880723

Did you log in mediaspace with your SSO?

Checkpoints

March 15: Divide into groups - pick up a topic you love – define the format

March 25: List of paper on file

April 05-15: Paper presentation

May 07: upload your podcast on mediaspace

May 27: ANNOTO, discussion peer evaluation

880723

PAST TOPICS

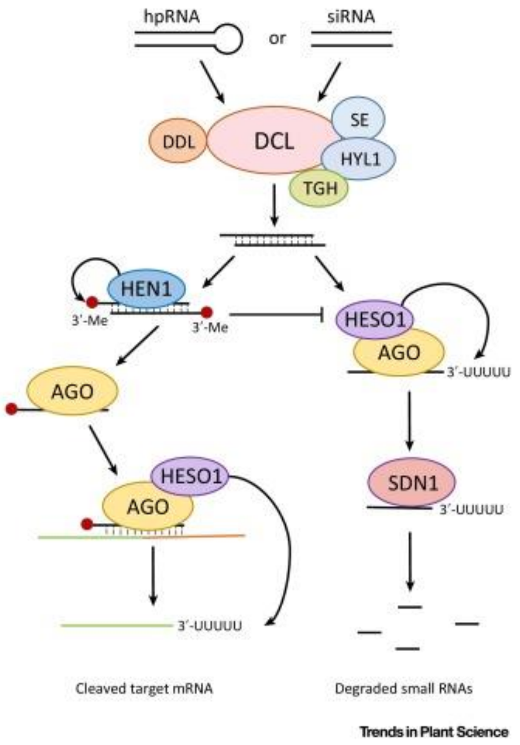
- Mitigation and Susiba2 rice
- Floodings
- Snorkel, Sub1 and RAP2.12 ERF VII

NEXT TOPICS:

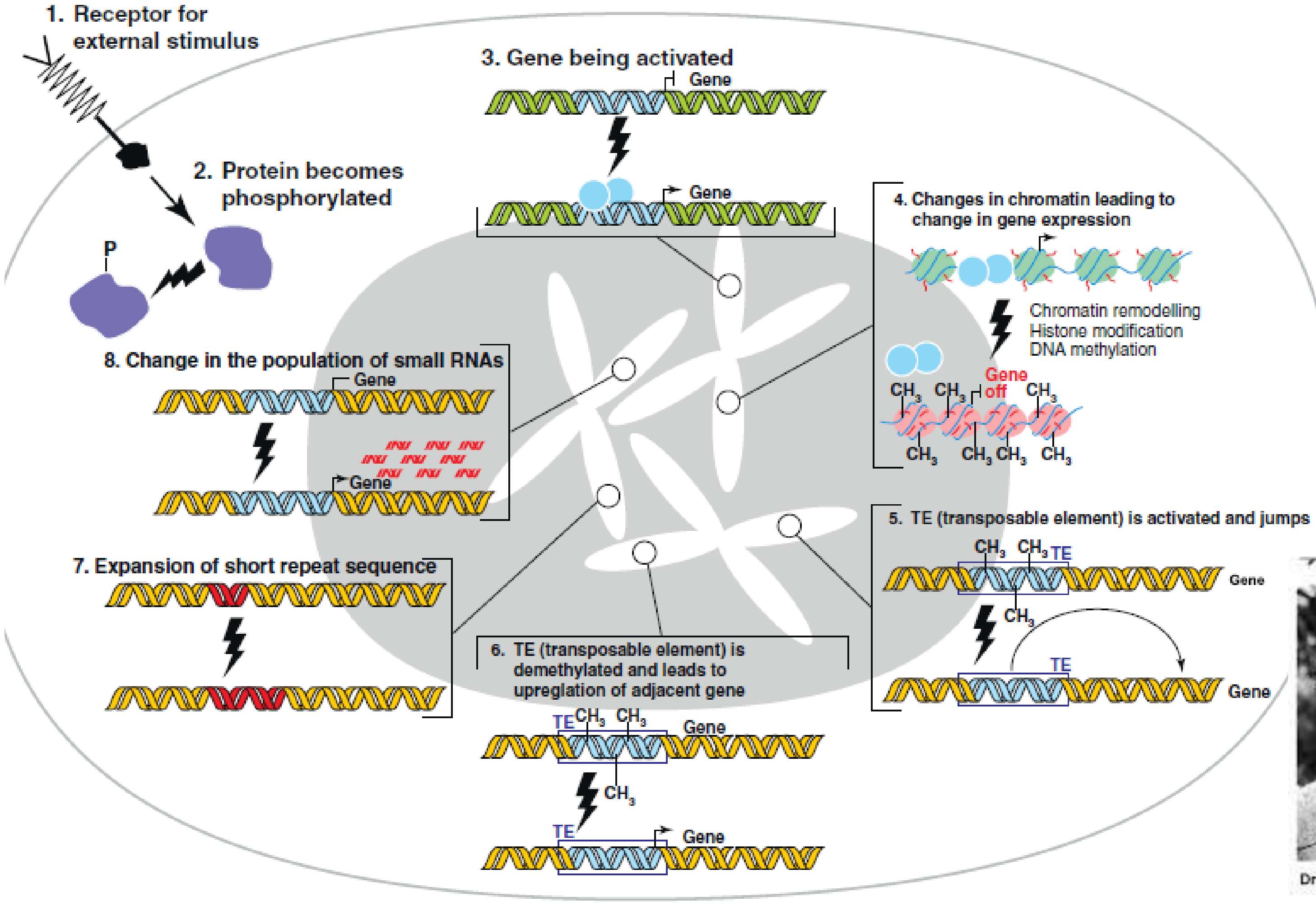
- Epigenetics and flowering time
- Epigenetics and drought resistance

Bridging evolution, ecology and molecular biology

Plastic molecular responses to environmental signals can occur in many ways.



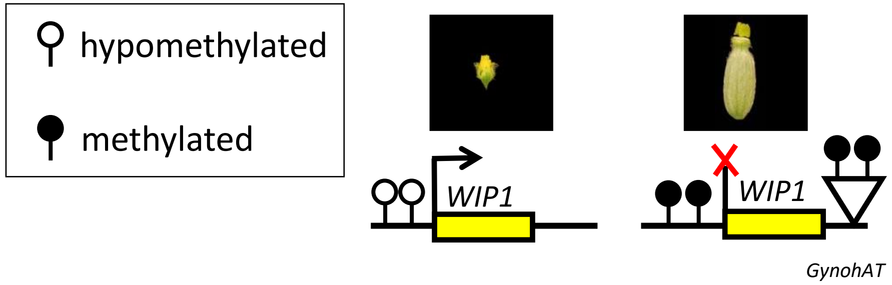
Trends in Plant Science



Dr.Barbara McClintock (June 16, 1902 – September 2, 1992)

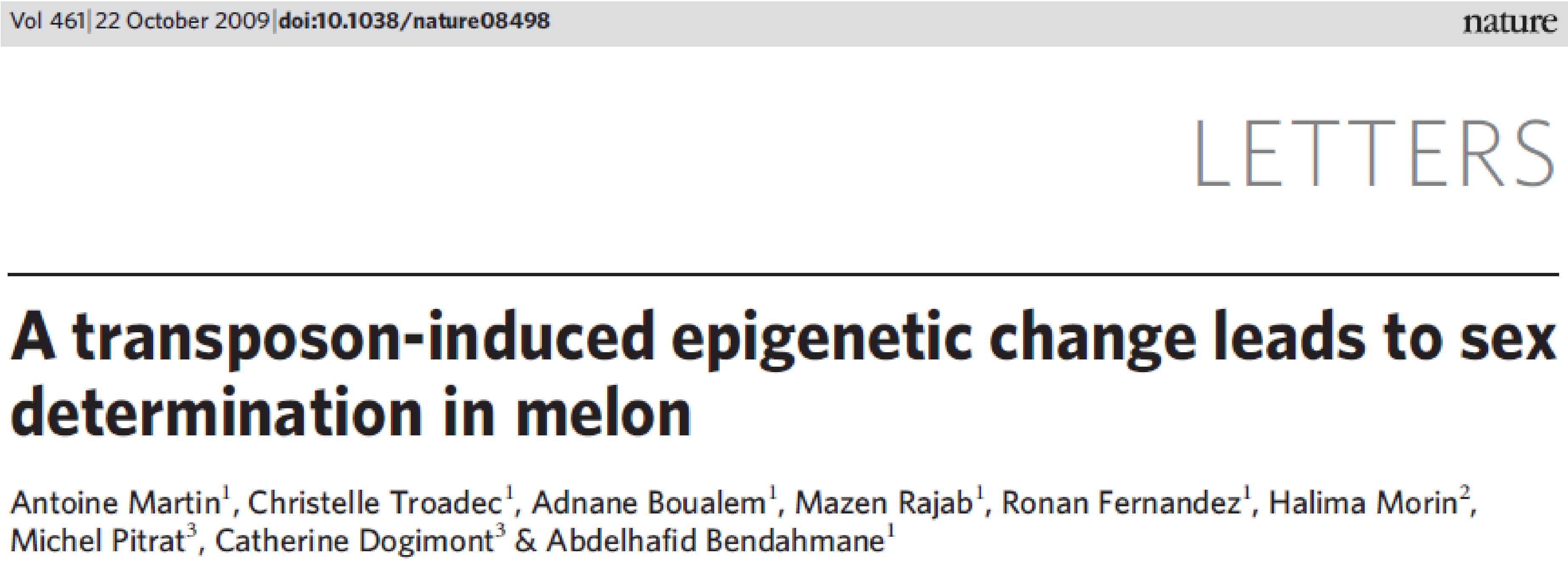
TRENDS in Plant Science

can lead to trans-generational effects? and adaptive?



gynoecious

Martin et al, Nature (2009)

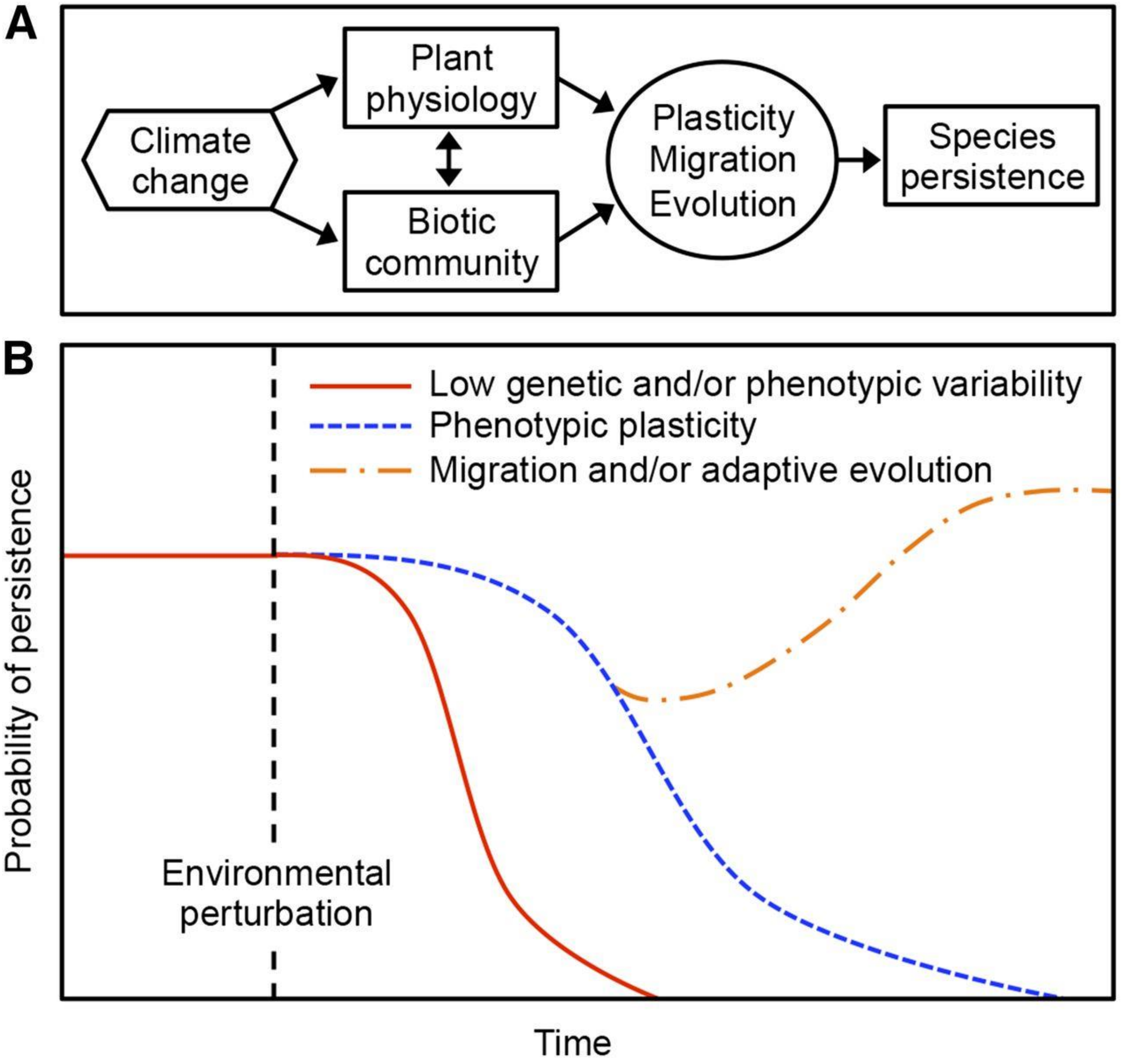


Vol 461| 22 October 2009| **doi:10.1038/nature08498** nature

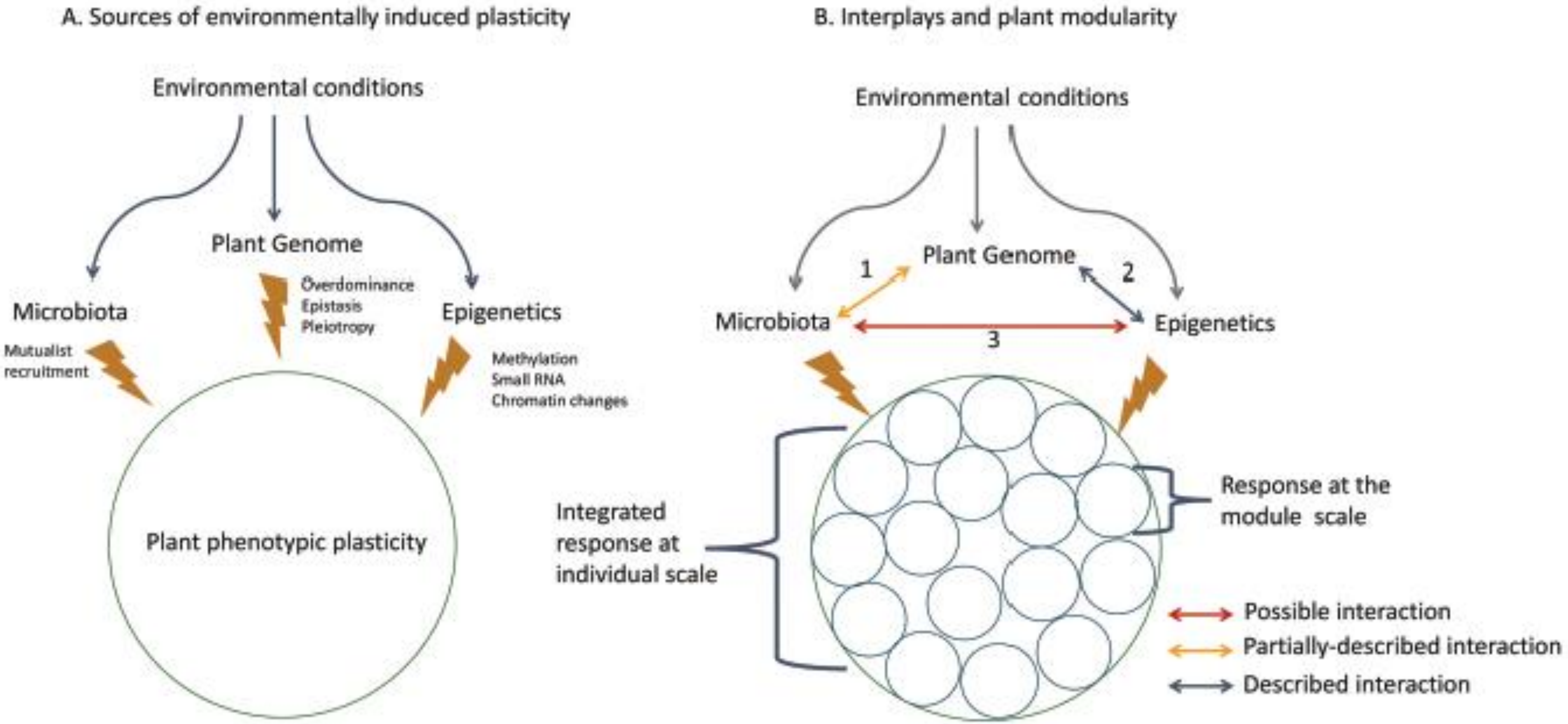
LETTERS

A transposon-induced epigenetic change leads to sex determination in melon

Antoine Martin[1], Christelle Troadec[1], Adnane Boualem[1], Mazen Rajab[1], Ronan Fernandez[1], Halima Morin[2], Michel Pitrat[3], Catherine Dogimont[3] & Abdelhafid Bendahmane[1]


A
Climate change
Plant physiology
Biotic community
Plasticity
Migration
Evolution
Species persistence
B
Low genetic and/or phenotypic variability
Phenotypic plasticity
Migration and/or adaptive evolution
Probability of persistence
Environmental perturbation
Time

Plant phenotypic plasticity is triggered by environmental constraints. Phenotypic changes induced are not solely genetically controlled but are also based on either epigenetic marks or plant microbiota by recruitment of mutualists. This plant ‘toolbox’ allows a rapid response to environmental constraints.



