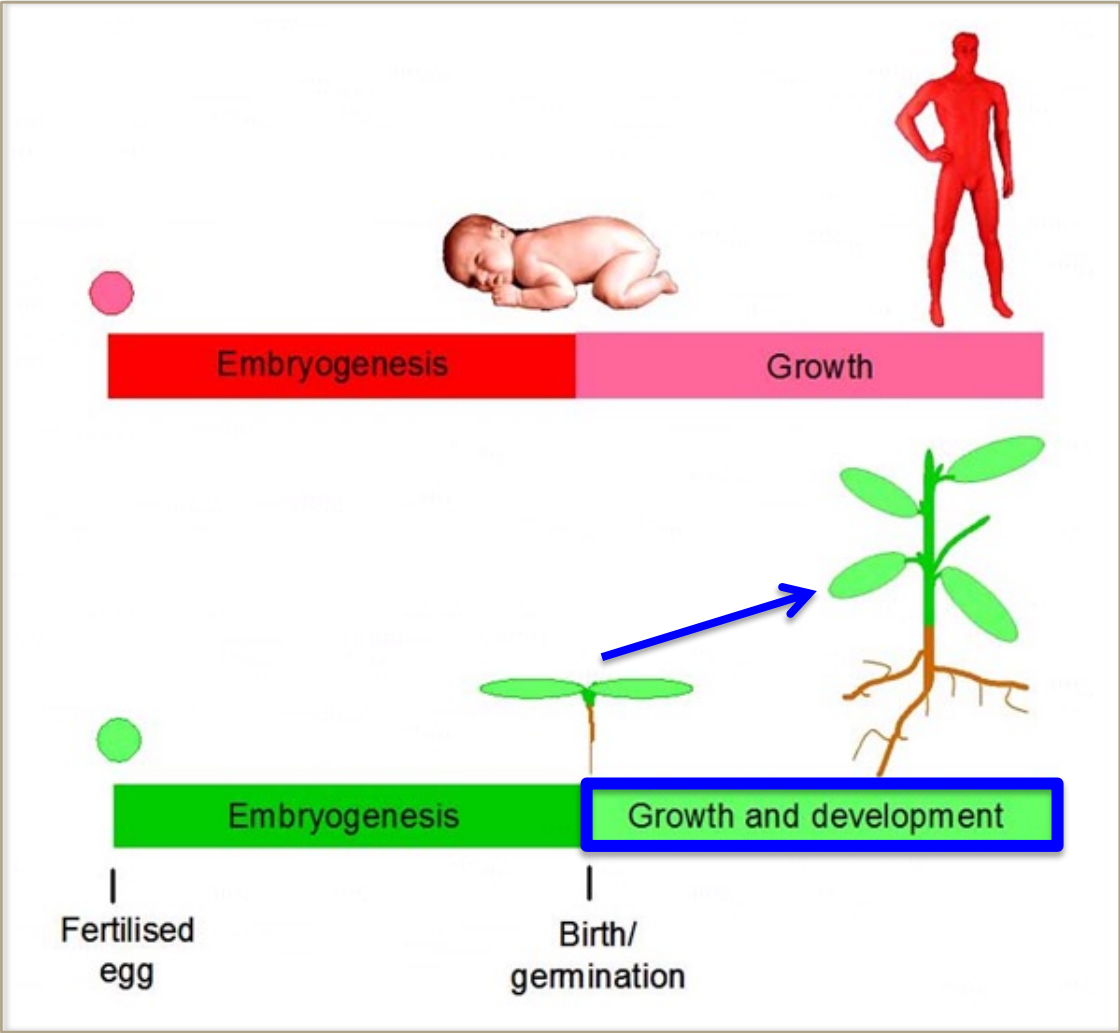
▷ to redirect plant development

▷ to depict the genuine function of chromatin marks

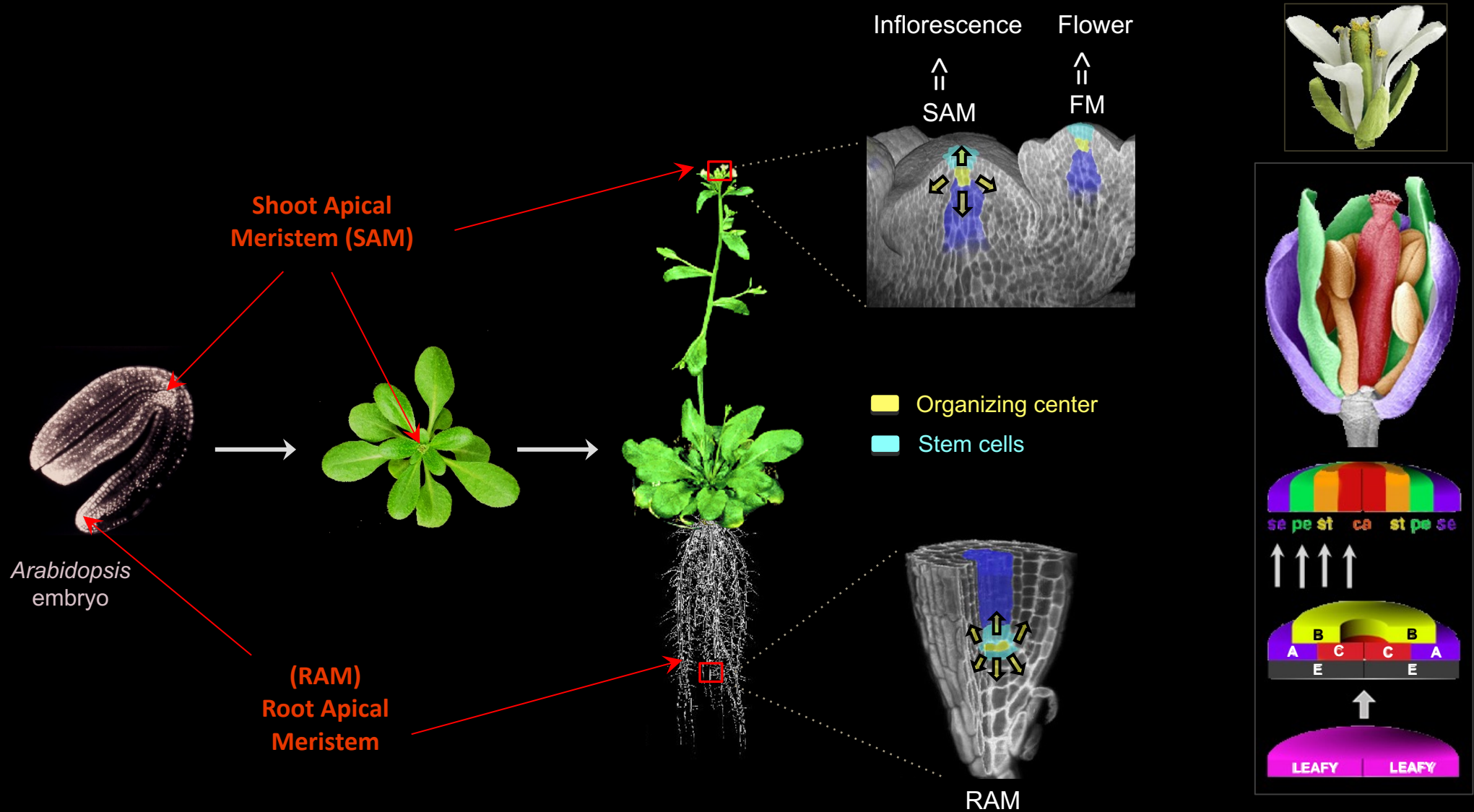
Eco-Devo project : Epiwarm (alpine meadows)

