

Did you log in mediaspace with your SSO?

Checkpoints

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

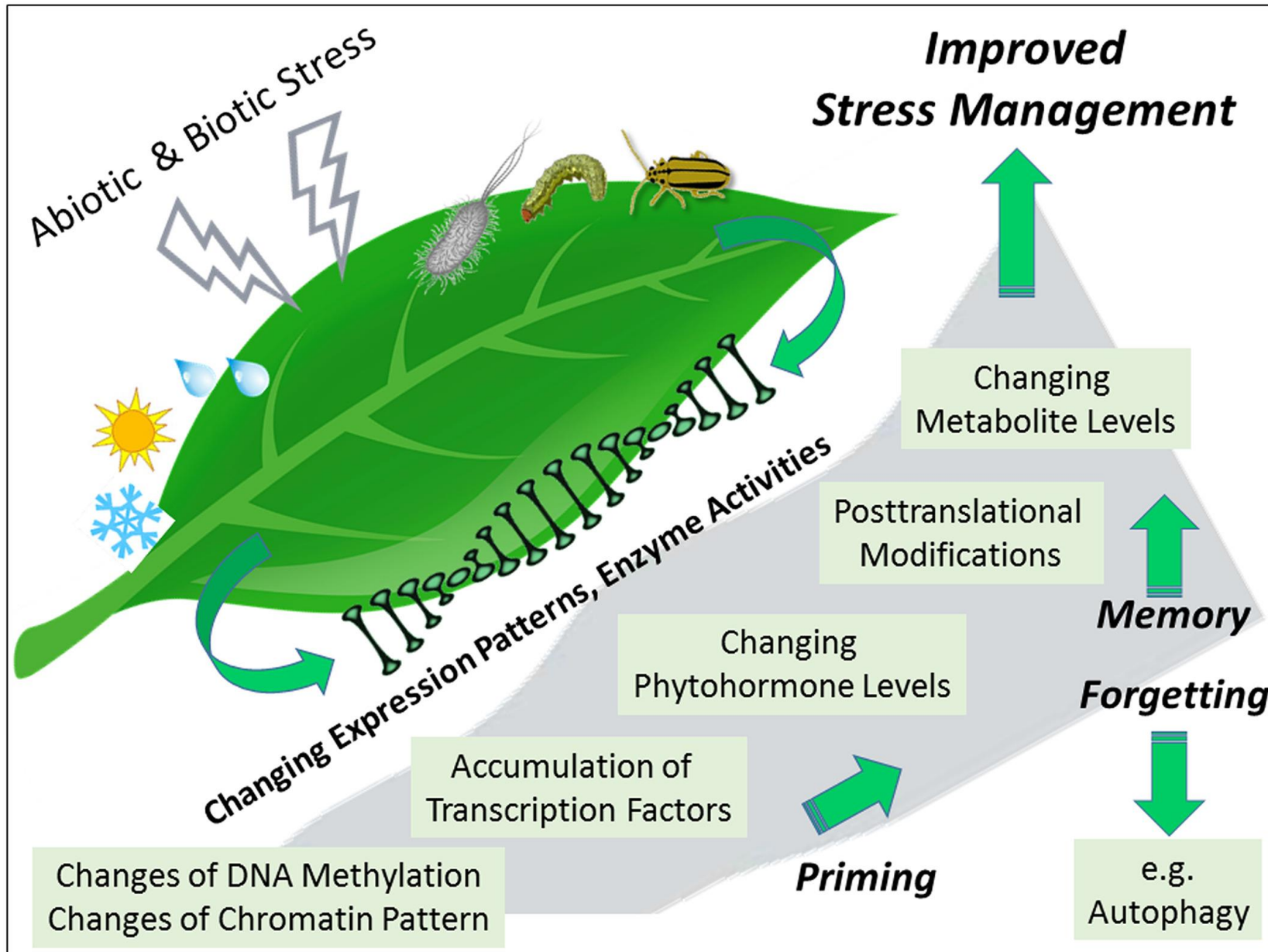
March 25: List of paper on file

April 05-15: Paper presentation

May 07: upload your podcast on mediaspace

May 27: ANNOTO, discussion peer evaluation

PRIMING MODIFIES RESPONSES TO A TRIGGERED STRESS



Plants need to cope with **changing environmental conditions**, be it variable light or temperature, different availability of water or nutrients, or attack by pathogens or insects.

Plants have evolved mechanisms by which they can **remember** past stress events and **prime** their responses in order to react more rapidly or more strongly to recurrent stress.