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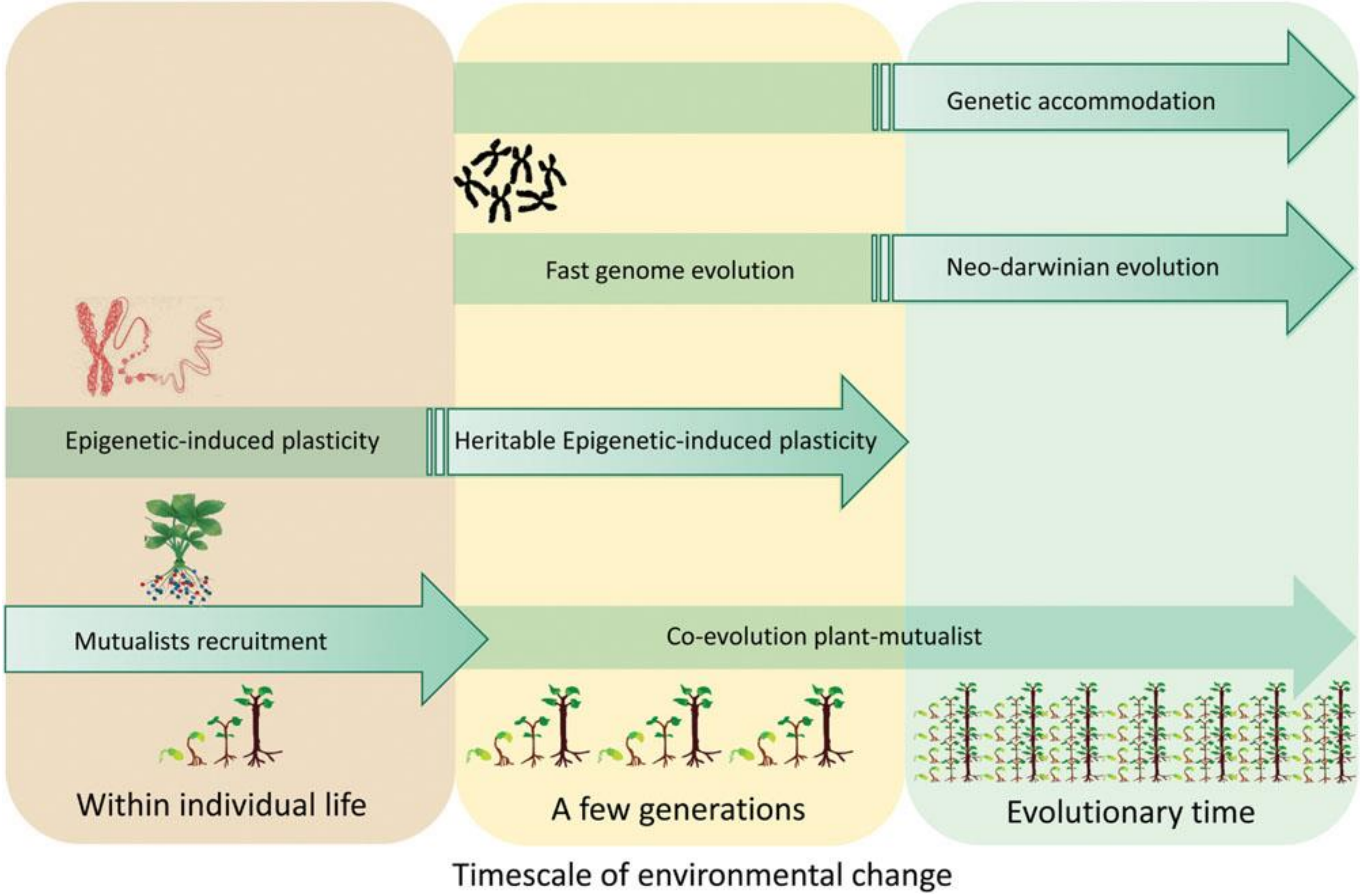
- Snorkel, Sub1 and RAP2.12 ERF VII

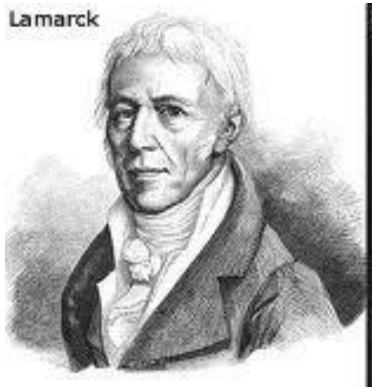
NEXT TOPICS:

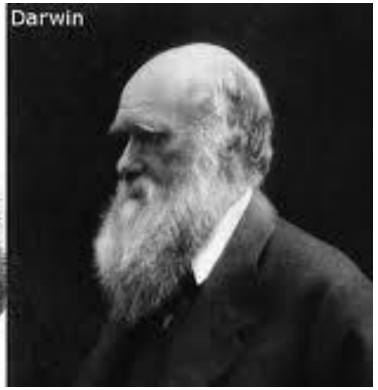
- Epigenetics and flowering time
- Epigenetics and drought resistance

A plant’s phenotypic variations can be inherited even in the case of a phenotypic trait not controlled by a gene/genome variation.



Lamarck revisited





Lamarck’s revenge: The epigenetics revolution may redeem one of Darwin’s oldest rivals

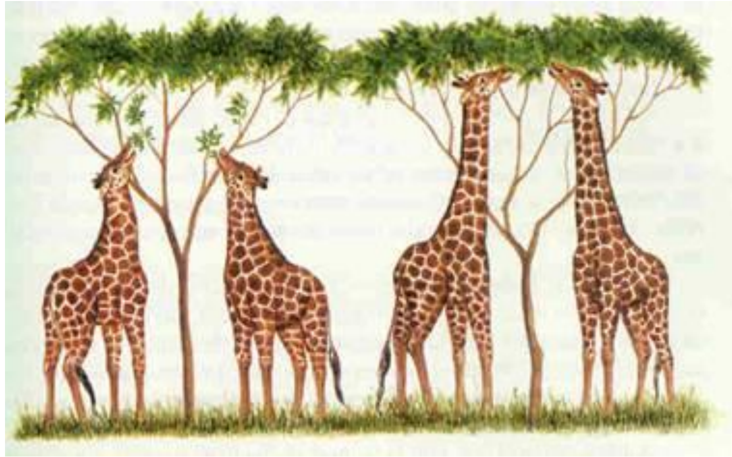
"Une des intuitions de Lamarck pourrait s'avérer juste..."

LE MONDE SCIENCE ET TECHNO | 13.04.2012 à 21h04 • Mis à jour le 13.04.2012 à 21h04

Epigenetics: In Defense of Lamarck

NEWS AND VIEWS

Lamarck revisited: epigenetic inheritance of ancestral odor fear conditioning



Climate change is inevitable within this century

Spotlight

The impact of climate change on plant epigenomes

Qiong A. Liu

Biochemistry and Cell Biology Department, Stony Brook University, Stony Brook, NY 11794, USA

Predicted that atmospheric CO2 will reach to 550–700 ppm by 2050 and 650–1200 ppm by 2100, which means a global climatic warming of 2.5 °C or more by 2050 and of up to 6.4 °C by the end of this century. **Severe and longer-lasting droughts**.

The opposing effects of CO2 and temperature on plant growth and other traits

elevated CO_2 concentrations increased photosynthetic carbon gain and net primary production, improved the efficiency of nitrogen usage, and increased tolerance to drought conditions

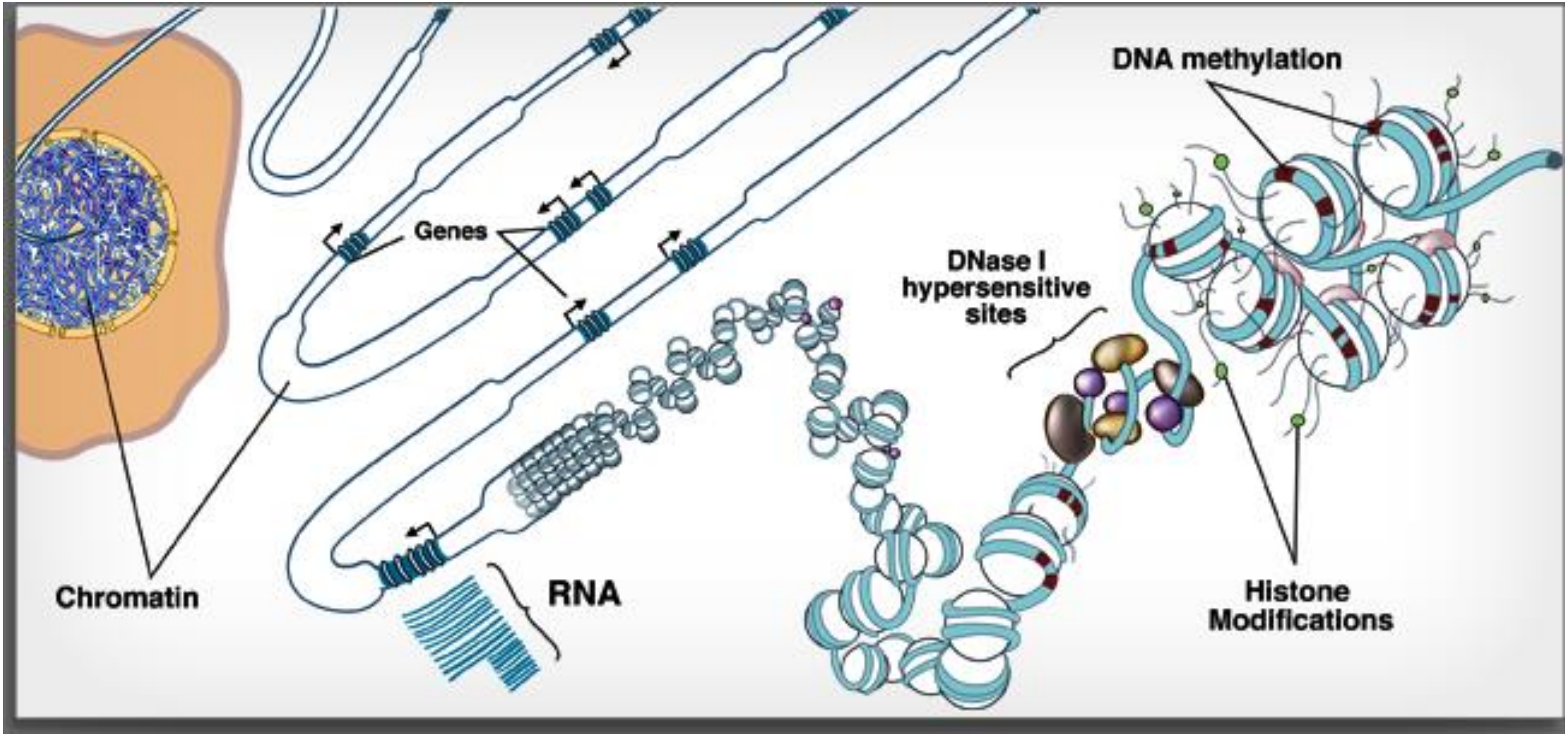
high seasonal temperatures significantly lowered biomass and grain production in a variety of crops and fruits

Climate changes are rapid, plants need to adapt rapidly

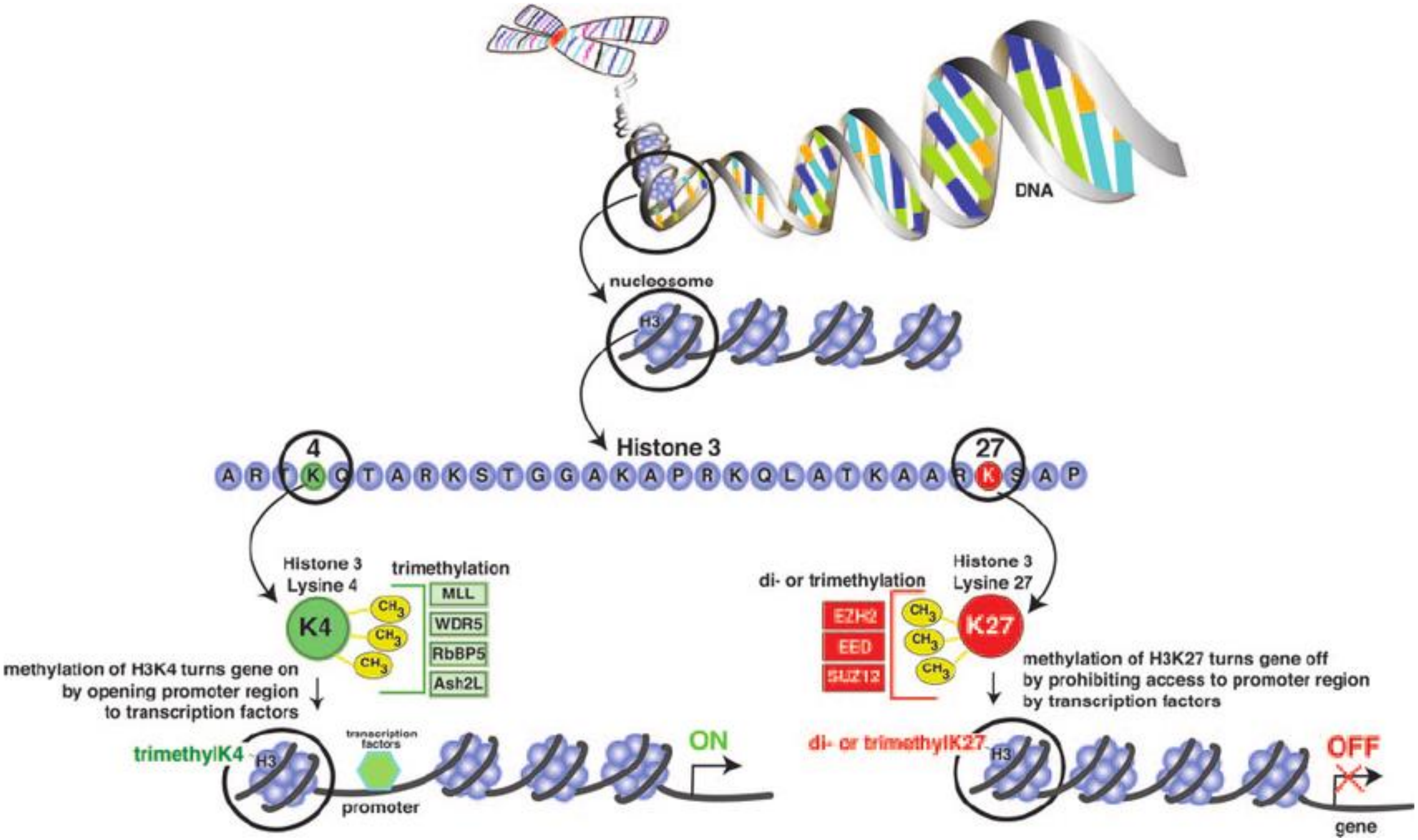
One avenue for rapid adaptation may be through **modification of DNA and histone proteins, as well as through expression of noncoding small RNAs (sRNA)**. Collectively, the arrangement and distribution of these modifications are referred to as the '**epigenome**' (http://www.roadmapepigenomics.org/).

Changes to the epigenome **may or may not be heritable**.

However, in cases of **a true epigenetic phenomenon, the change, which is stably inherited, cannot be correlated with a genetic change**.


DNA methylation
Genes
DNase I hypersensitive sites
Chromatin
RNA
Histone Modifications

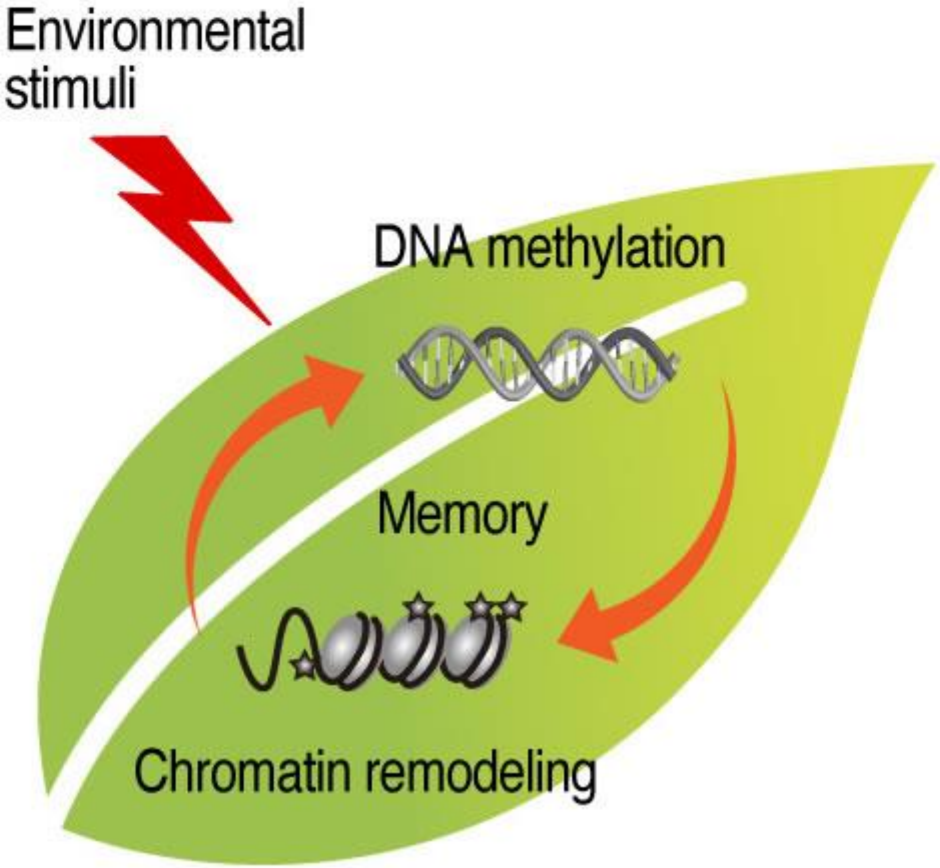
Chromatin modification are both **positive** and **negative** regulators



methylation of H3K4 turns gene on by opening promoter region to transcription factors

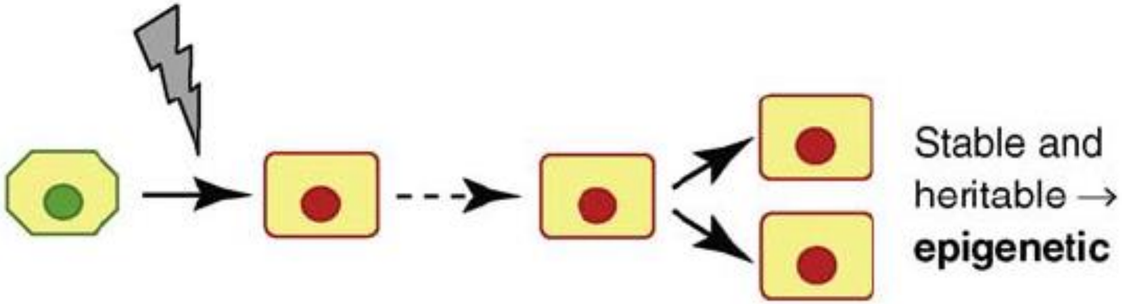
methylation of H3K27 turns gene off by prohibiting access to promoter region by transcription factors

Histone H3K27



H3K27 is known for one thing: shutting down transcription. When H3K27 is trimethylated, it is tightly associated with inactive gene promoters.

Can chromatin changes induced by environmental stimuli be inherited when the stress is released?



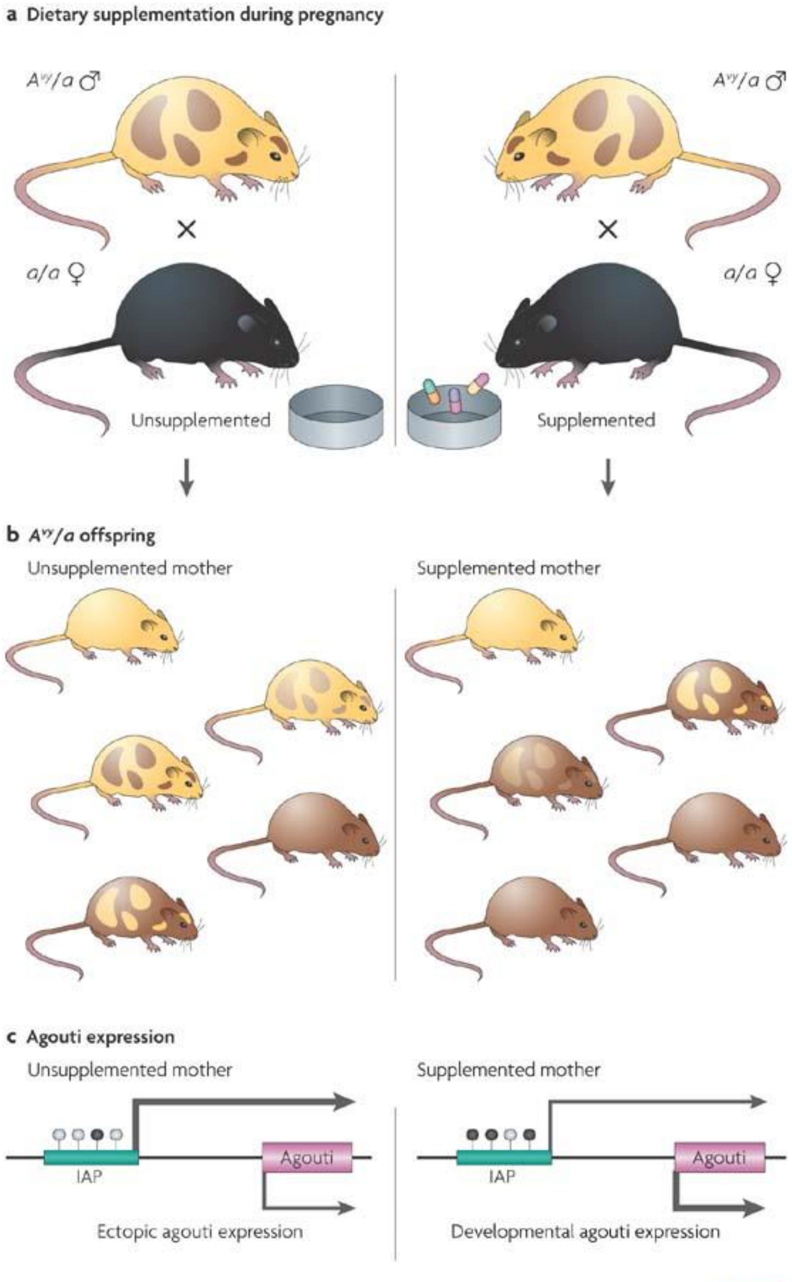
Ex. H3K27me3 or DNAme

through somatic divisions?

or

through generation?