**Coordinators
of Dynamics**

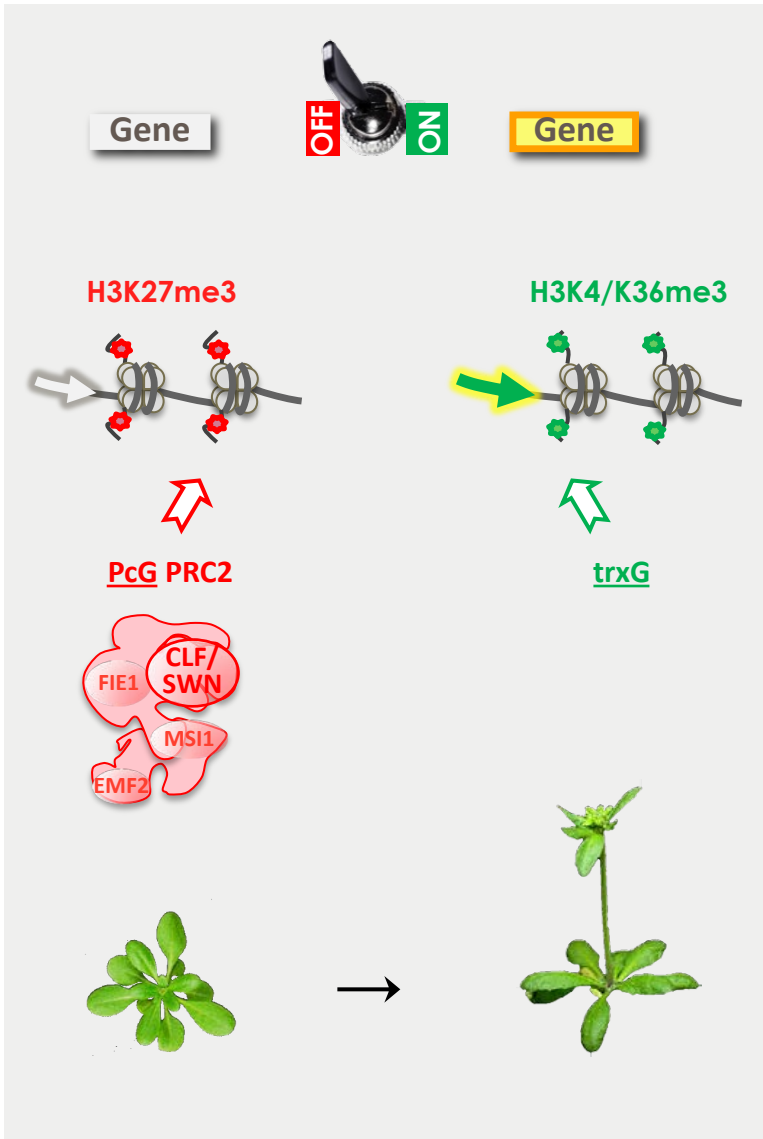
Plant organogenesis operates post-embryogenesis



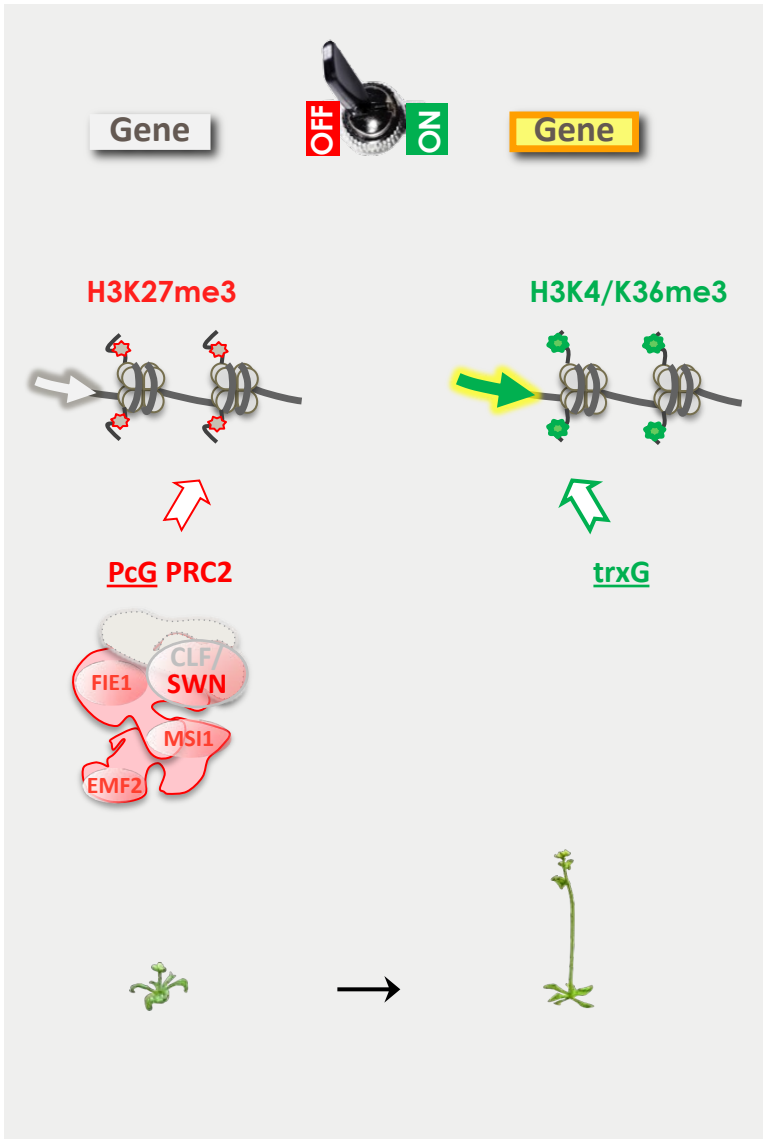
Organs are continuously produced from Meristems