DOI: 10.1111/pce.13526

EDITORIAL

WILEY

Stress priming, memory, and signalling in plants

Epigenetic control systems offer an alternative mechanism for responses that are dynamic and persistent: a gene, or a network, is activated in response to a stimulus, but once the stimulus is removed, a mark could be left to facilitate altered, quicker or more potent responses to subsequent stresses.

‘transcriptional memory’ to mean that a type of information persists after the plant has recovered from the initial stress and that the ‘memory’ influences subsequent transcriptional responses.

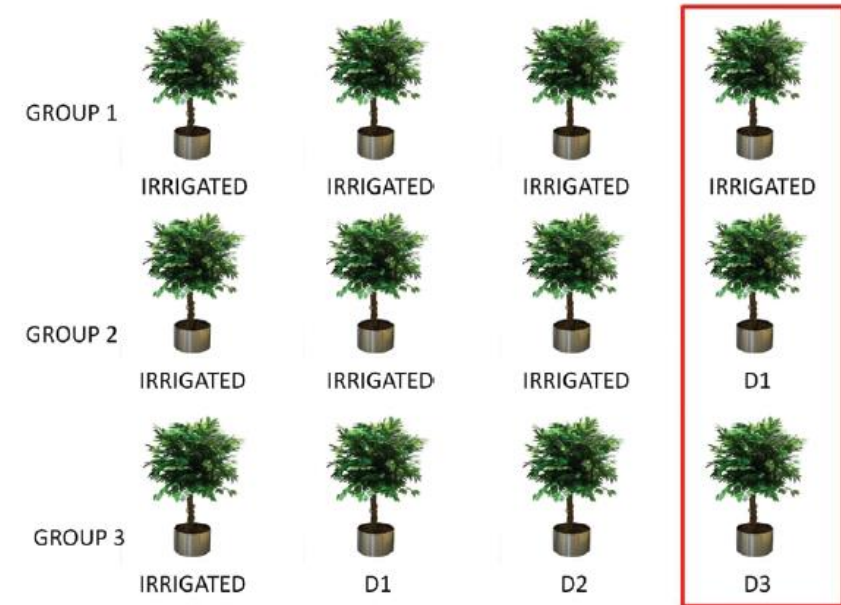
RESEARCH PAPER

Photosynthetic and metabolic acclimation to repeated drought events play key roles in drought tolerance in coffee

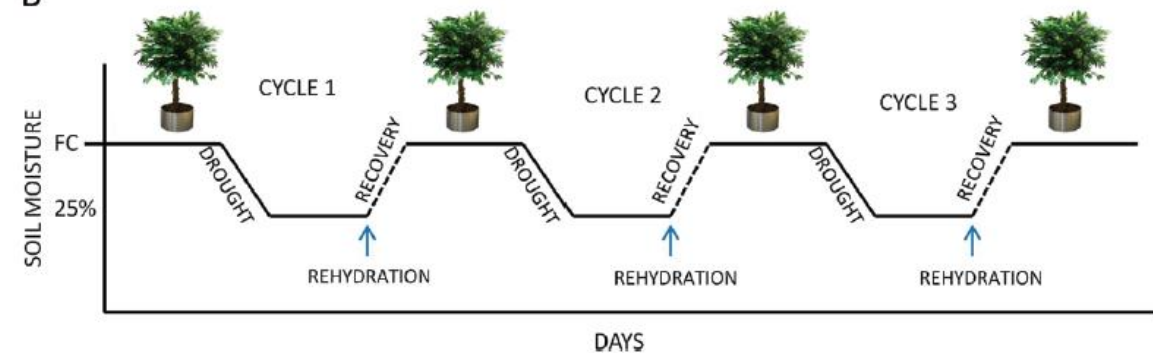
Paulo E. Menezes-Silva^{1,2}, Lilian M. V. P. Sanglard¹, Rodrigo T. Ávila¹, Leandro E. Morais^{1,3}, Samuel C. V. Martins¹, Priscilla Nobres⁴, Camila M. Patreze⁵, Marcio A. Ferreira⁴, Wagner L. Araújo⁶, Alisdair R. Fernie⁷ and Fábio M. DaMatta^{1,*}

Acclimation to repeated drought episodes seemed to depend on an orchestrated reprogramming of plant metabolism, involving key processes such as **photosynthesis, respiration, photorespiration, and the antioxidant system**. In addition, the exposure to recurrent stress events also resulted in differential molecular adjustments, as noted in the qPCR data, suggesting the existence of so-called **trainable genes** in coffee. It is therefore tempting to suggest that the differential acclimation observed in D3 plants might be the results of the generation of a **‘drought memory’**

A



B



What are trainable genes?