Adaptative Potentiel



Nature Reviews | Genetics

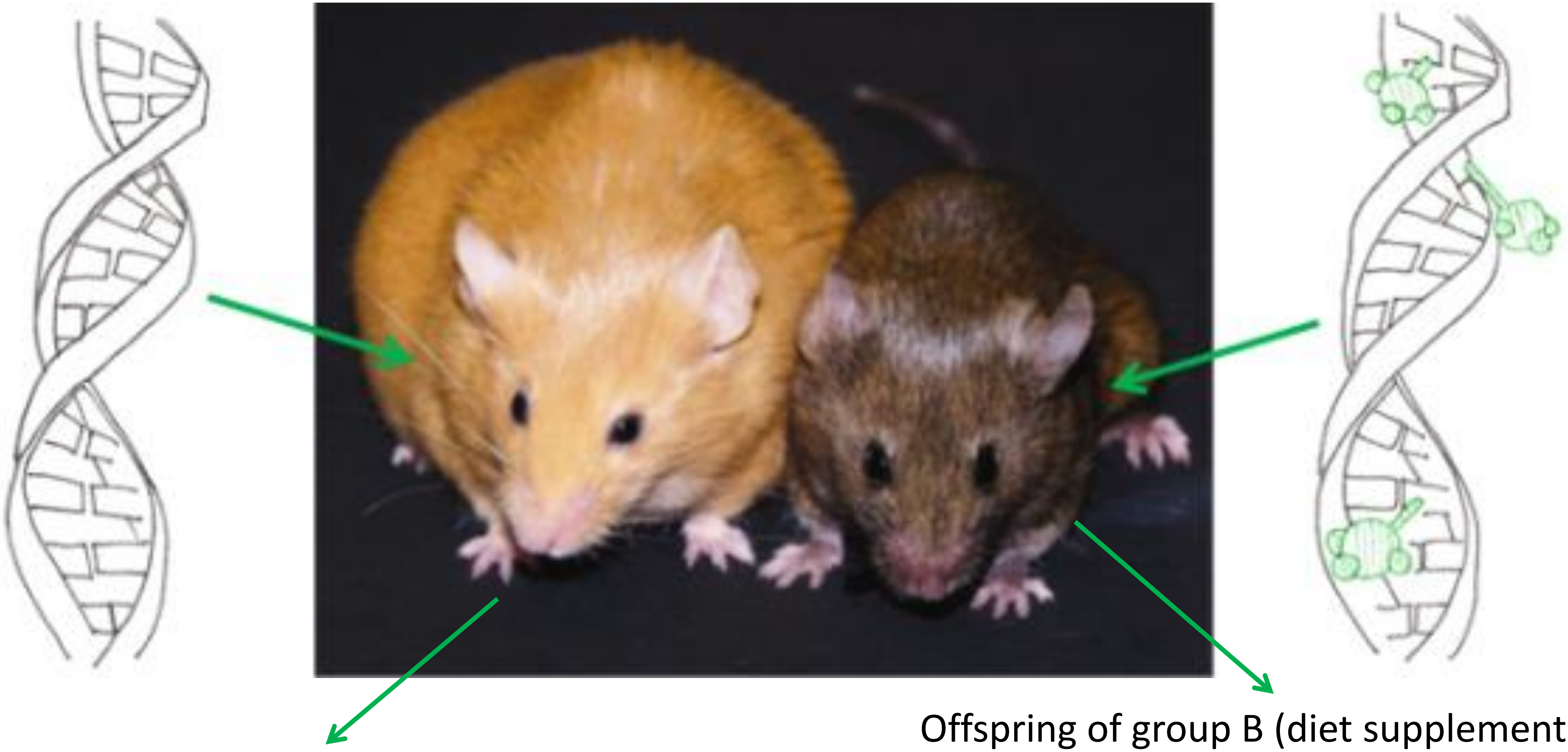
Offspring of group A (restricted diet):

- Yellow coats
- Obese
- More prone to cancer and diabetes

Offspring of group B (diet supplemented with choline, folic acid, betaine and Vitamin B12):

- Brown coats
- Healthy weight
- Less prone to disease

Agouti mice and epigenetics



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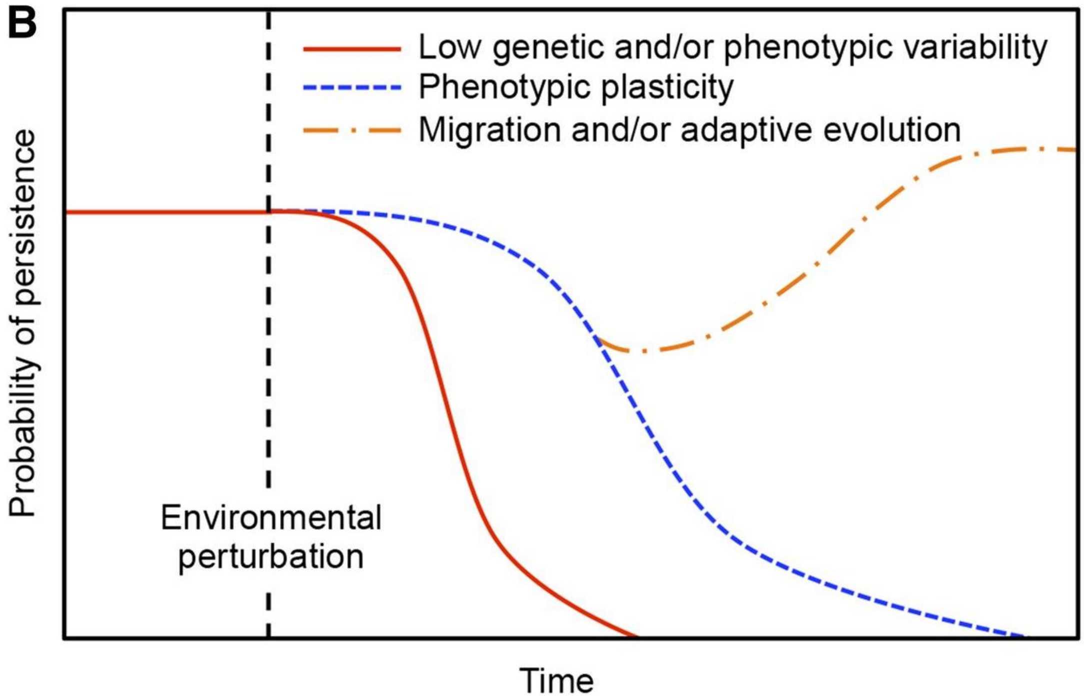
Flowering time

- The study of cyclical biological events in the natural world is called phenology. Flowering time is a seasonal phenological process.

- Altered flowering time and disruption of meet pollinators.

- Early flowering and late freezing events.

- Adaptative potential

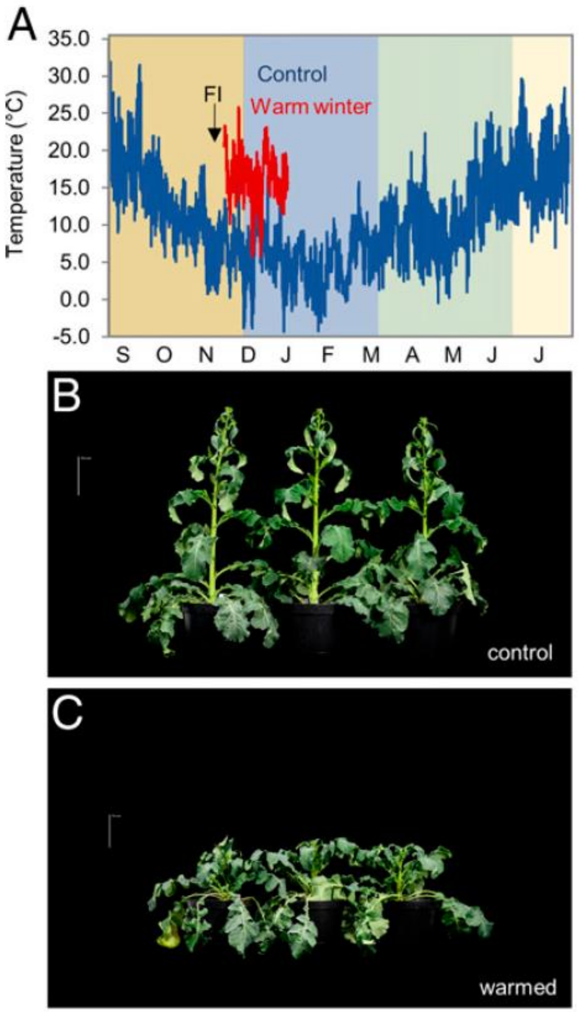


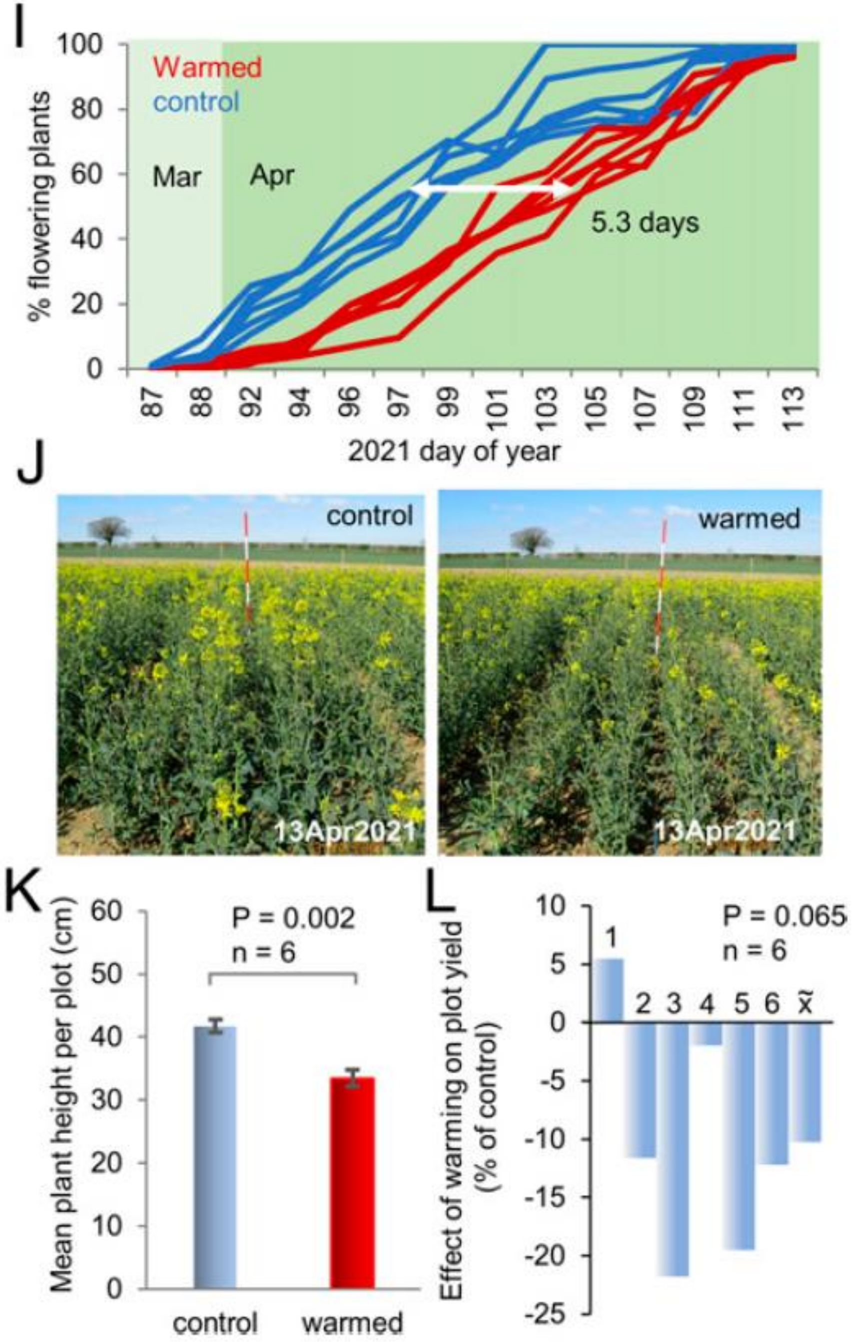
PNAS RESEARCH ARTICLE | PLANT BIOLOGY OPEN ACCESS

Winter warming post floral initiation delays flowering via bud dormancy activation and affects yield in a winter annual crop

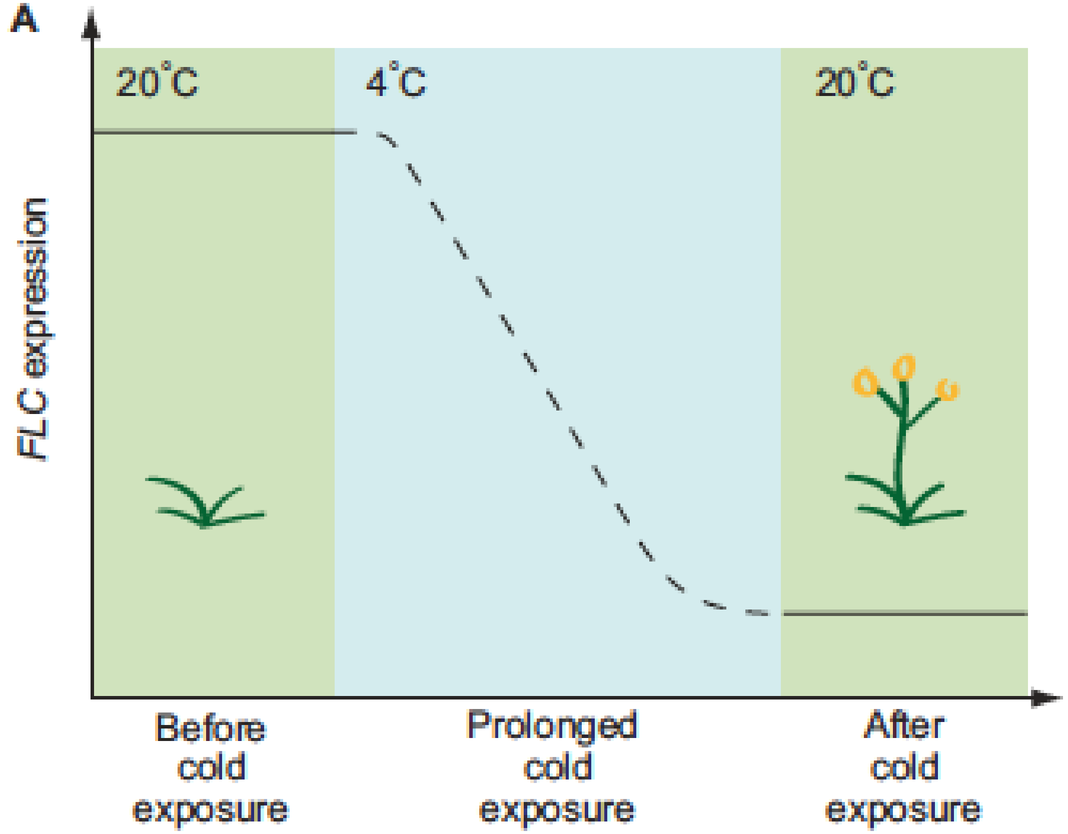
Xiang Lu[a,1,2], Carmel M. O'Neill[a,2], Samuel Warner[a], Qing Xiong[a,1], Xiaochao Chen[a], Rachel Wells[a], and Steven Penfield[a,3]

Edited by Richard Amasino, University of Wisconsin–Madison, Madison, WI; received March 14, 2022; accepted July 28, 2022





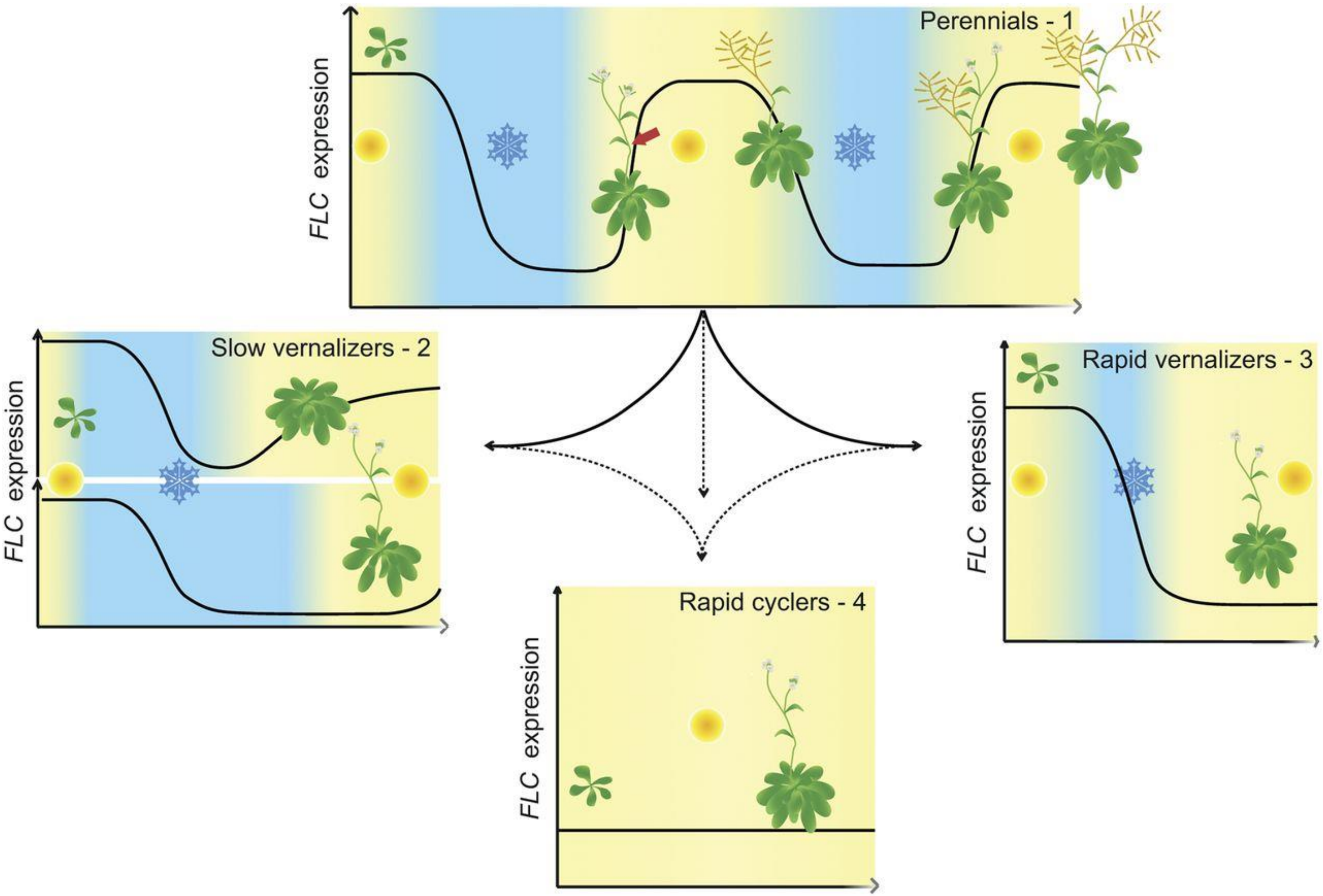
Vernalization – a cold-induced epigenetic switch (cold memory)



The floral repressor gene, FLC is repressed when plants are exposed to the cold (WINTER) in a quantitative manner.