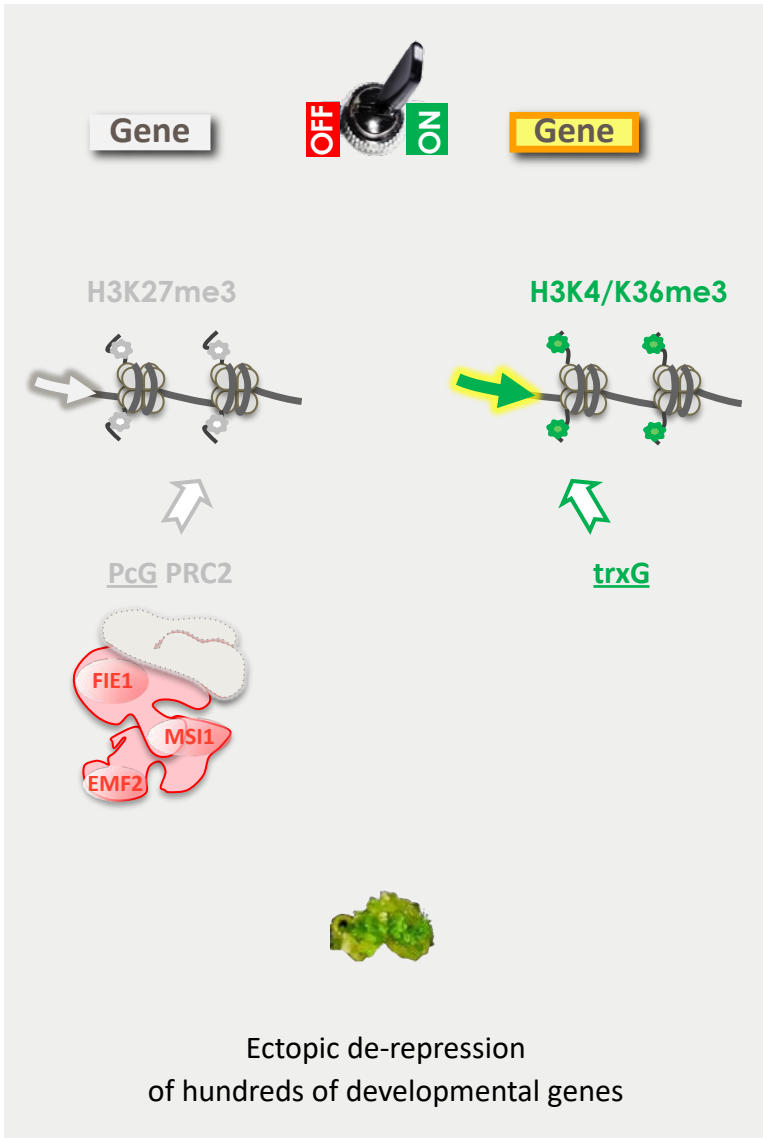
Chromatin dynamics : the ULTRAPETALA1 (ULT1) dual switch