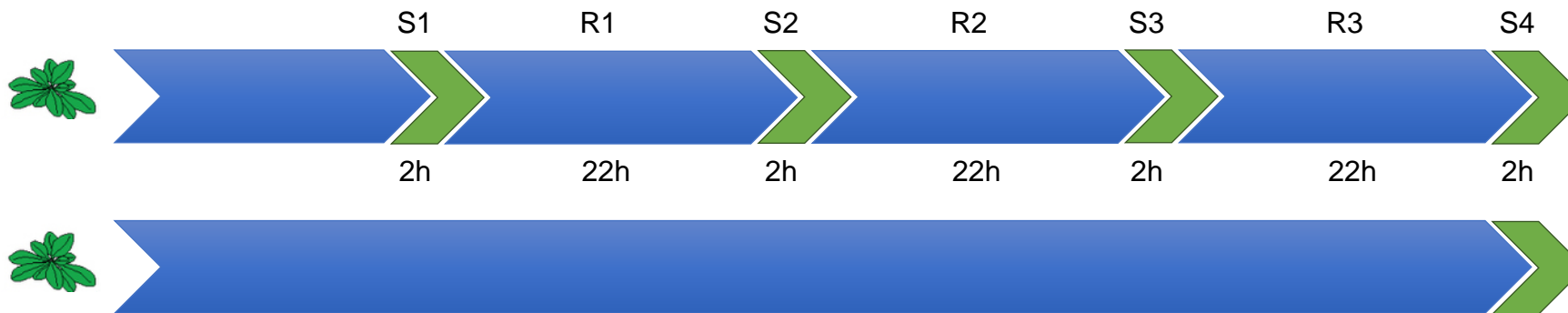


Multiple exposures to drought 'train' transcriptional responses in *Arabidopsis*

Yong Ding¹, Michael Fromm² & Zoya Avramova¹

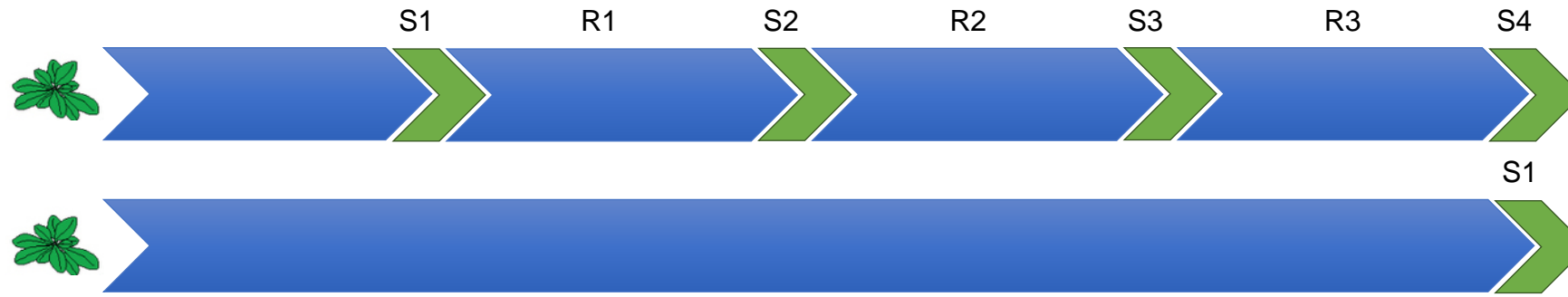
Example: Response to recurrent dehydration stress

Previous exposure to a stress may alter a plant's subsequent stress response by producing faster and/or stronger reactions that may provide the benefits of enhanced protection