Subsequently, remains stably repressed on the return to warm temperature (SPRING).

- Vernalization: the acceleration of flowering by the prolonged cold of winter.
- FLC (FLOWERING LOCUS C): a MADS box transcriptional repressor involved in silencing the genes that are required for the switch to flowering.



Epigenetic Regulation in Plant Responses to the Environment

David C. Baulcombe[1] and Caroline Dean[2]

[1]Department of Plant Science, University of Cambridge, Cambridge CB2 3EA, United Kingdom; [2]Department of Cell and Developmental Biology, John Innes Centre, Norwich NR4 7UH, United Kingdom

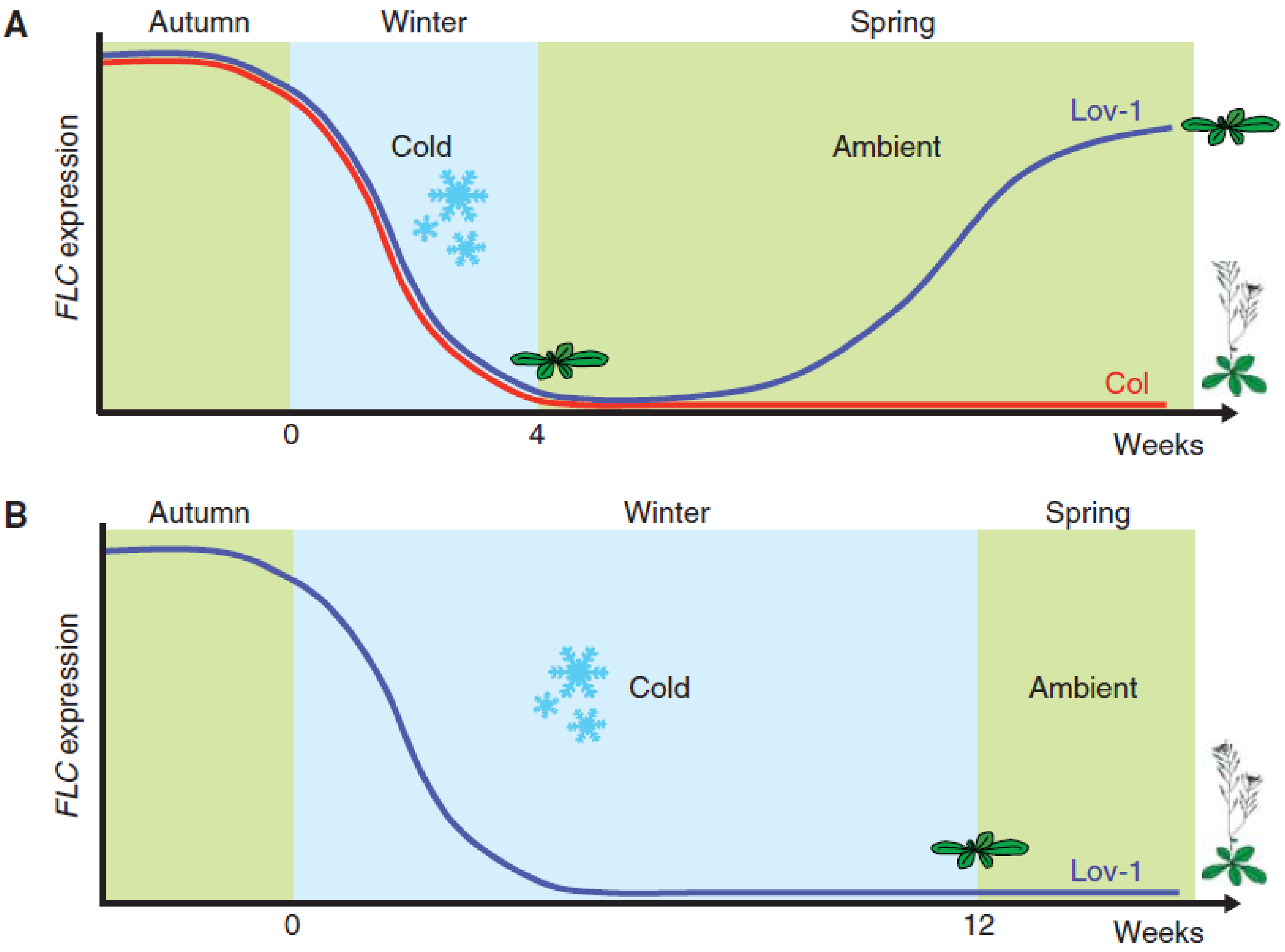
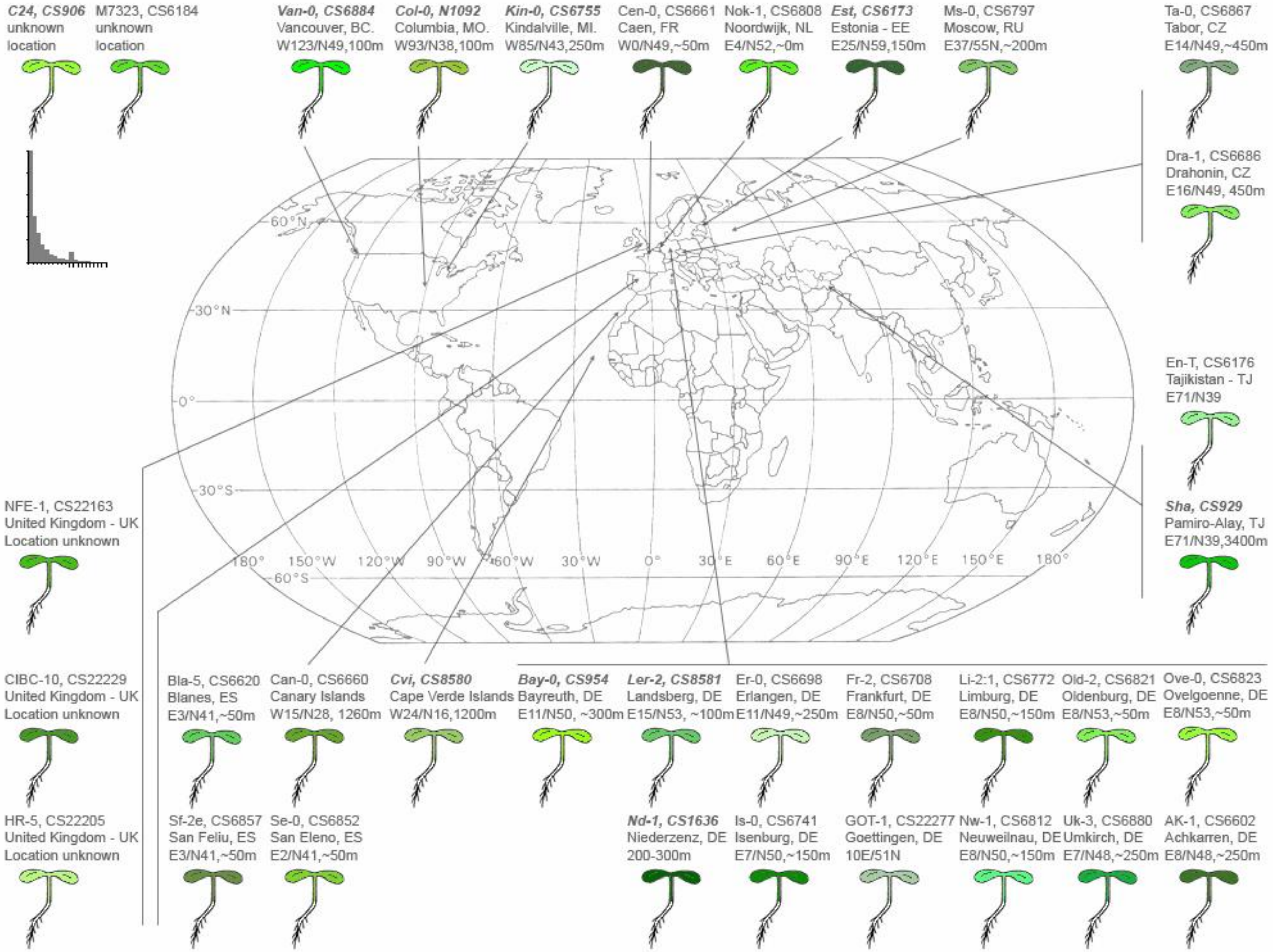
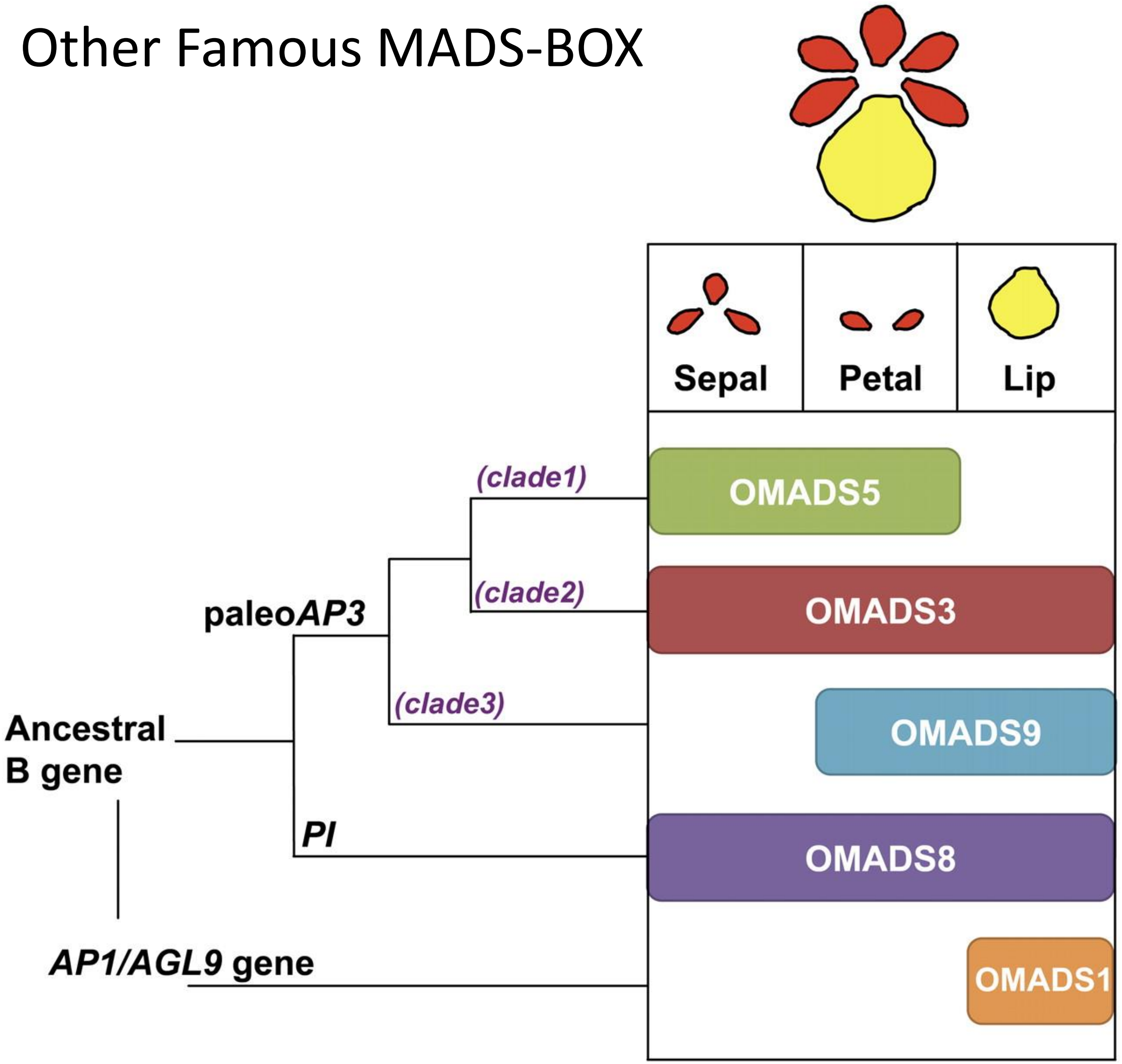
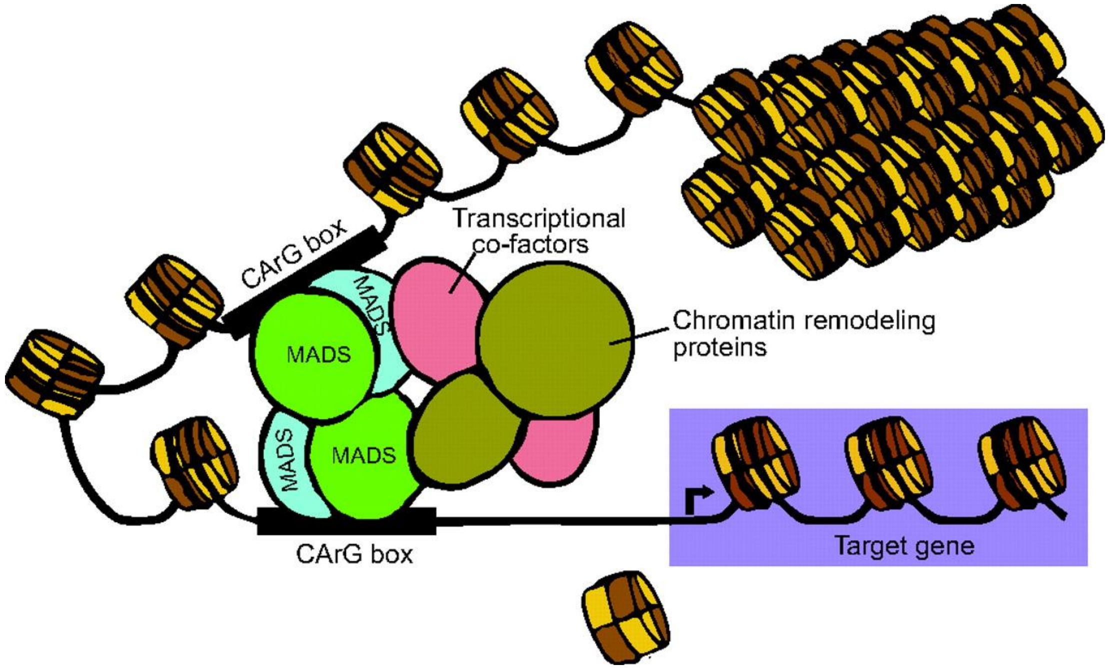


Figure 5. Quantitative variation in the epigenetic silencing of *FLC* in *Arabidopsis* accessions from different climates. (*A*) An *Arabidopsis* accession from Germany (Col, red line) requires only 4 wk of cold to epigenetically silence *FLC*. Lov-1, from the northern limit of its range in Northern Sweden (latitude 62.5°N), sees reactivation of the *FLC* gene if the cold period is so short, resulting in an inability to become vernalized and, hence, does not flower. (*B*) Lov-1 needs a much longer period of cold (12 wk) for full epigenetic silencing. Molecular analysis has shown this difference is the result of a small number of *cis* polymorphisms near the PHD-PRC2 nucleation region in intron 1.

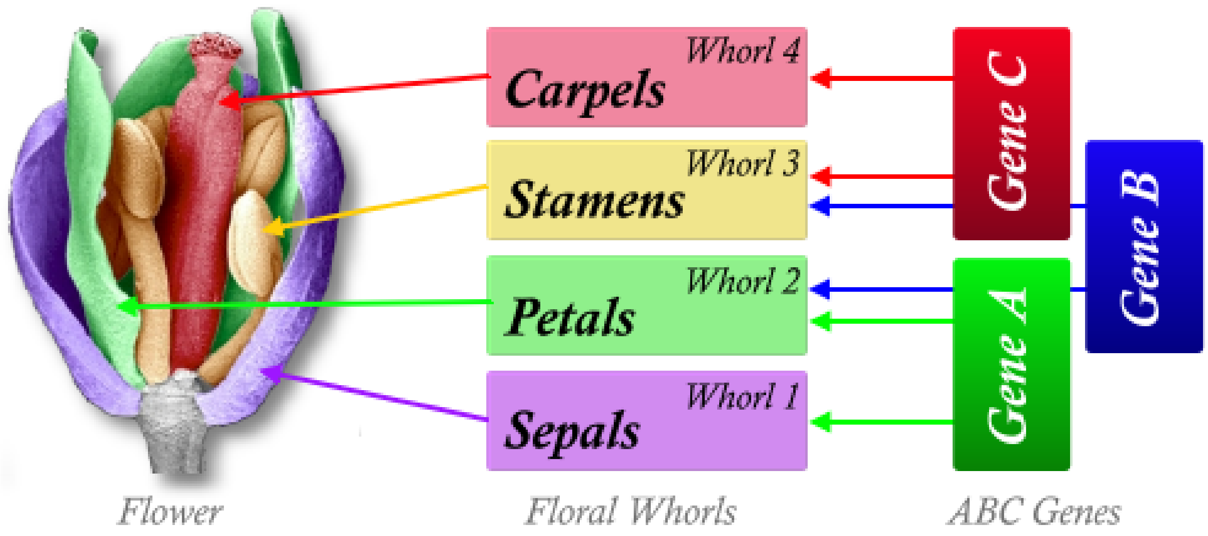

C24, CS906
unknown location
M7323, CS6184
unknown location
Van-0, CS6884
Vancouver, BC.
W123/N49,100m
Col-0, N1092
Columbia, MO.
W93/N38,100m
Kin-0, CS6755
Kindalville, MI.
W85/N43,250m
Cen-0, CS6661
Caen, FR
W0/N49,~50m
Nok-1, CS6808
Noordwijk, NL
E4/N52,~0m
Est, CS6173
Estonia - EE
E25/N59,150m
Ms-0, CS6797
Moscow, RU
E37/55N,~200m
Ta-0, CS6867
Tabor, CZ
E14/N49,~450m
Dra-1, CS6686
Drahonin, CZ
E16/N49, 450m
En-T, CS6176
Tajikistan - TJ
E71/N39
Sha, CS929
Pamiro-Alay, TJ
E71/N39,3400m
60°N
30°N
0°
30°S
60°S
180°
150°W
120°W
90°W
60°W
30°W
0°
30°E
60°E
90°E
120°E
150°E
180°
NFE-1, CS22163
United Kingdom - UK
Location unknown
CIBC-10, CS22229
United Kingdom - UK
Location unknown
HR-5, CS22205
United Kingdom - UK
Location unknown
Bla-5, CS6620
Blanes, ES
E3/N41,~50m
Can-0, CS6660
Canary Islands
W15/N28, 1260m
Cvi, CS8580
Cape Verde Islands
W24/N16,1200m
Bay-0, CS954
Bayreuth, DE
E11/N50, ~300m
Ler-2, CS8581
Landsberg, DE
E15/N53, ~100m
Er-0, CS6698
Erlangen, DE
E11/N49,~250m
Fr-2, CS6708
Frankfurt, DE
E8/N50,~50m
Li-2:1, CS6772
Limburg, DE
E8/N50,~150m
Old-2, CS6821
Oldenburg, DE
E8/N53,~50m
Ove-0, CS6823
Ovelgoenne, DE
E8/N53,~50m
Sf-2e, CS6857
San Feliu, ES
E3/N41,~50m
Se-0, CS6852
San Eleno, ES
E2/N41,~50m
Nd-1, CS1636
Niederzenz, DE
200-300m
Is-0, CS6741
Isenburg, DE
E7/N50,~150m
GOT-1, CS22277
Goettingen, DE
10E/51N
Nw-1, CS6812
Neuweilnau, DE
E8/N50,~150m
Uk-3, CS6880
Umkirch, DE
E7/N48,~250m
AK-1, CS6602
Achkarren, DE
E8/N48,~250m