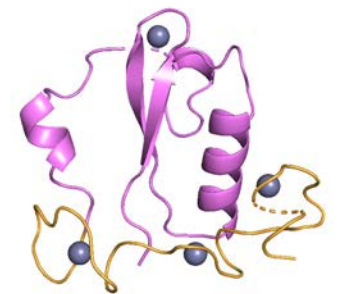
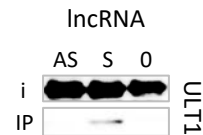
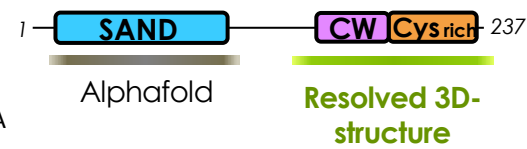
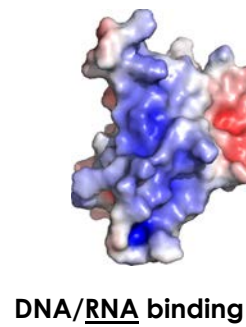
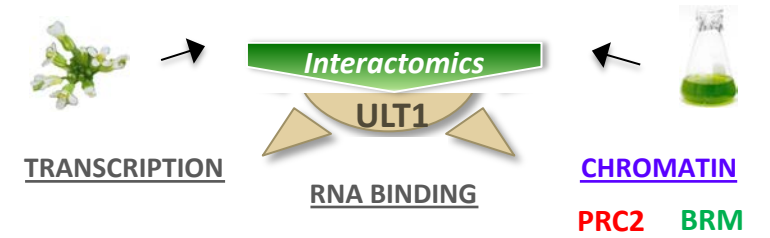
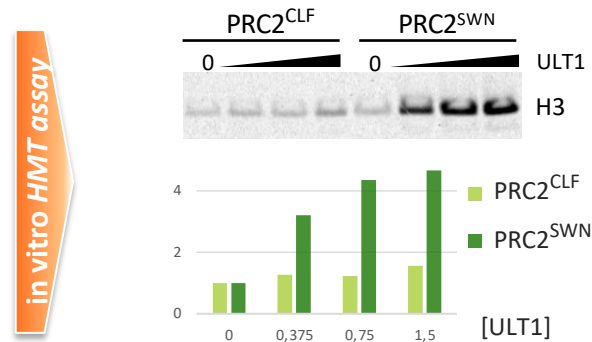
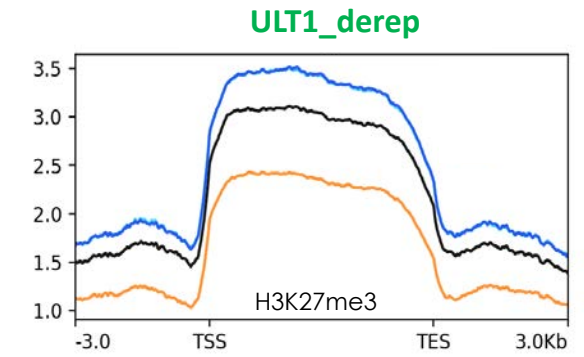
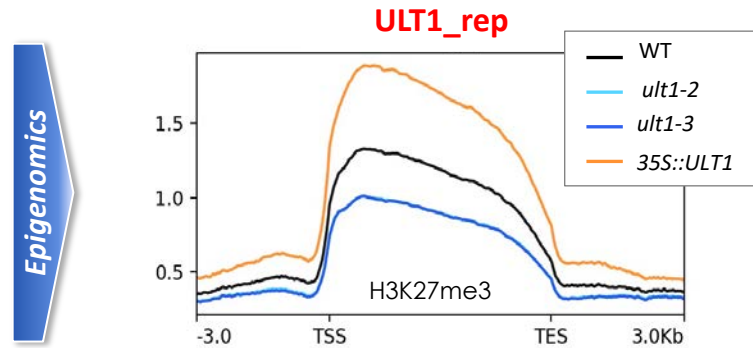
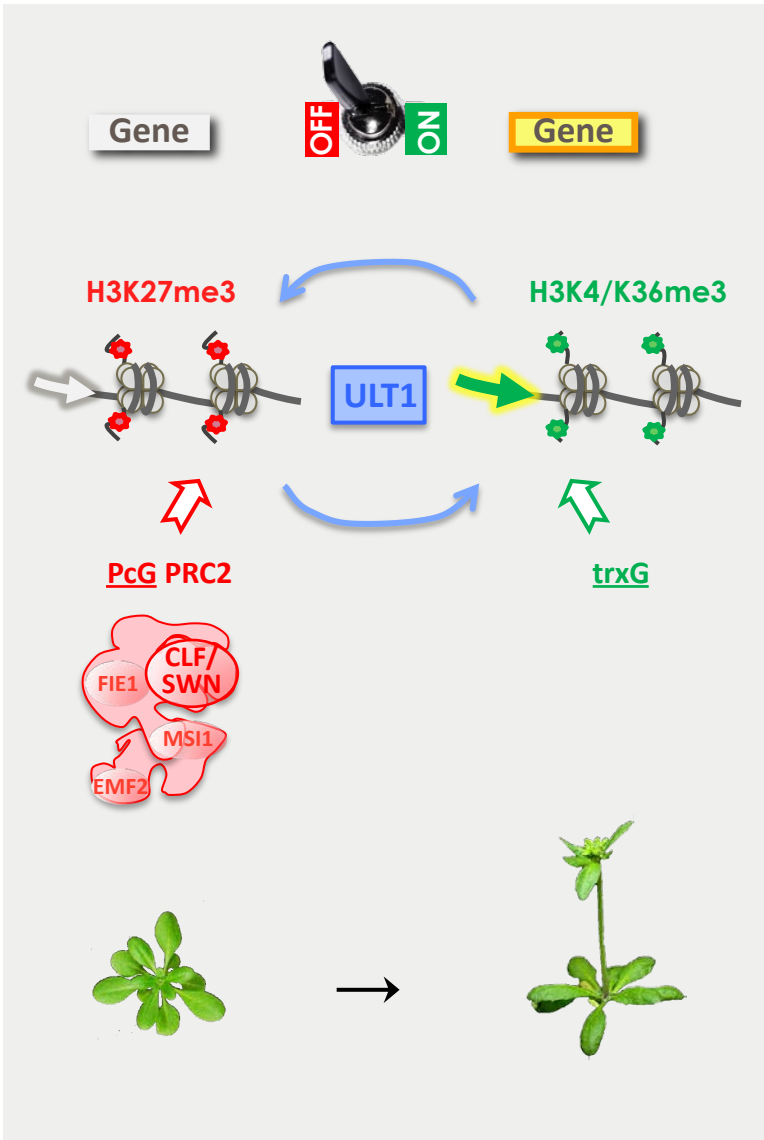
Chromatin dynamics : the ULTRAPETALA1 (ULT1) dual switch



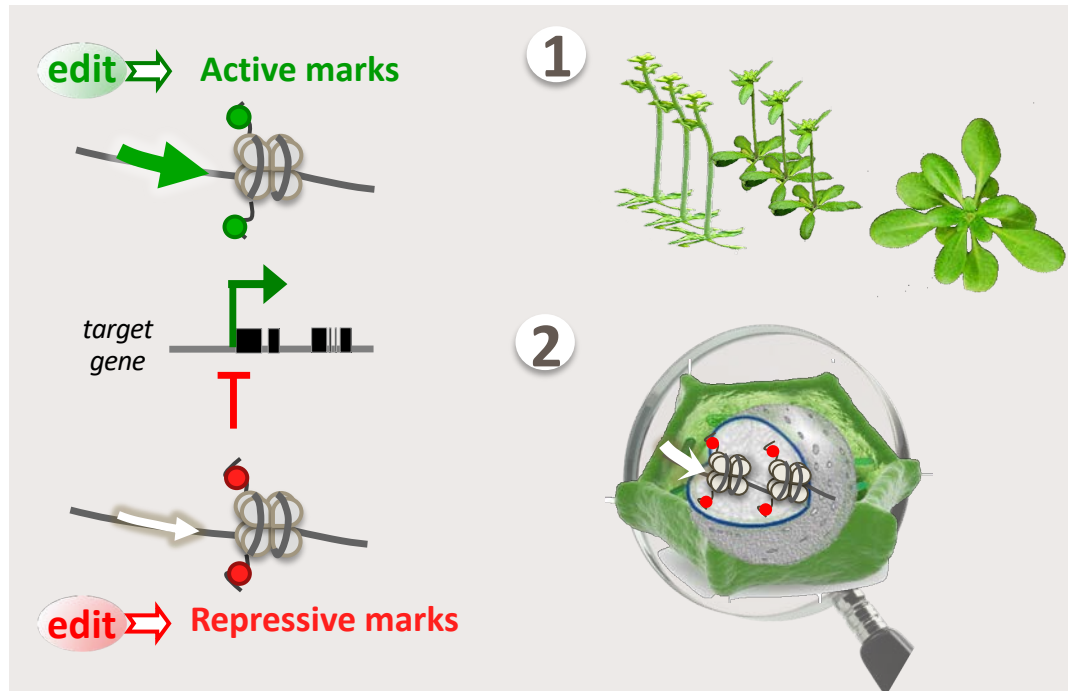
Chromatin dynamics : the ULTRAPETALA1 (ULT1) dual switch