Other Famous MADS-BOX





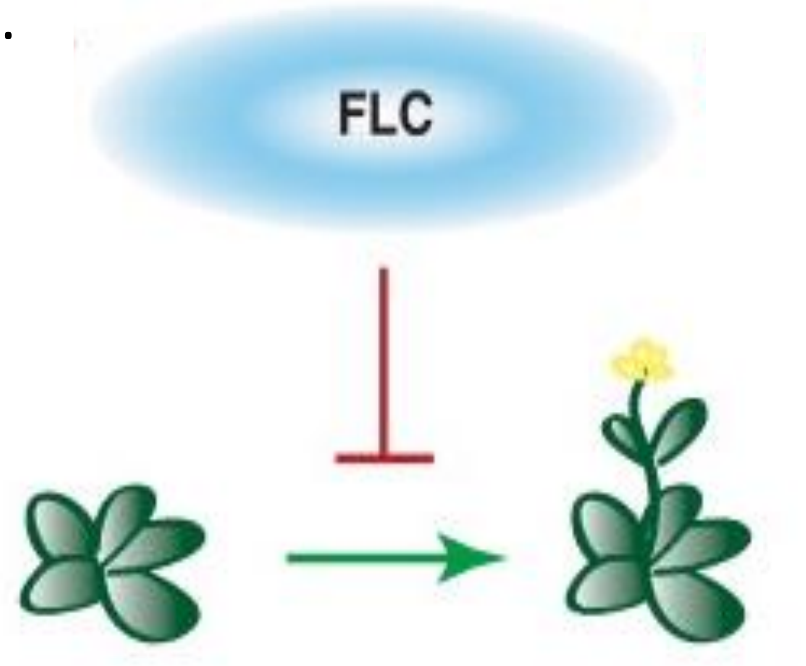
ABC models

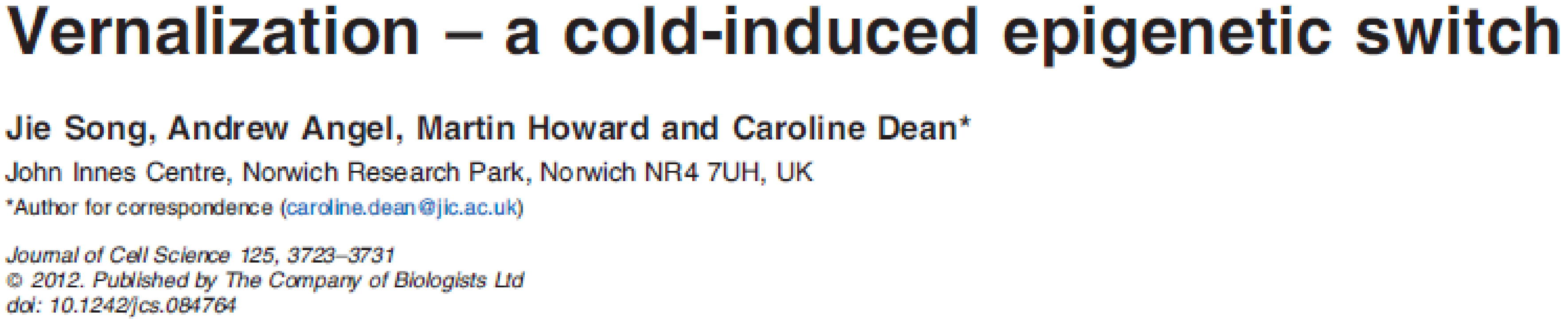

Whorl 4
Carpels
Whorl 3
Stamens
Whorl 2
Petals
Whorl 1
Sepals
Gene C
Gene B
Gene A
Flower
Floral Whorls
ABC Genes


A
D
G
B
H
E
C
F
I
J

Vernalization – a cold-induced epigenetic switch (cold memory)

- Vernalization: the acceleration of flowering by the prolonged cold of winter.
- FLC (FLOWERING LOCUS C): a MADS box transcriptional repressor involved in silencing the genes that are required for the switch to flowering.




Vernalization – a cold-induced epigenetic switch

Jie Song, Andrew Angel, Martin Howard and Caroline Dean*
John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK
*Author for correspondence (caroline.dean@jic.ac.uk)

Journal of Cell Science 125, 3723–3731

doi: 10.1242/jcs.084764

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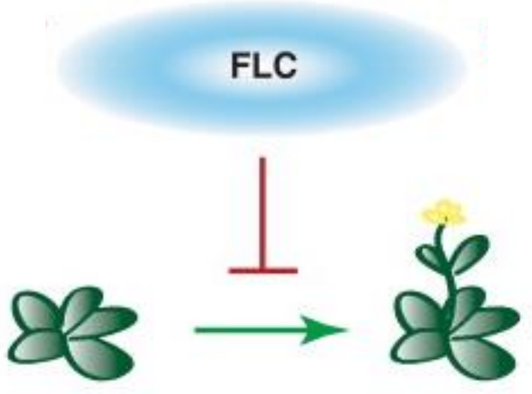
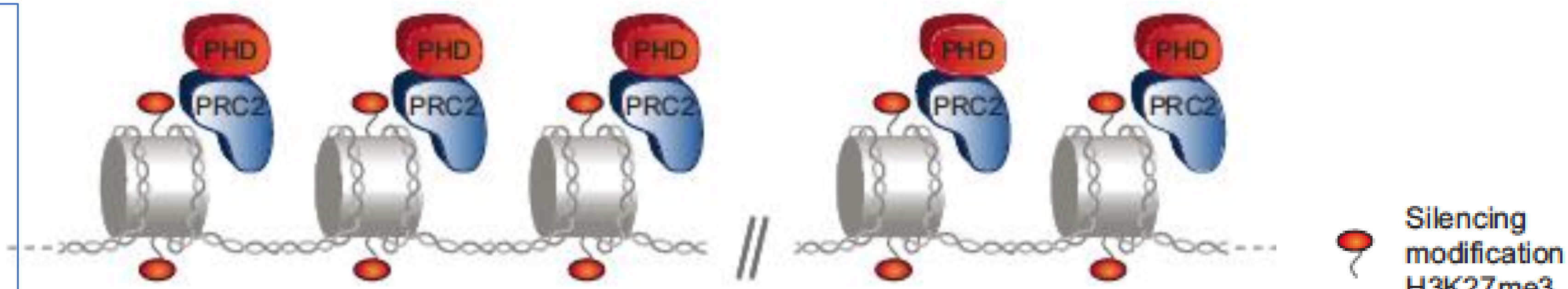


The quantitative nature of vernalization is reflected in the progressive accumulation of H3K27me3 at the nucleation region with increasing lengths of cold exposure

PRC2 o polycomb repressive complex 2: a conserved protein complex that is involved in chromatin silencing through methylation of the lysine 27residue on histone H3.



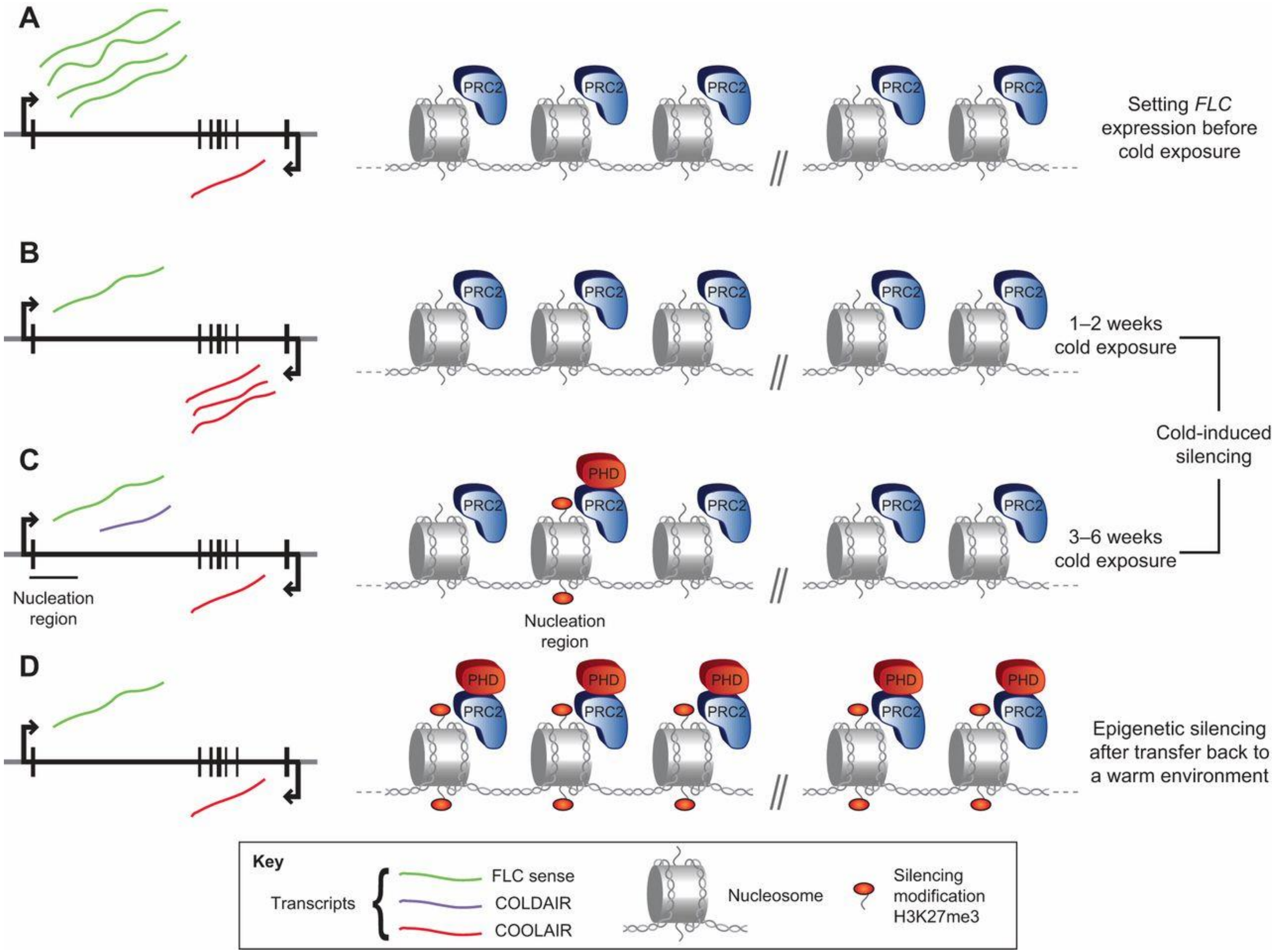
FLC expression during different stages of vernalization.

full-length sense transcripts (green)

non-coding antisense transcripts, COOLAIR (red)

Cold induced non-coding sense transcripts, COLDAIR (purple).

DIFFERENT LEVELS OF REGULATION



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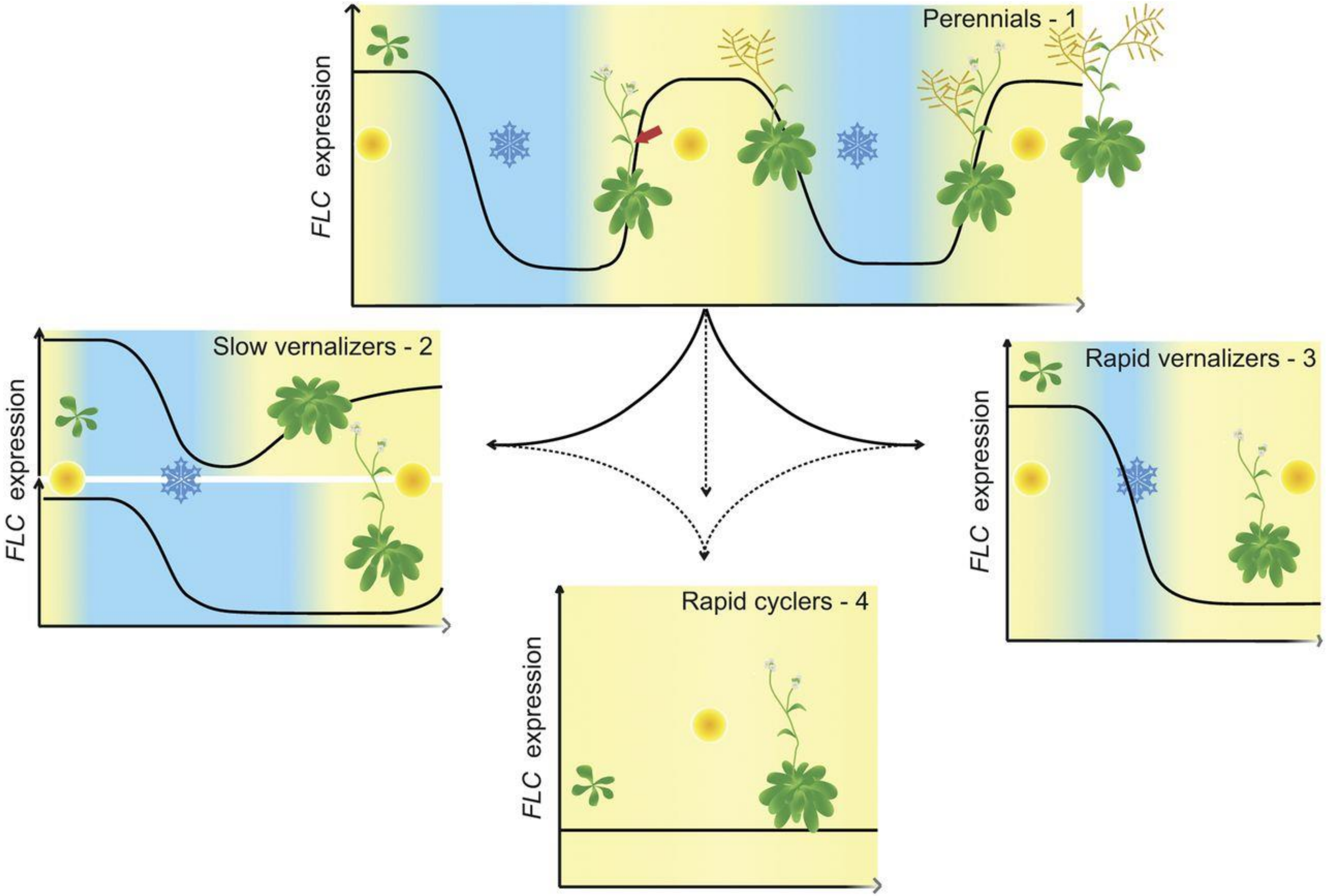
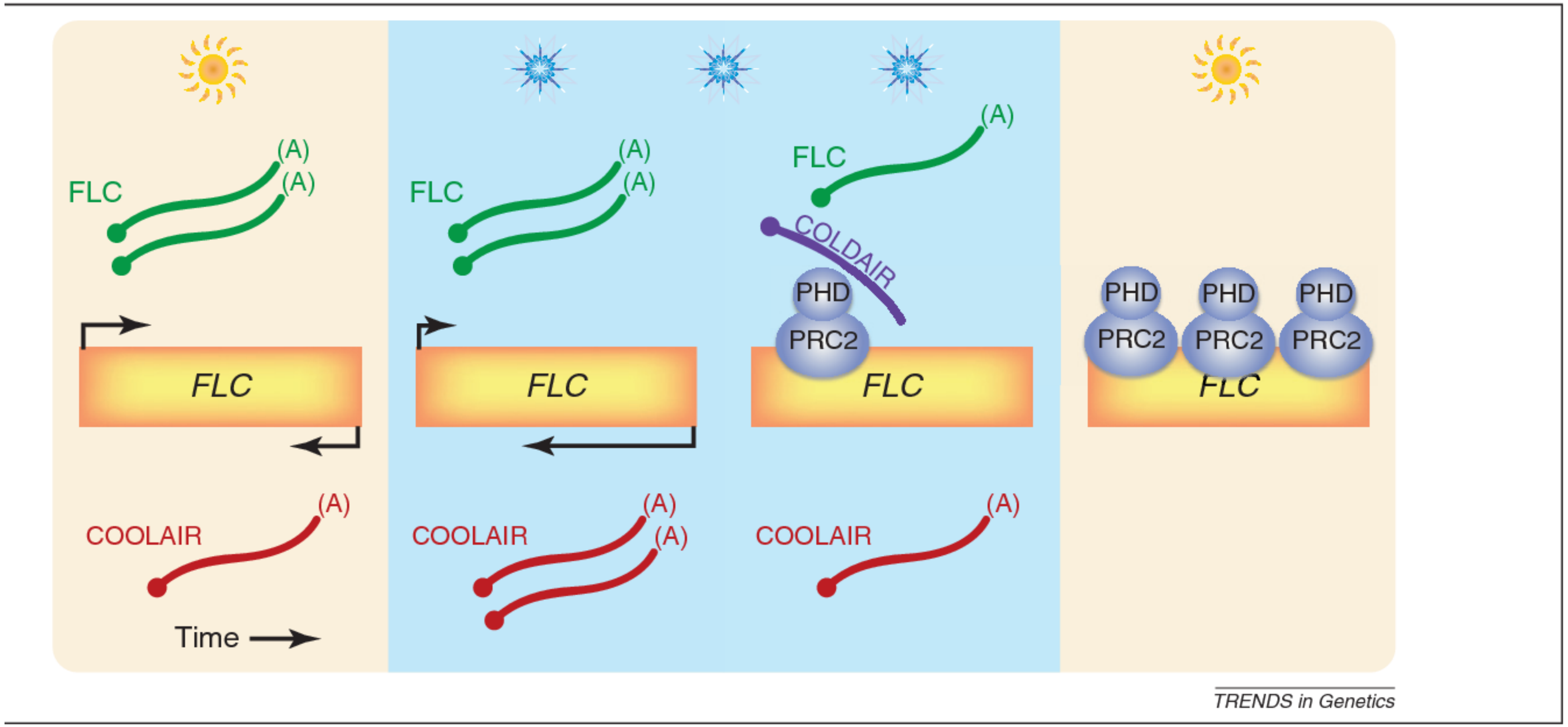
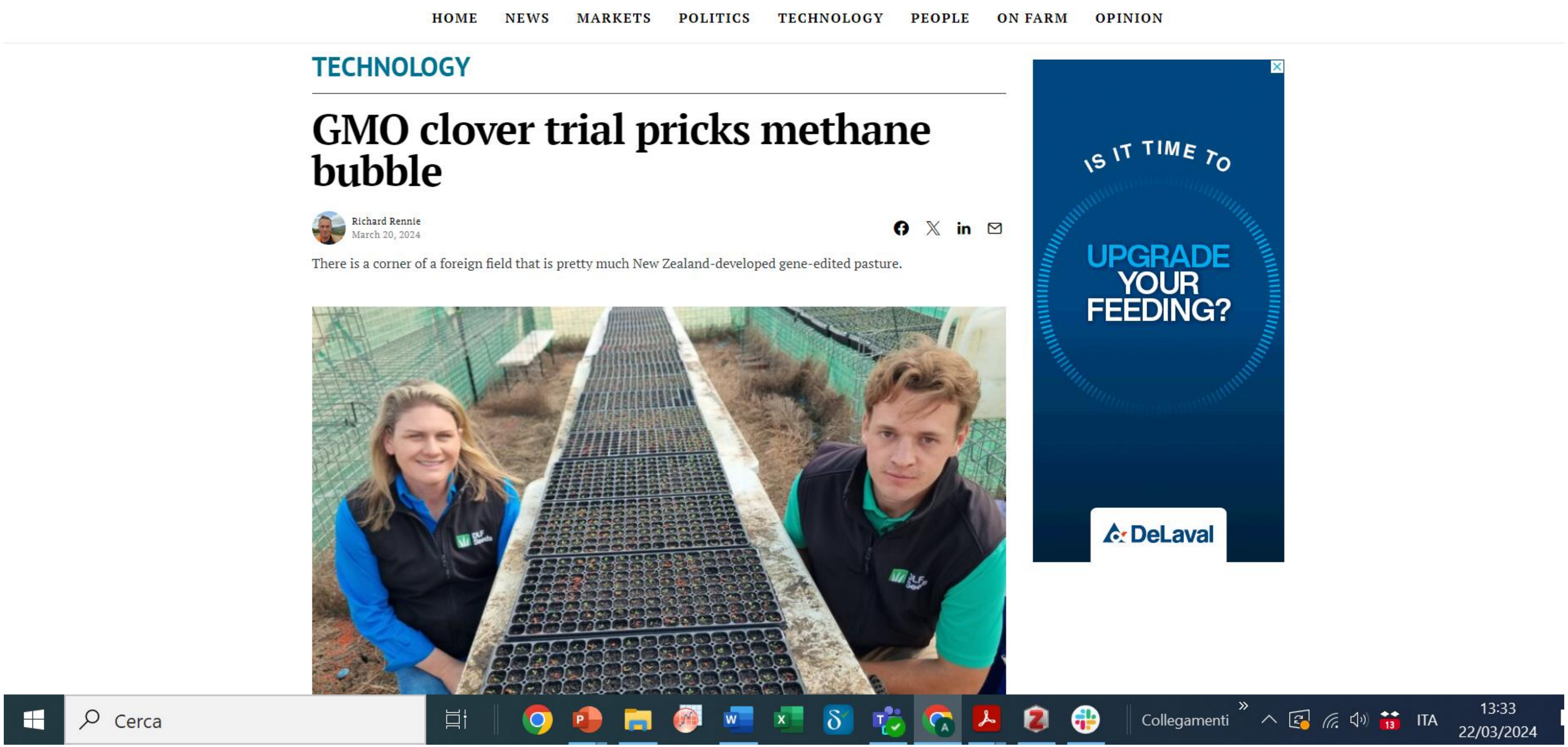




rnalization silences *FLC* epigenetically. Vernalization is the process whereby flowering is accelerated in response to the prolonged cold of winter. Time runs

- COLDAIR is required for stable repression of FLC after vernalization and a lack of COLDAIR lead to late flowering after vernalization.
- COLDAIR binds PRC2 complex protein CURLY LEAF (CLF), with maximal interaction after 20 days of vernalization / cold exposure.
- COLDAIR is required to recruit PRC2 to the FLC locus allowing deposition of the repressive H3K27me3 chromatin mark.
- COLDAIR did not impact the expression of other genes that repress flowering.