Chromatin dynamics : the ULTRAPETALA1 (ULT1) dual switch



REWIRE: Editing histone marks to depict their **genuine function** & redirect plant development



★ **Innovative tools** : Chromatin rewiring [WP1]

Objective 1 . Development [WP2]

- Morphogenesis and cell fates
- Gene expression

★ **Cutting-edge methods**: *in situ* quantification and visualisation of chromatin & transcription

Objective 2 . Nucleus dynamics [WP3]

- Chromatin topology & structure
- Transcription

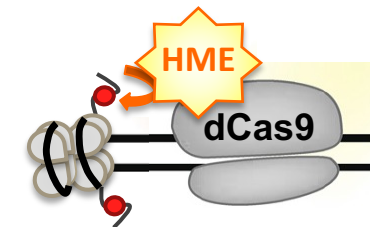
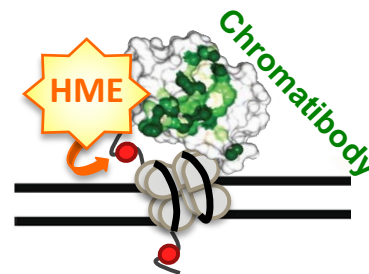
★ **The epigenetic editing tools:**

HME: Histone Modifying Enzyme

Genome-wide,
Chromatibody-induced

H3 mark
editing

Local,
dCas9-induced

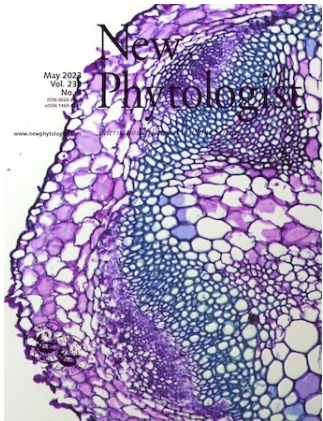


REWIRE: Editing histone marks to depict their genuine function & redirect plant development

Genome-wide



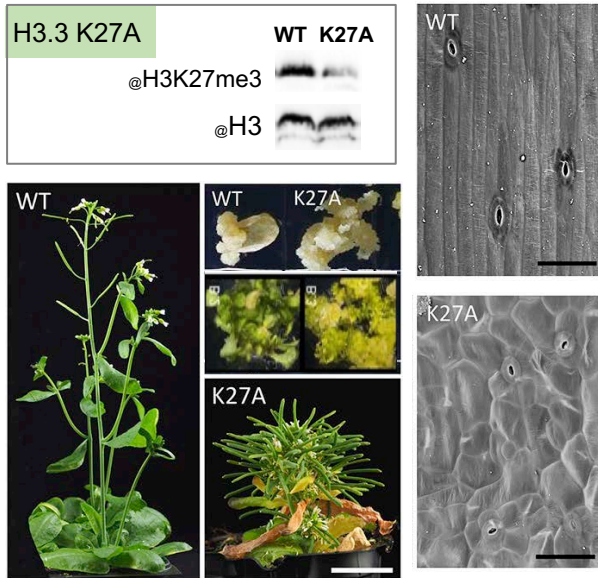
CNRS communication
© Christel Carles



Histone editing, a novel approach to explore the epigenetic regulation of plant development

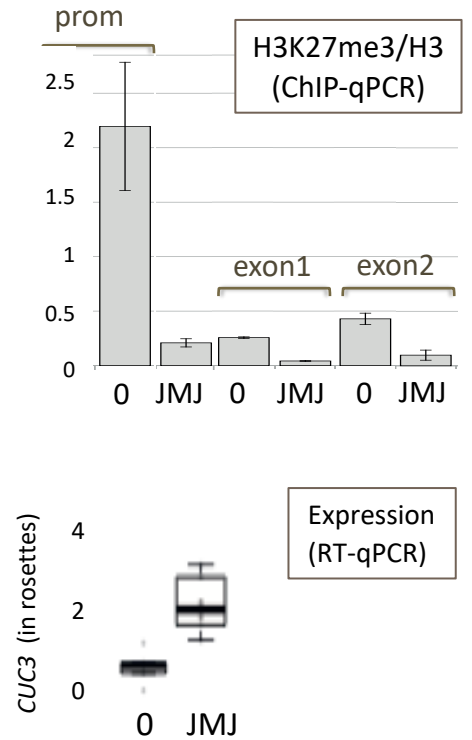
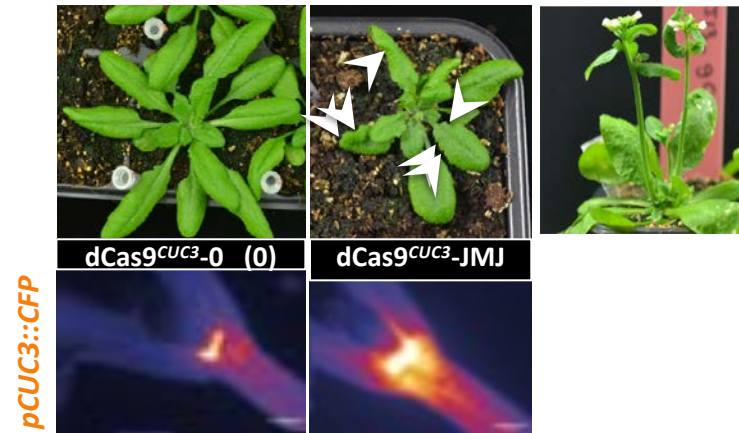
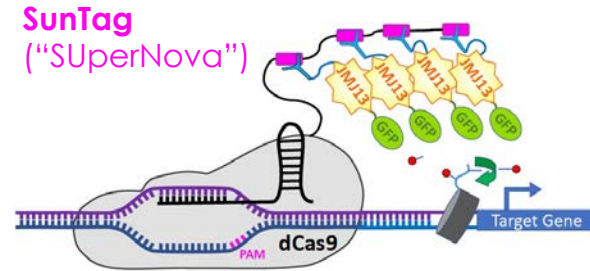
16 février 2023