TECHNOLOGY

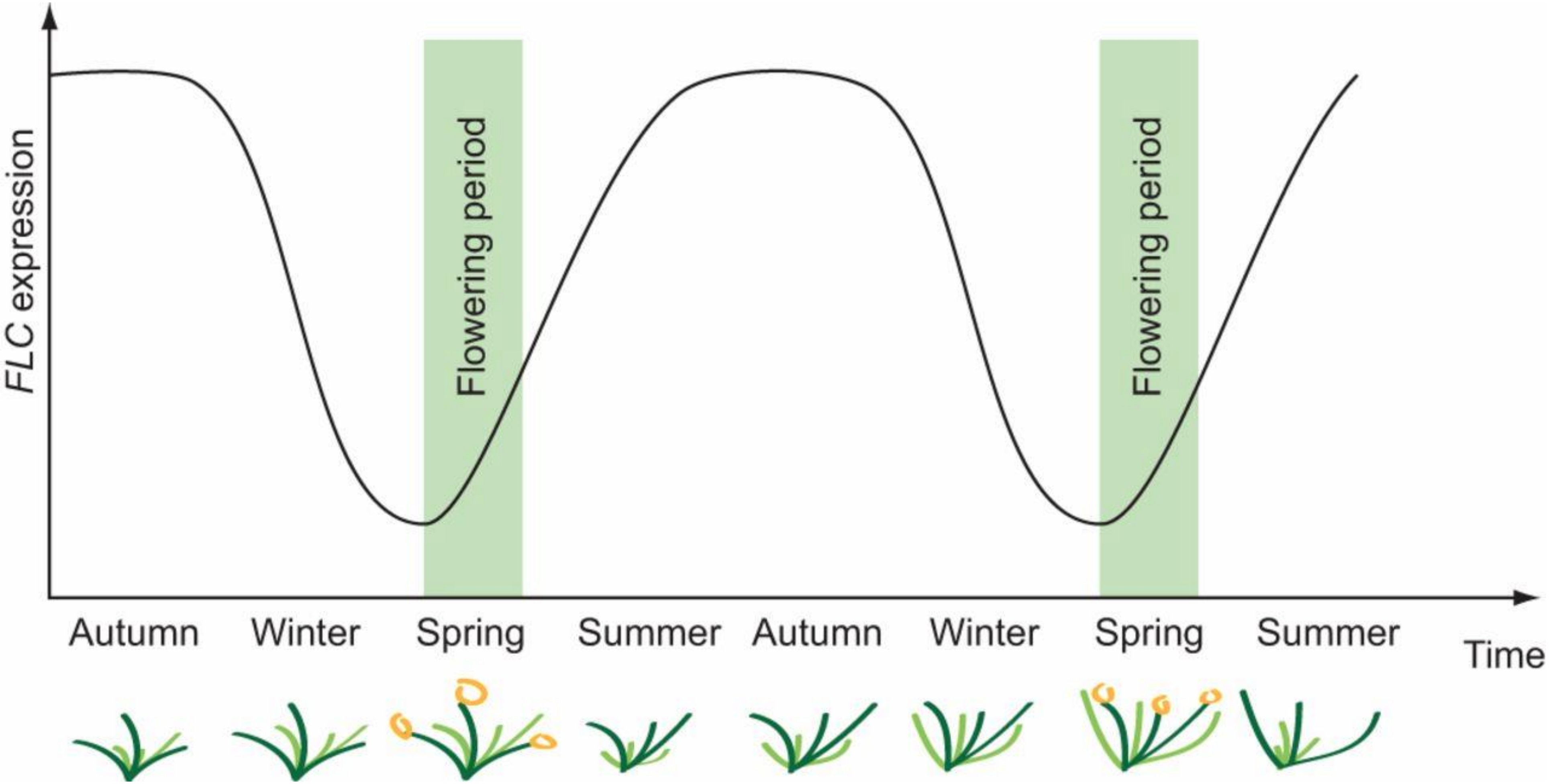
GMO clover trial pricks methane bubble

Richard Rennie
March 20, 2024

There is a corner of a foreign field that is pretty much New Zealand-developed gene-edited pasture.

https://www.farmersweekly.co.nz/technology/gmo-clover-trial-pricks-methane-bubble/

Changes in epigenetic silencing underlie differences in life history.



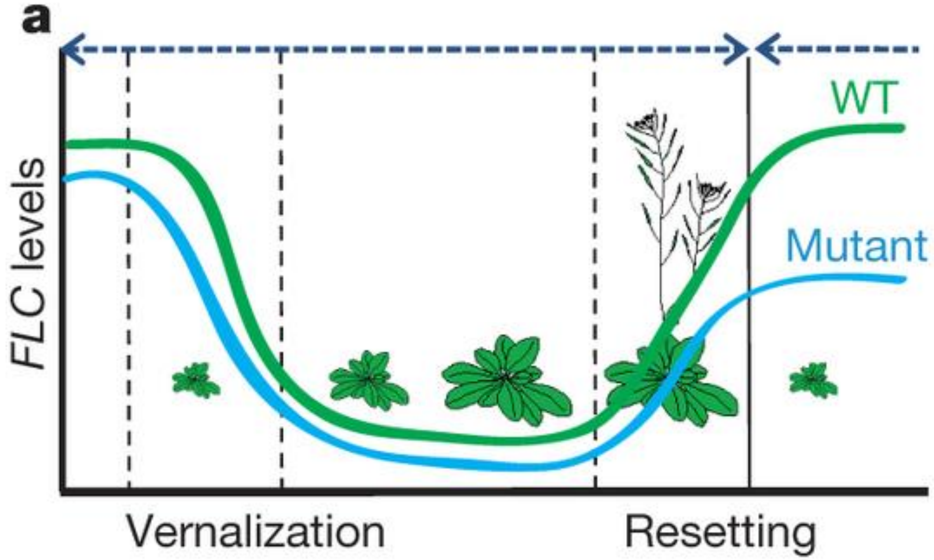
In some perennials, some parts of the plant do not switch to reproductive development after one winter, and remain vegetative, thereby maintaining the adult plant over many years.

In **perennial** *Arabis alpina* plants, FLC expression is transiently but not epigenetically silenced by exposure to cold. Older meristems flower after one winter but newer meristems remain vegetative until the subsequent winter.

Epigenetic reprogramming that prevents transgenerational inheritance of the vernalized state

The resetting of FLC expression occurs in the early globular embryo.

Isolation and characterization of the resetting mutant.



What happens to a mutant with a progeny carrying low FLC expression levels?

Crevillen et al., 2014

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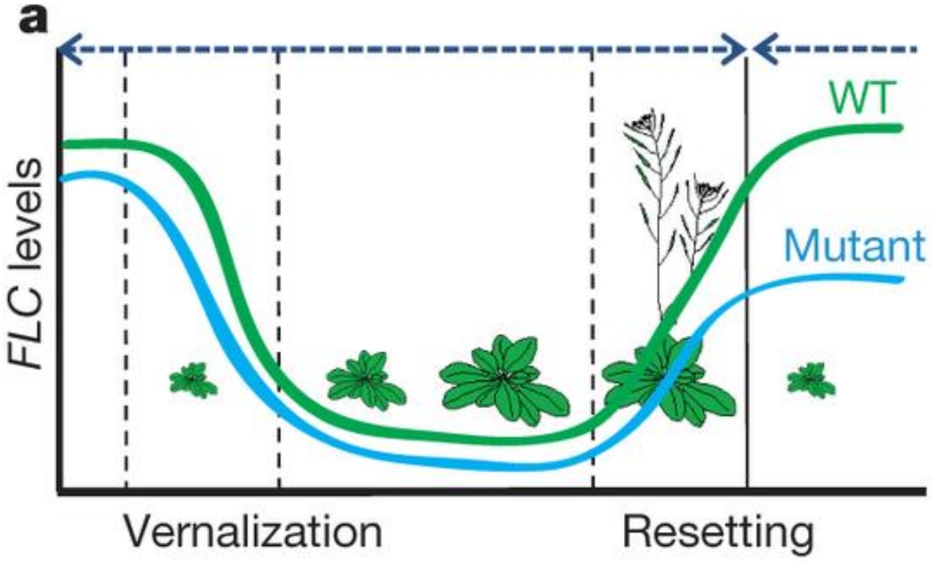
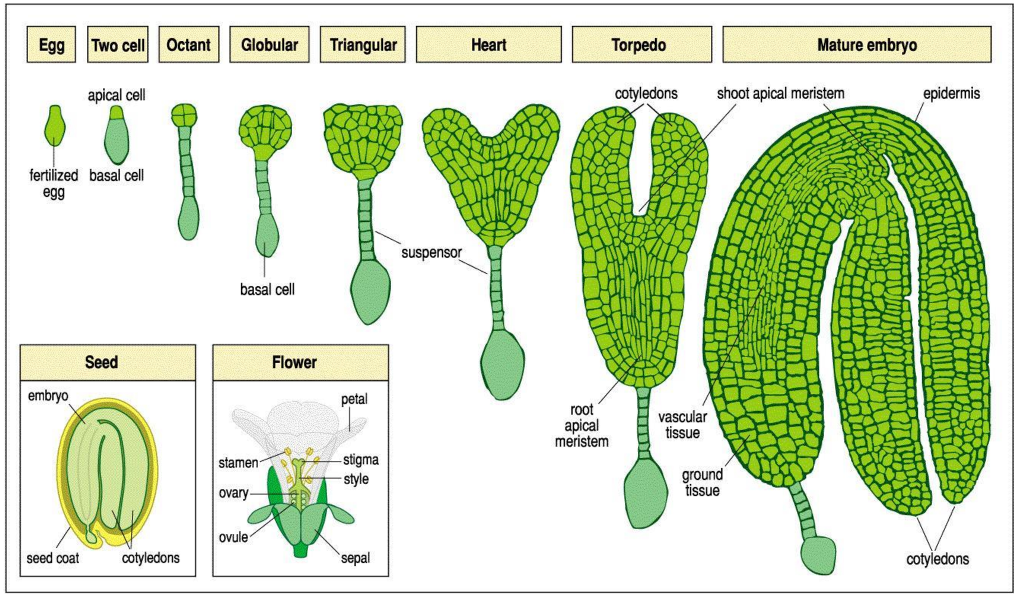




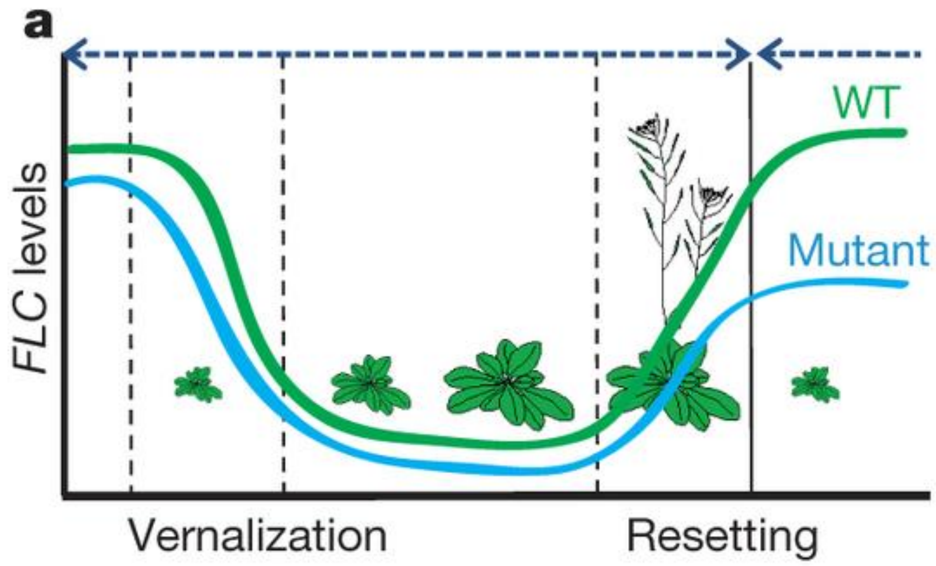
LETTER

doi:10.1038/nature13722

Epigenetic reprogramming that prevents transgenerational inheritance of the vernalized state

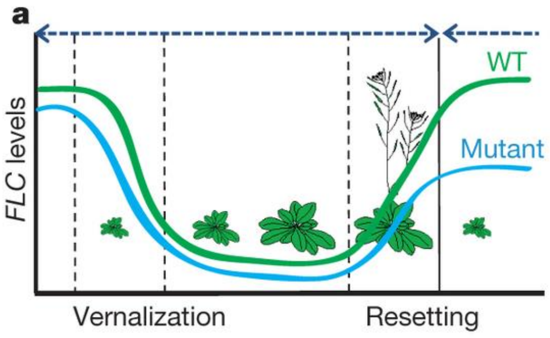
Pedro Crevillén[1]†, Hongchun Yang[1], Xia Cui[2], Christiaan Greeff[1]†, Martin Trick[1], Qi Qiu[2], Xiaofeng Cao[2] & Caroline Dean[1]

Crevillen et al., 2014

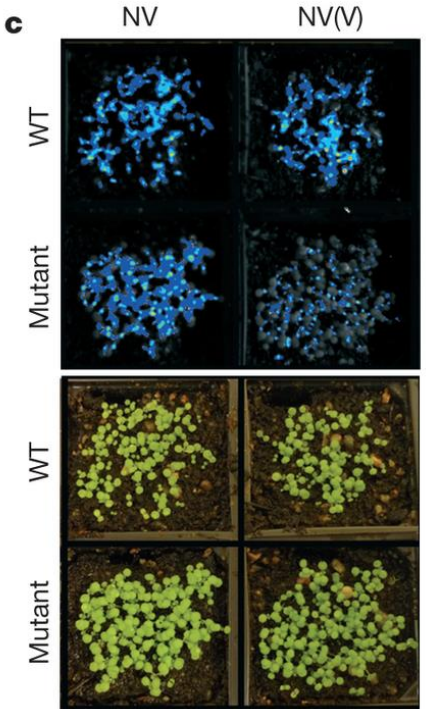


How could you quickly look for mutants with an altered FLC expression level?

FLC::LUC reporter gene and mutant analysis



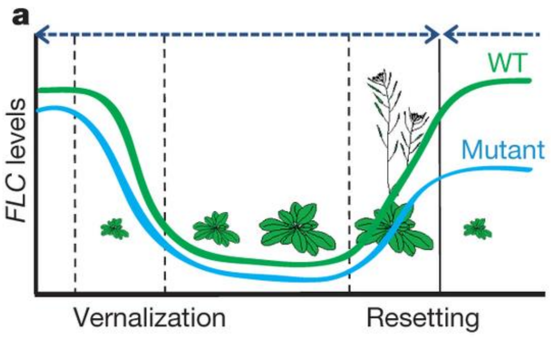
FLC:LUC

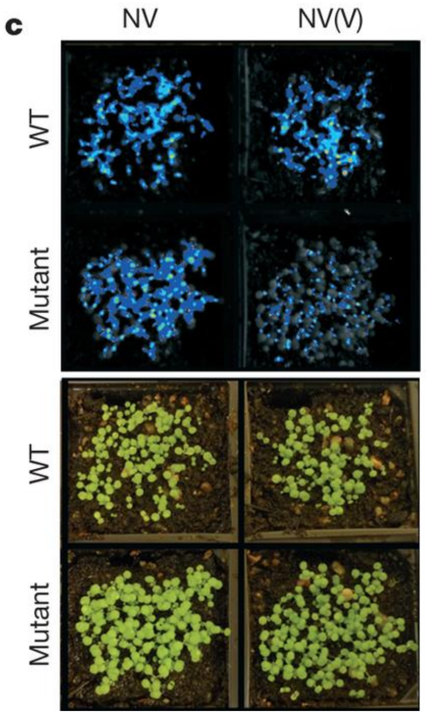


NV, non-vernalized;
NV(V), non-vernalized following vernalization in the previous generation;