RÉSULTATS SCIENTIFIQUES BIOLOGIE VÉGÉTALE



Fal et al., New Phytol 2023

Locus specific Chimeric dCas9 System for Enhanced Targeting



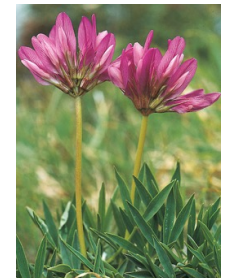
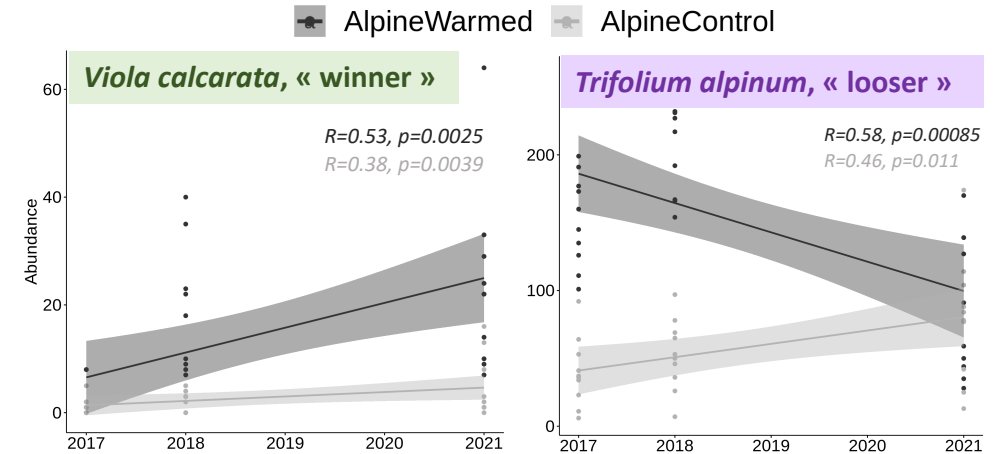
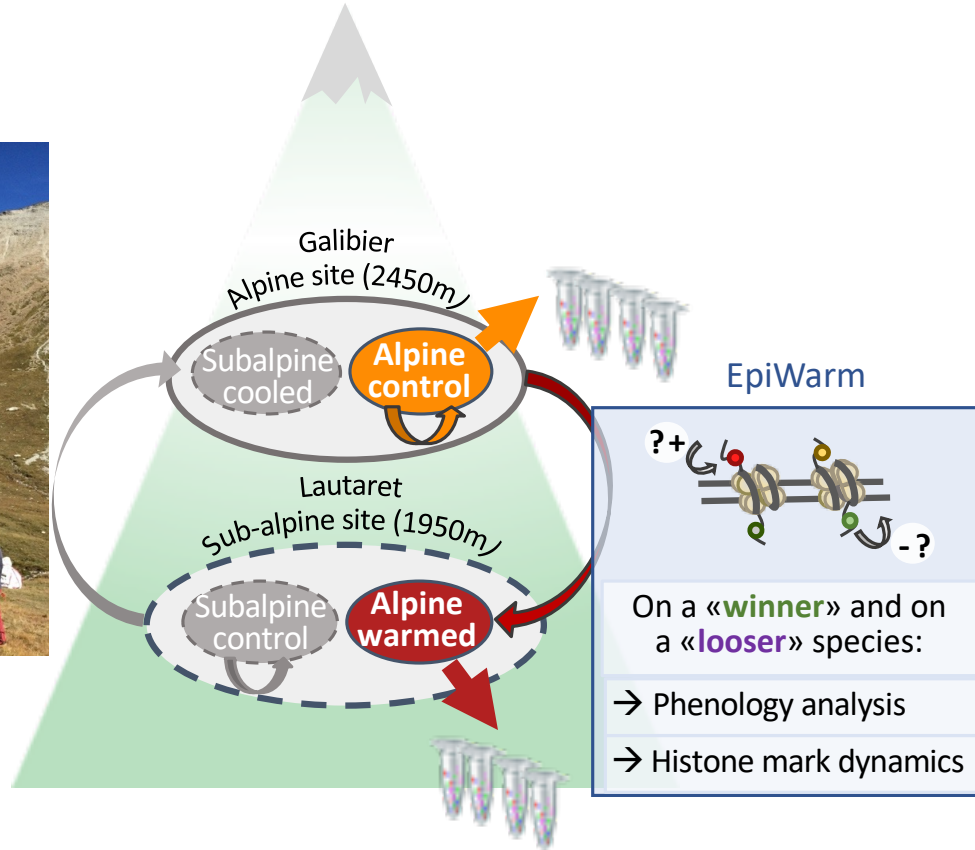
Multi-scale impact of epigenetic editing : from chromatin and transcription dynamics to cell fate

PhD Project Salim El Khoury
Co-dir. : J-Philippe Kleman (IBS)



EpiWarm

Environmental Epigenetics :



Question:

How do epigenetics of the transplanted population change ? → Analysis of epigenetics mark dynamics upon warming of the alpine species

ACKNOWLEDGEMENTS

Team members



ChromDev, January 2024



Colleagues for teaching activities @ UGA & UniMi:



Faycal Boussouar



Florence Courtois



Gabrielle Tichtinsky



Luca Gianfranceschi



Paolo Pesaresi



Camilla Betti



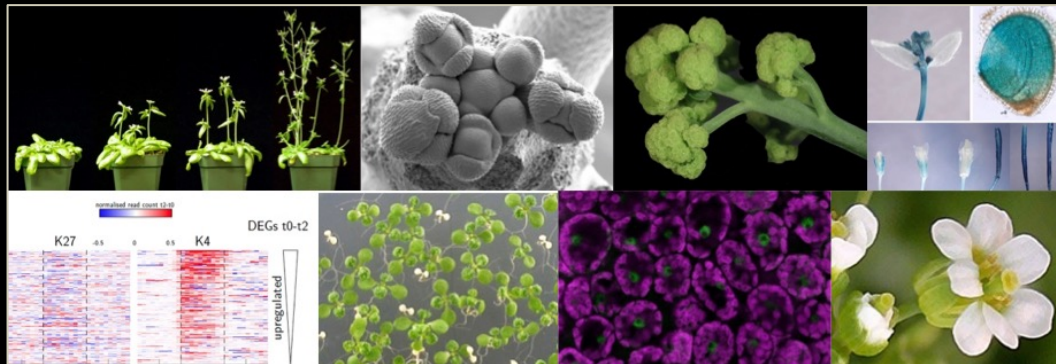
Stephan Nonchev



Sylvie Canavesio

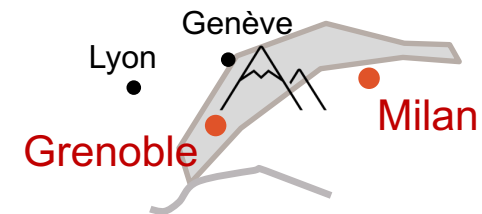


Anahide Faye



PLANT-Int

Master's degree in Plant Biology



Master of Plant Biology

Coord.: Christel CARLES



Master of Biology

Coord.: Alain BUISSON



M2

**PLANTA
International**

Plant
Sciences



**Double
Diploma**
UGA / UniMi



M1



UGA +
INPG
NNN

Nanoscience
and
Nano
technology



PhEDC

Physiology
Epigenetics
Development
Differentiation



NN

Neurosciences
Neurobiology



ISB

Integrative
Structural
Biology



IMID

Immunology
Microbiology
Infectious Dis.



Pro2Bio

« Professional » M2

LST

Lab
Science
Trading



BioTechCO

Biologie,
Chimie,
Commerce
(alternance)



Molecular and Cellular
Biology (MCB)



Bachelor (L3)

The Master's degree in Plant Biology PLANTA-International



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PLANT-Int Academic Coordinator :
Christel Carles (for course enquiries)
christel.carles@univ-grenoble-alpes.fr

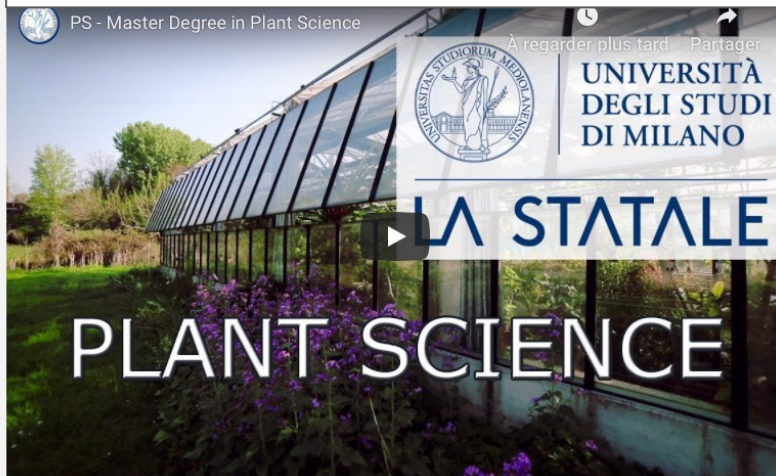
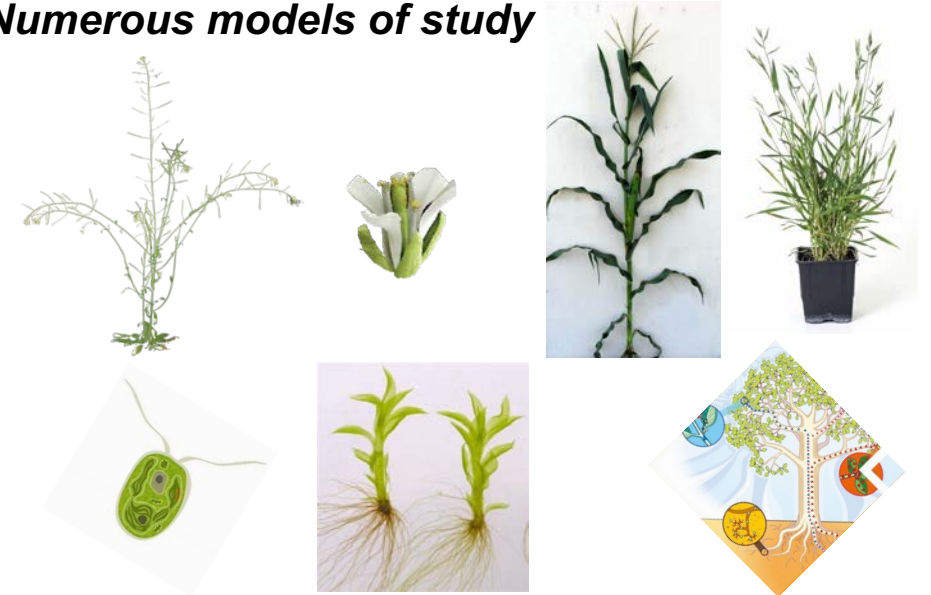
PLANT-Int Clerical Assistant:

Objectives

- Training scientists in **Plant Sciences**
→ careers in the academic/private sector
- Encouraging the development of **an international scientific & professional network**



Numerous models of study



ZOOM

Article "Algal remodeling in a ubiquitous planktonic photosymbiosis"

LINKS TO...

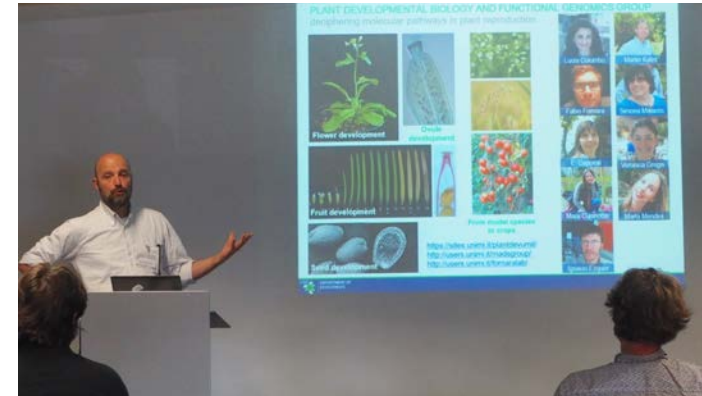
- The UNIMI PLANT-Int website
- The UGA teaching catalogue



PLANTA International (PLANT-Int) / Plant Science



- **International Training, double diploma (UGA / UniMi)**
 - ❖ **M1: Semester 1 @ UGA, Semester 2 @ UniMi**
 - ❖ **M2: “à la carte”(UGA or UniMi ou elsewhere ; remote teaching)**

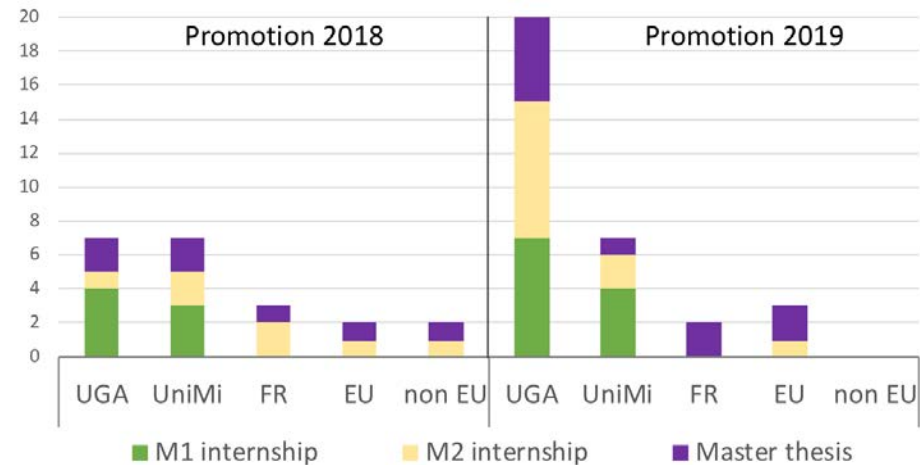


- **Plant sciences**, approached on a **multi-scale** basis :
(community >) organism > cell > molecule (> atome)

- **Choice of courses in the disciplines** of Developmental biology, Cell biology, molecular genetics, epigenetics, biochemistry, physiology, biostatistics, applied sciences

- **3 internships** with mobility strongly recommended

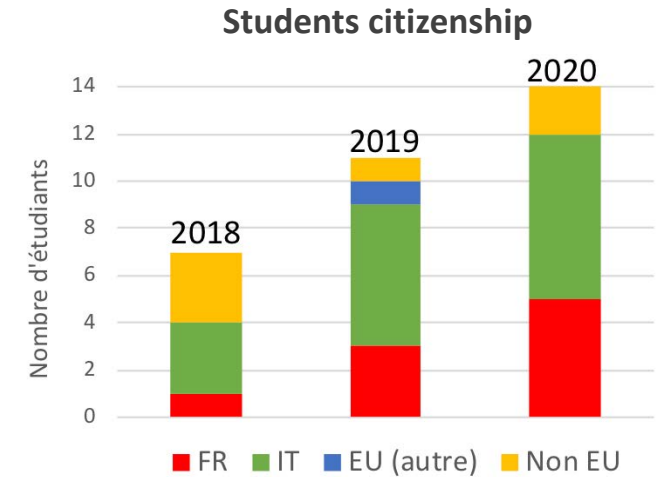
Places of internships



- **Innovative teaching methods** : Projects, collaborative work, tutorials, internships

Strengths of the PLANT-Int Master

- ✓ **Attractiveness & Internationalisation**
Groups of around twenty students
From Europe and beyond (Macedonia, South America, India, ...)
- **Annual scientific conference with hosting laboratories**



- ✓ **Professionalisation and further study**
 - Jobs in companies or start-ups
 - PhD in Plant Sciences
- **Financial support for student mobility**
Mobility grants, Scholarships



Selection Campaigns for the PLANTA-International Master's degree in Plant Biology

MonMaster 2024 : <https://candidature.monmaster.gouv.fr/>

- Ouverture de campagne : **Du 26 février 2024 au 24 mars 2024**
- Sélection des dossiers et entretiens: avant le 29 mai 2024
- Phase Principale d'admission sur MM : du **4 juin 2024 au 24 juin 2024**

PEF :

- Ouverture de campagne sur Portail d'Études en France : **le 1^{er} octobre 2023**
- Sélection des dossiers et entretiens: avant le 29 avril 2024
- Saisie des résultat sur Portail d'Études en France : **le 3 mai 2024**

Coordinators



PLANTA International (PLANT-Int)

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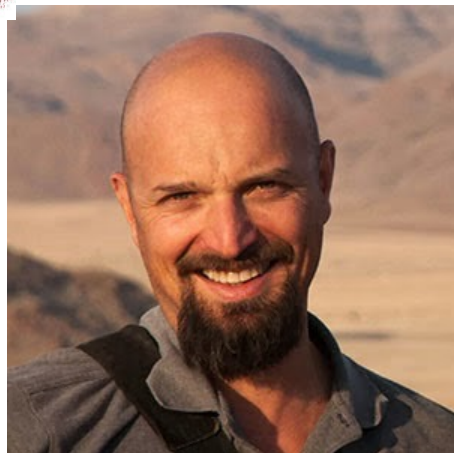
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