Crevillen et al., 2014

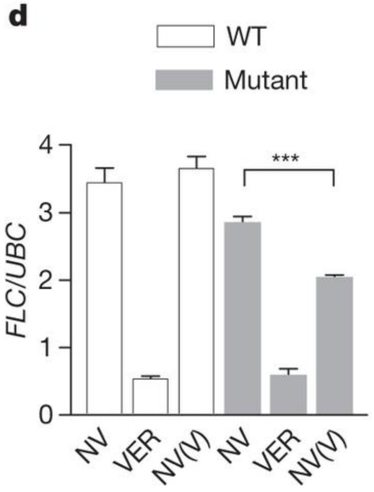
FLC::LUC reporter gene



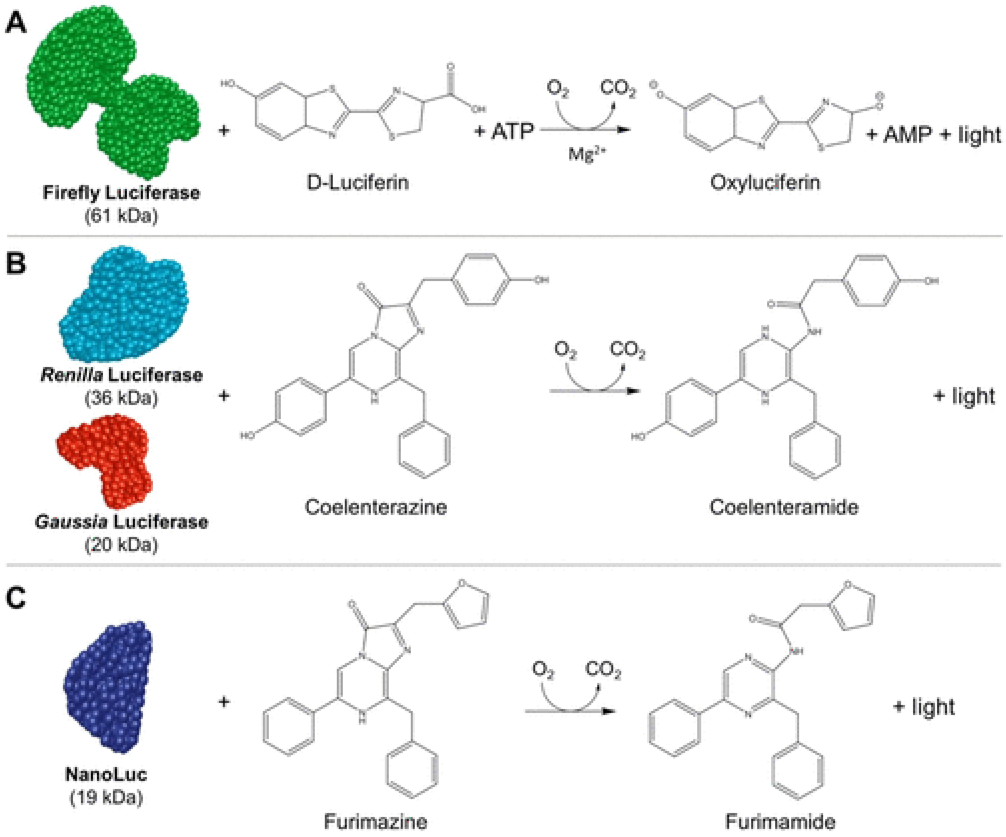


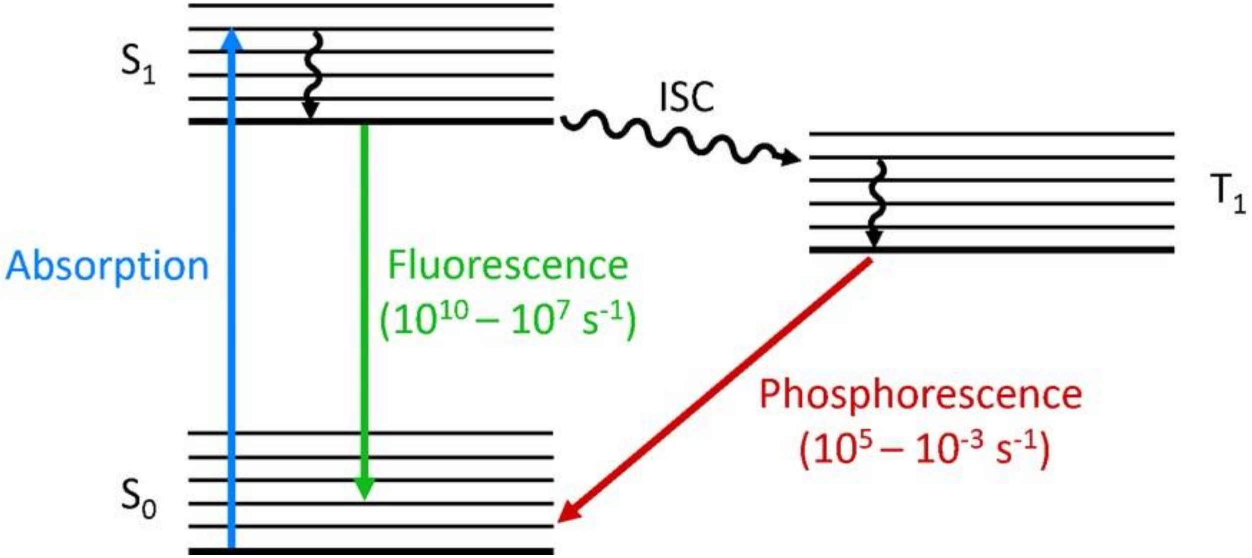
FLC:LUC

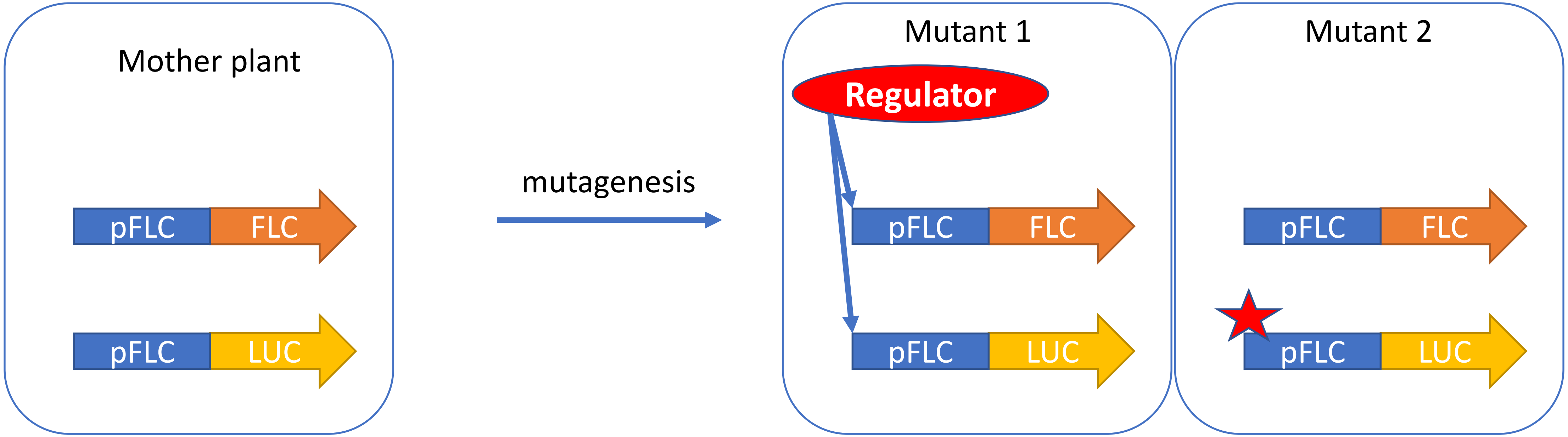
NV, non-vernalized;
VER, vernalized
NV(V), non-vernalized following vernalization in the previous generation;



Crevillen et al., 2014


A
Firefly Luciferase
(61 kDa)
+
D-Luciferin
+ ATP
O_2
CO_2
Mg^{2+}
Oxyluciferin
+ AMP + light
B
Renilla Luciferase
(36 kDa)
Gaussia Luciferase
(20 kDa)
+
Coelenterazine
O_2
CO_2
Coelenteramide
+ light
C
NanoLuc
(19 kDa)
+
Furimazine
O_2
CO_2
Furimamide
+ light

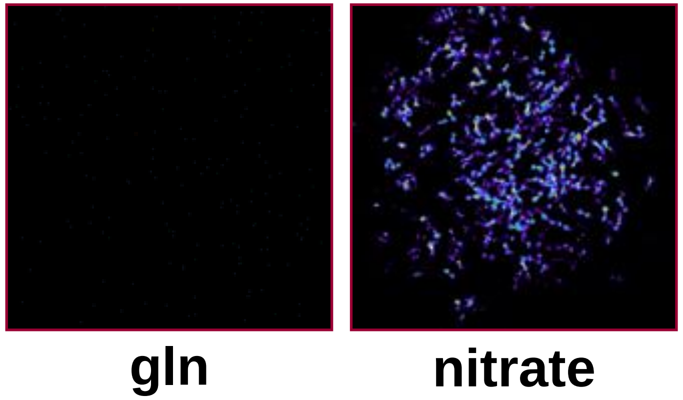

S_1
ISC
T_1
Absorption
Fluorescence
($10^{10} – 10^{7}$ s^{-1})
Phosphorescence
($10^{5} – 10^{-3}$ s^{-1})
S_0


Mother plant
pFLC
FLC
pFLC
LUC
mutagenesis
Mutant 1
Regulator
pFLC
FLC
pFLC
LUC
Mutant 2
pFLC
FLC
pFLC
LUC

NII::Luc mutants analysis

- ✓ *NII1* promoter from tobacco foliar nitrite reductase fused to *Luc*.

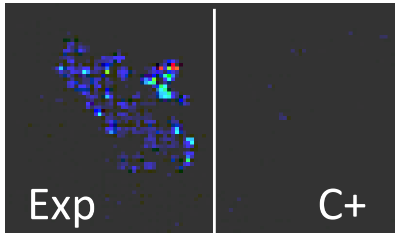
{*T. Engelsted, T. Hoff, J. Mundy, N. Durand,*
MT Leydecker and HN Truong}



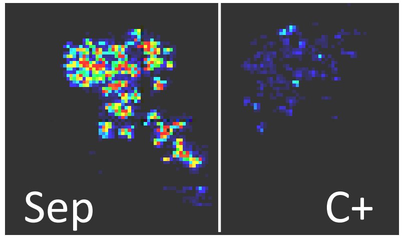
EMS mutagenesis

1st screening in Denmark and 2nd screening in Versailles

- ✓ 2 Exp_mutants: overexpressing luciferase on Gln

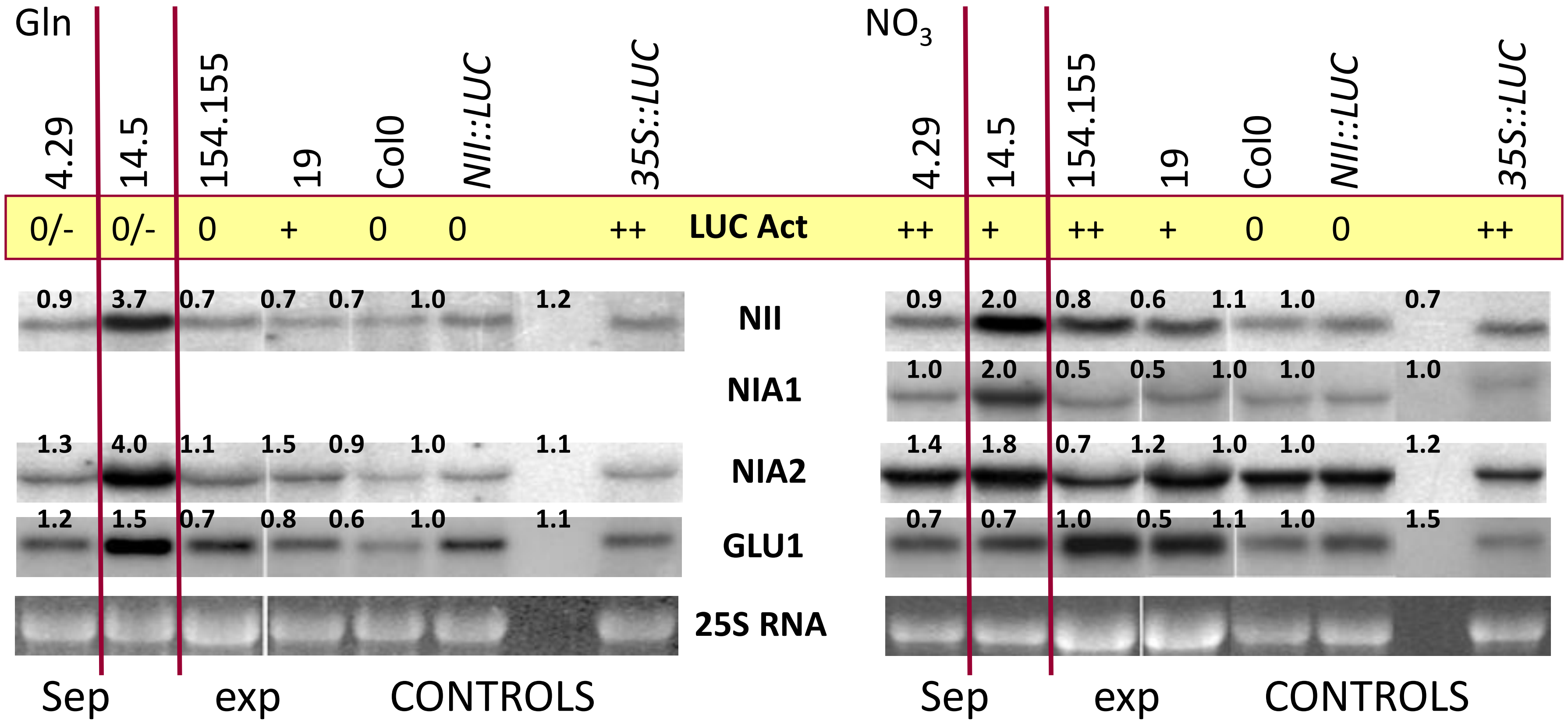


- ✓ 6 Sep_mutants: overexpressing luciferase on NO3



Gene expression analysis

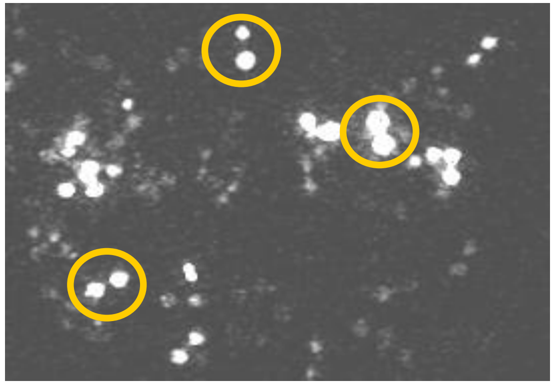
- Northern Blotting, 10 days old *in vitro* plantlets:



✓ 14.5Sep mutant has a higher expression of *NII* and *NIA*, expecially on Gln

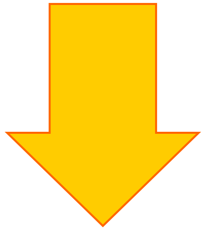
Mapping 14.5Sep mutation

- ✓ Crossing Ler X *NIILUC* (F2)
  Ler X 14.5Sep (F2)



14.5Sep backcross (F2)

Visualisation on NO_3

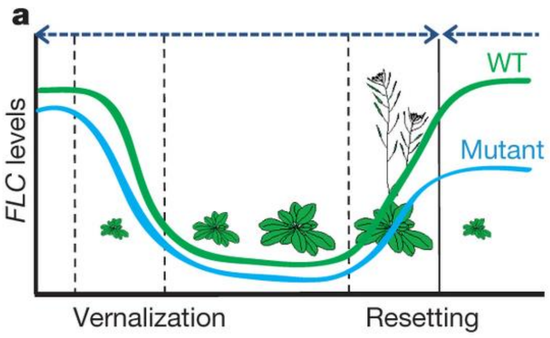


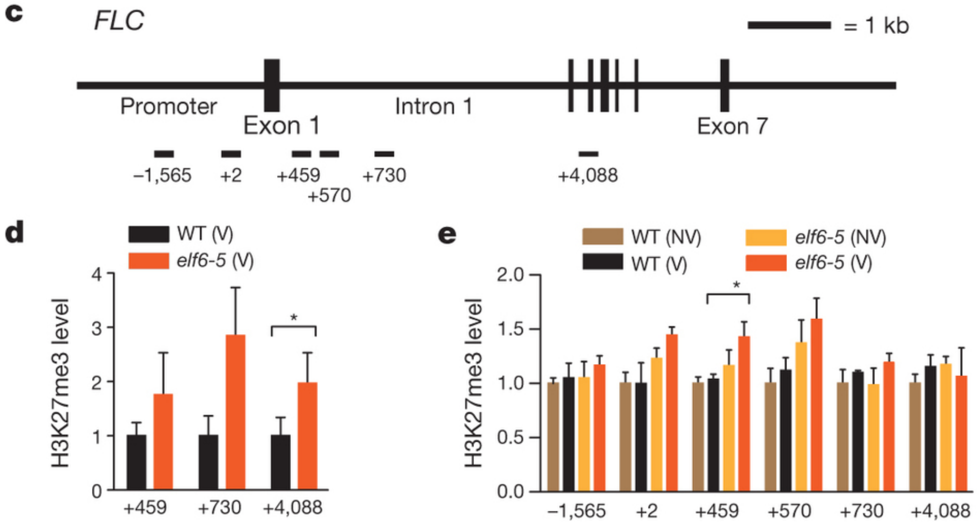
Transfer in the greenhouse

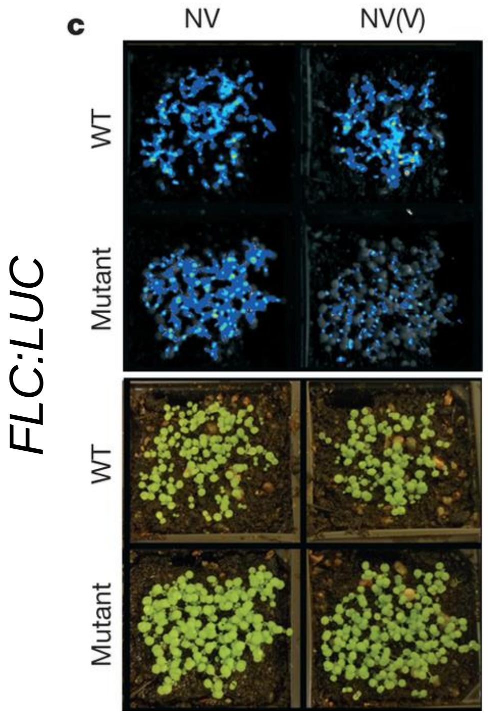
DNA extraction+PCR

ELF6 demethylase activity

ELF6 has H3K27me3 demethylase activity, and its mutation reduced this enzymatic activity in planta.







Crevillen et al., 2014

Resetting FLC is a process activated by H3K27 demethylation (example, **ELF6**).

Epigenetic reprogramming avoid trans-generational transmission of certain phenotypes.

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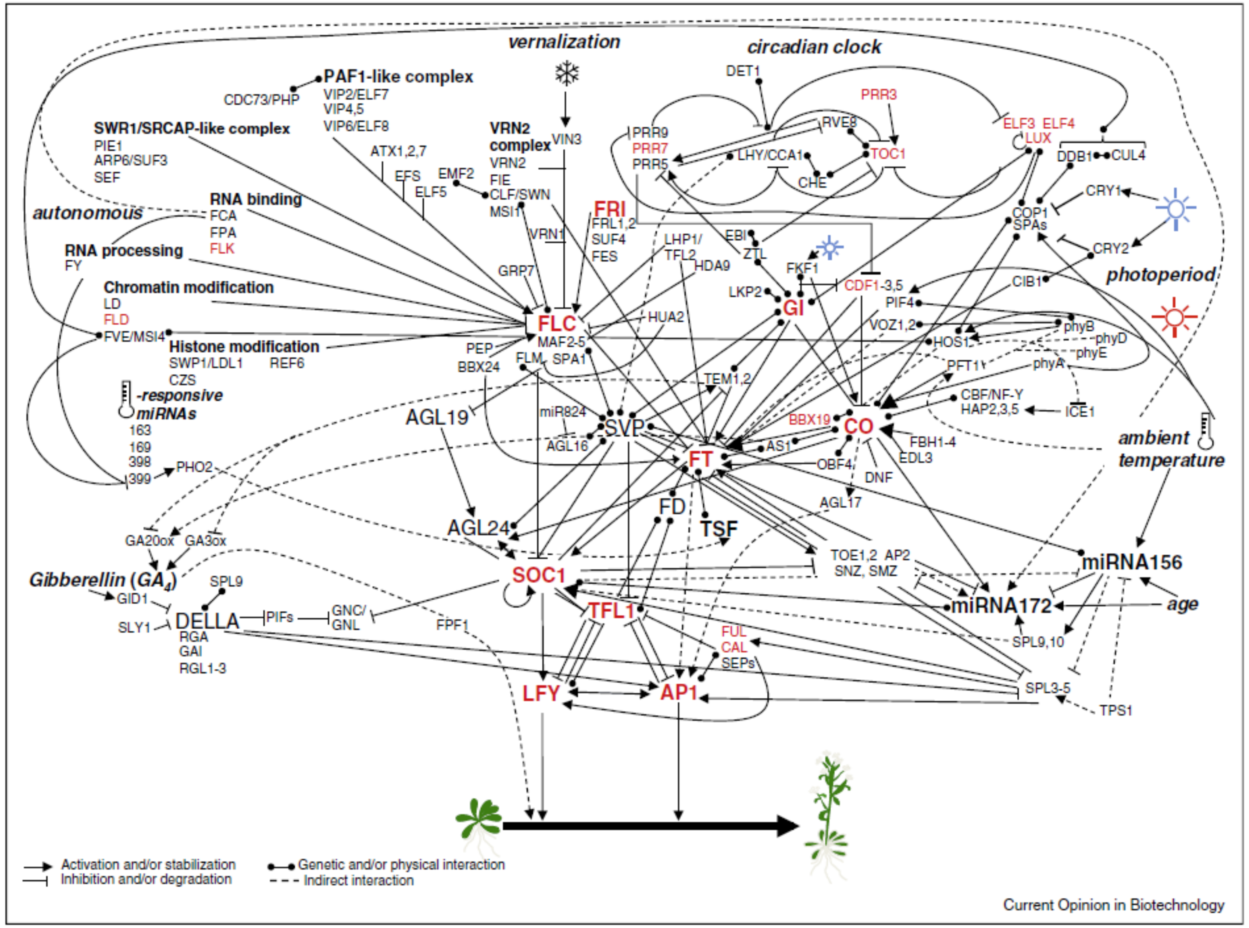
Current Opinion in Biotechnology

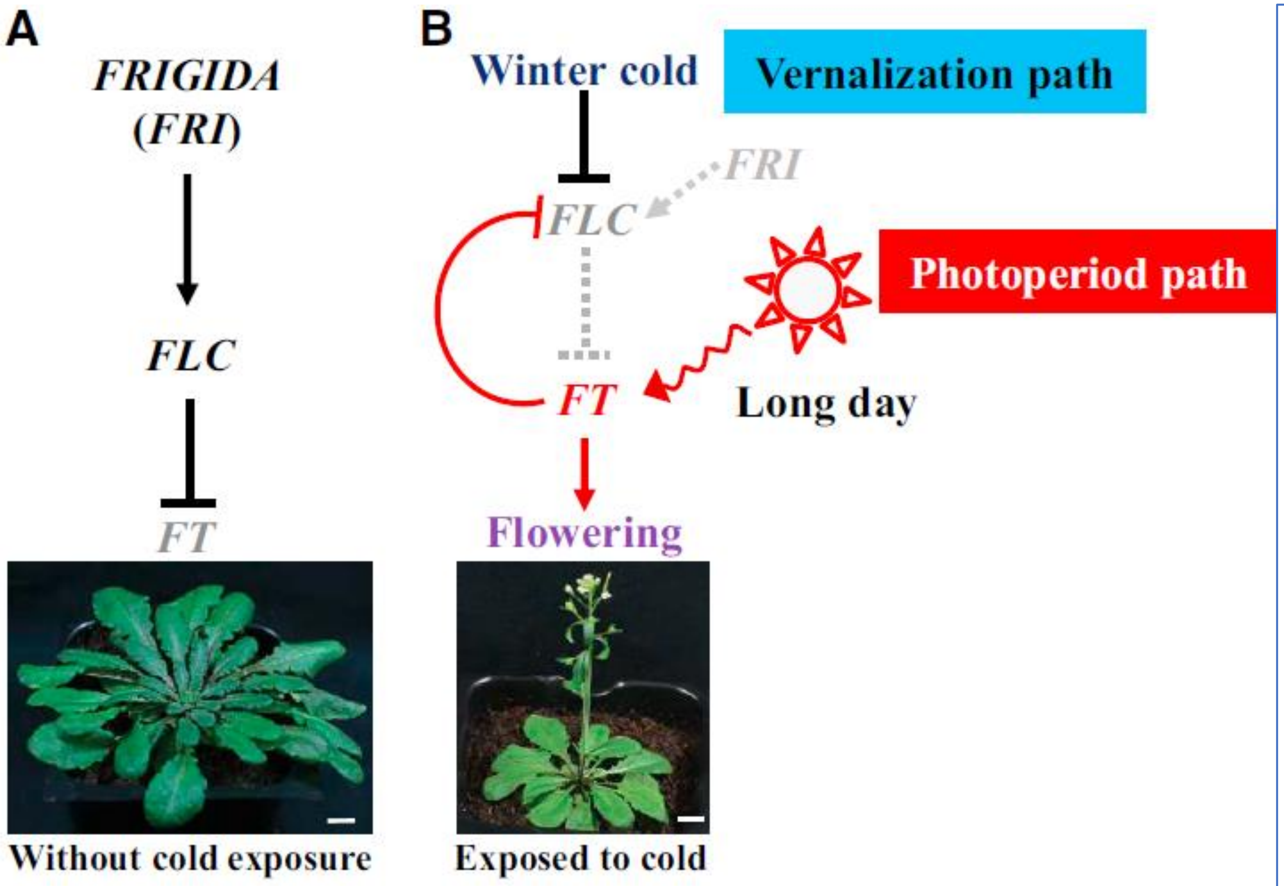
Flowering time regulation in crops — what did we learn from Arabidopsis?

Martina Blümel[1], Nadine Dally[1] and Christian Jung[1]



VERY COMPLEX PATHWAY

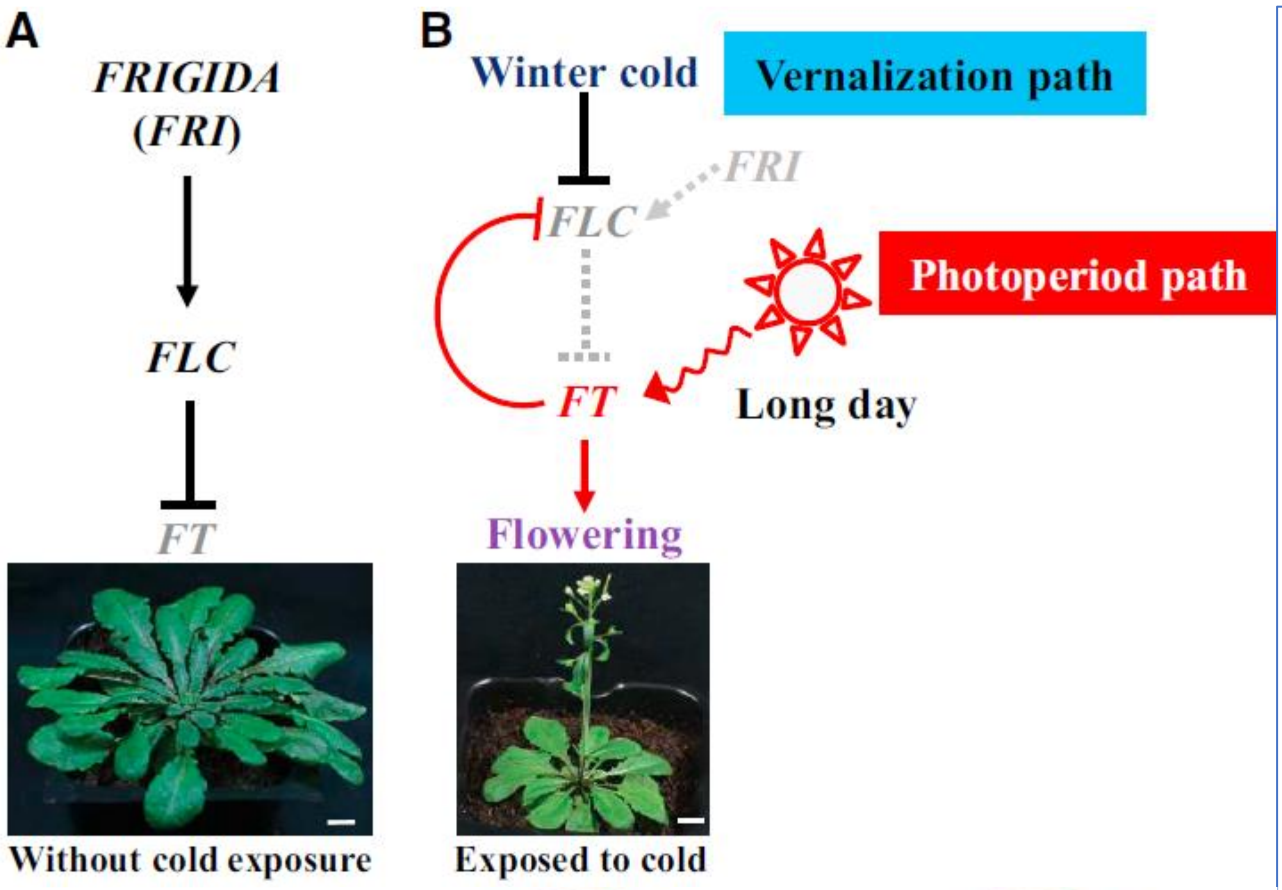
Flowering time gene network with known genetic and epigenetic regulators in Arabidopsis thaliana. Arrows indicate a promoting, T-ends indicate an inhibiting genetic interaction. Round dots at both ends mark an interaction without a known direction. Dashed lines denote an indirect interaction. Genes attributed as major regulators in the different flowering time pathways are written in bold. Red writing indicates the functional characterization of a gene as a flowering time regulator in cultivated species — although not necessarily with the same function as in Arabidopsis — by mutant analysis, sequencing and complementation analysis or heterologous expression, RNA interference, or clear linkage with a major QTL.



FLC TO FOCUS ON EPIGENETIC CONTROL

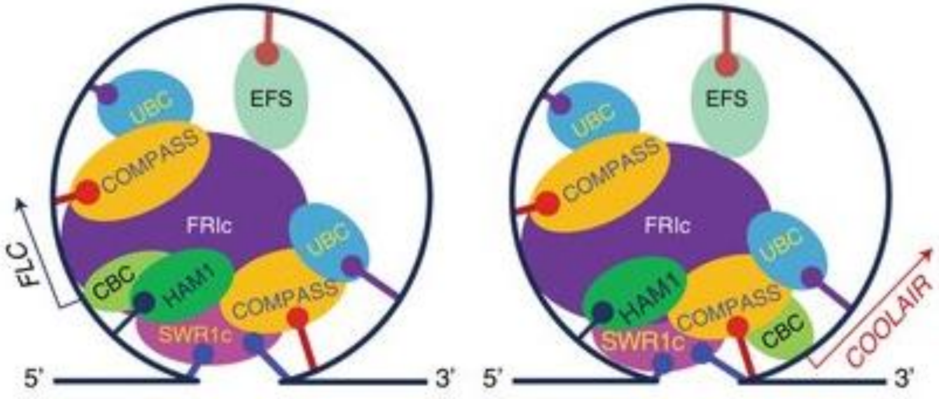
(A) **No VERNALIZATION AND SHORT-DAY PHOTOPERIOD**. A winter annual Arabidopsis line without prolonged cold exposure. FRIGIDA activates the expression of the floral repressor FLC (for FLOWERING LOCUS C), which directly represses the expression of the florigenic FT (for FLOWERING LOCUS T) gene to inhibit flowering.

(B) **After experiencing winter cold**, Arabidopsis winter annuals in temperate regions flower in late spring in response to increasing day length. Winter cold, through the vernalization pathway, represses FLC expression and thus relieves FT repression. This enables long-day induction of FT expression by the photoperiod pathway to promote flowering. FT feedback represses FLC expression.

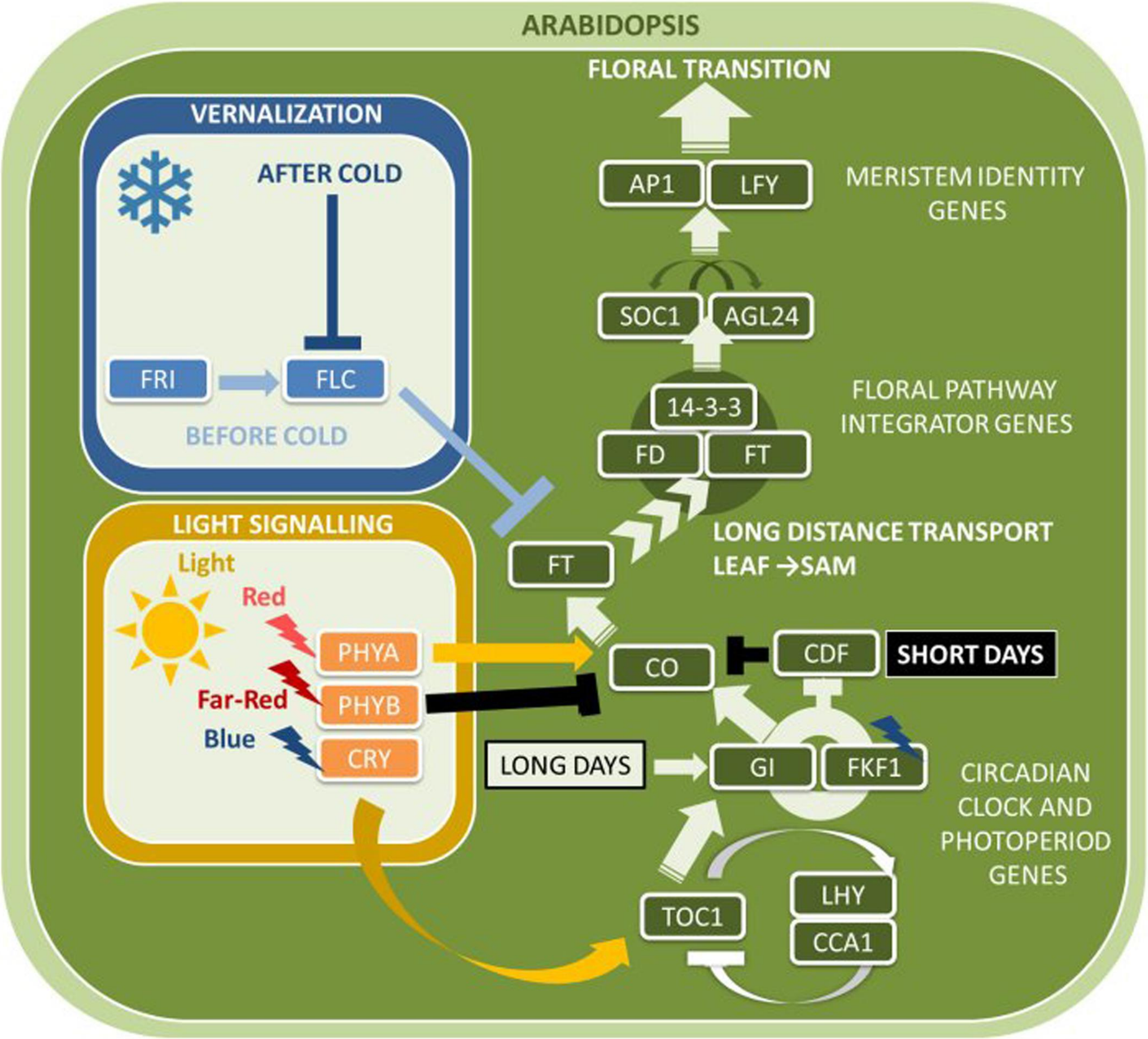


The winter annual growth habit is conferred by FRIGIDA (FRI) and FLC.
FRI encodes a plant-specific **scaffold protein** and functions dominantly to upregulate FLC expression to a high level that inhibits flowering.

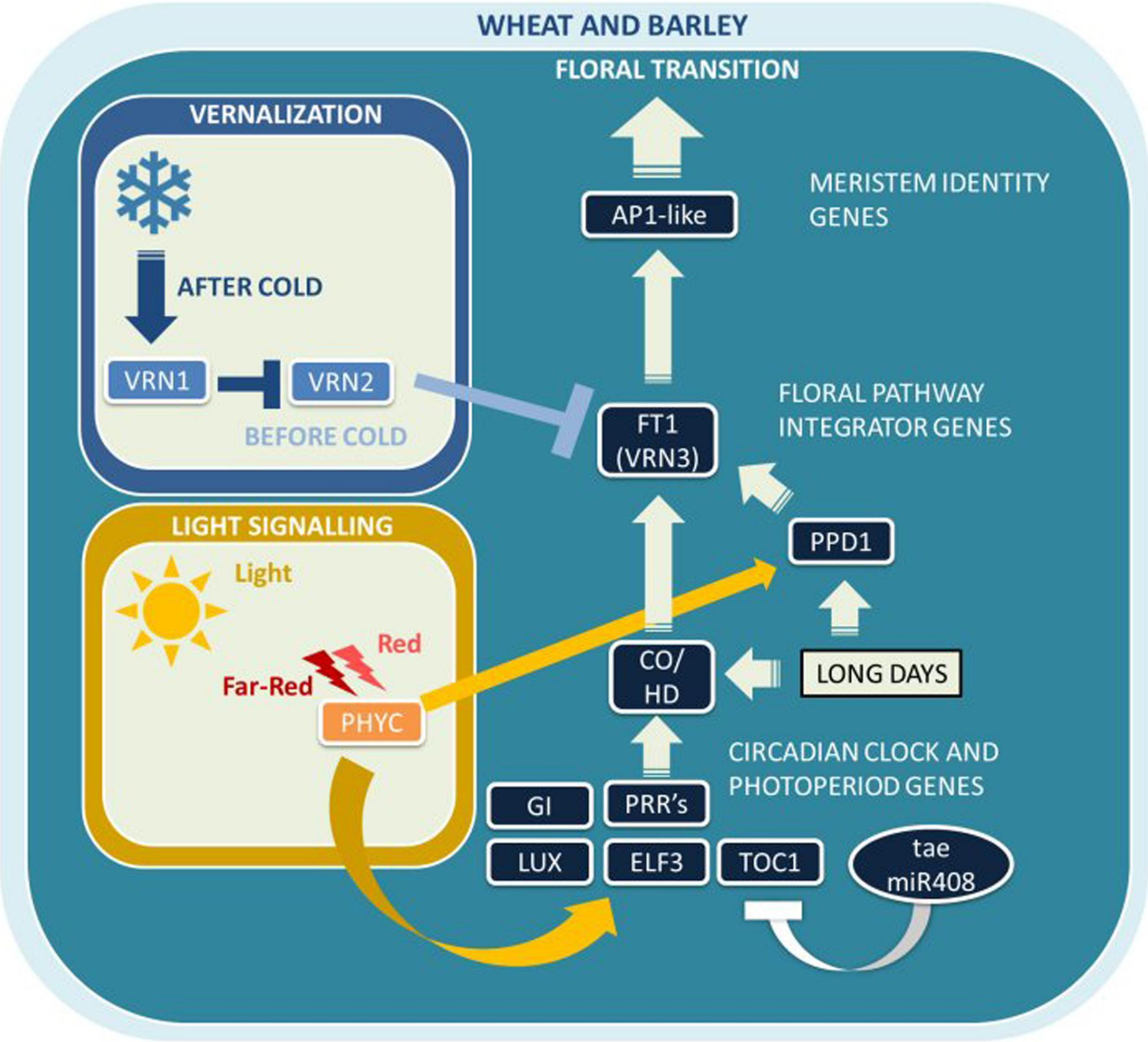
Before winter cold exposure, the scaffold protein FRI is located at FLC in a region around the transcription initiation site, and physically associates with a few transcriptional coactivators, among which are the histone 3 lysine 4 (H3K4) methyltransferase complex COMPASS-like, the histone acetyltransferases HAM1 (for HISTONE ACETYLTRANSFERASE OF THE MYST FAMILY 1).



Working models for FRIsc-mediated upregulation of FLC and COOLAIR.



Major flowering pathway genes of *Arabidopsis thaliana*. Positive and negative regulatory connections are indicated by arrows and lines with T-ends, respectively. White and black arrows or T-ends indicate regulatory connections occurring primarily under long days and short days, respectively.



Major flowering pathway genes of bread wheat (*Triticum aestivum L.*) and barley (*Hordeum vulgare* L.). Positive and negative regulatory connections are indicated by arrows and lines with T-ends, respectively. White arrows or T-ends indicate regulatory connections occurring primarily under long days.

Traditional breeding and phenotypic selection of natural genetic variants at flowering loci was used to optimize flowering time within a given production environment to achieve greater yields

AGRICULTURAL IMPACT