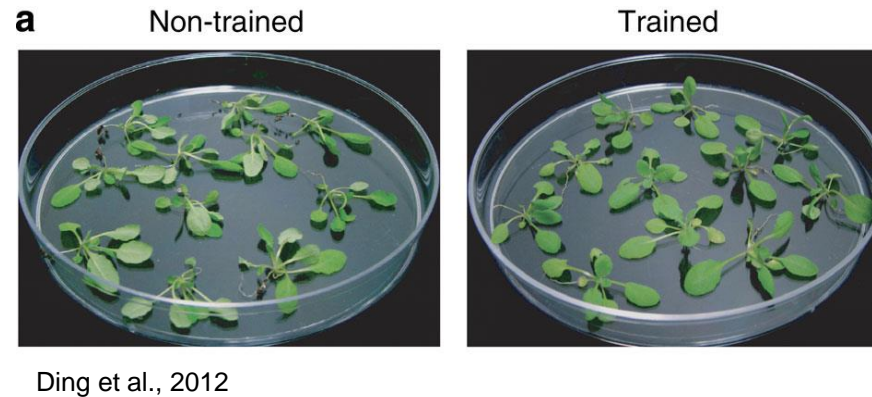


How do plants exercise a form of 'stress memory'?

Response to dehydration stress of trained or non-trained plants.

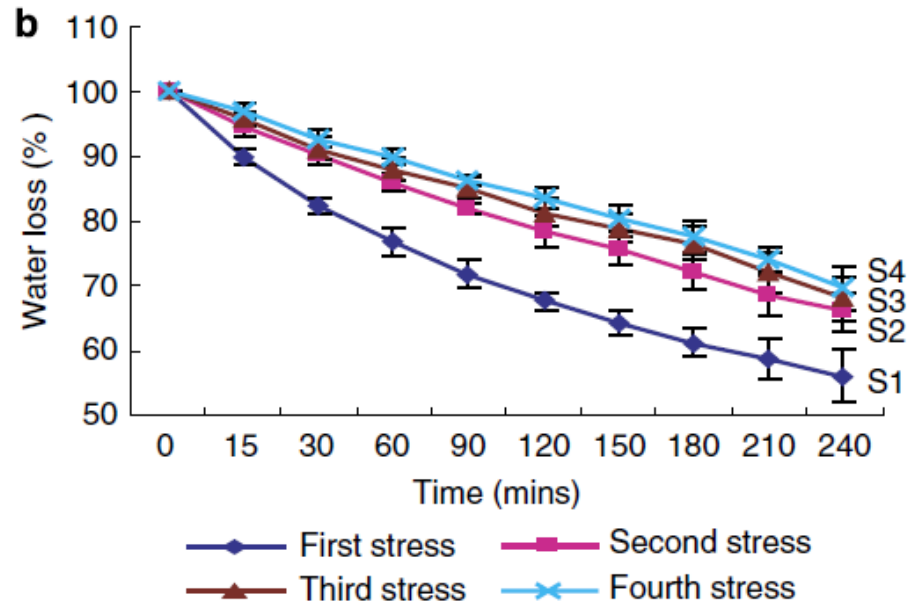
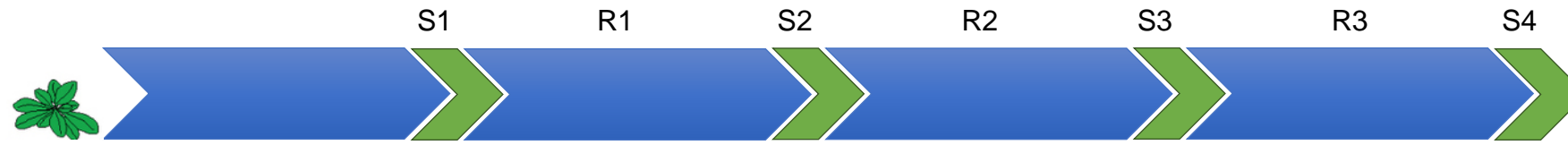


Appearance of 3-week-old *Arabidopsis* plants to 1-h exposure to air if not previously stressed (non-trained) or previously stressed with three consecutive cycles of stress/recovery treatments (trained).

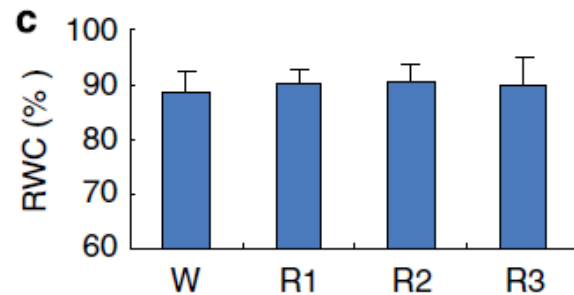


Non-trained plants wilted faster than trained plants

Response to dehydration stress of trained or non-trained plants.



Non-trained leaves lost water at a faster rate than trained plants



RWC of initial preinduced watered (W) state

Ding et al., 2012

drought hardening observed in horticultural plants

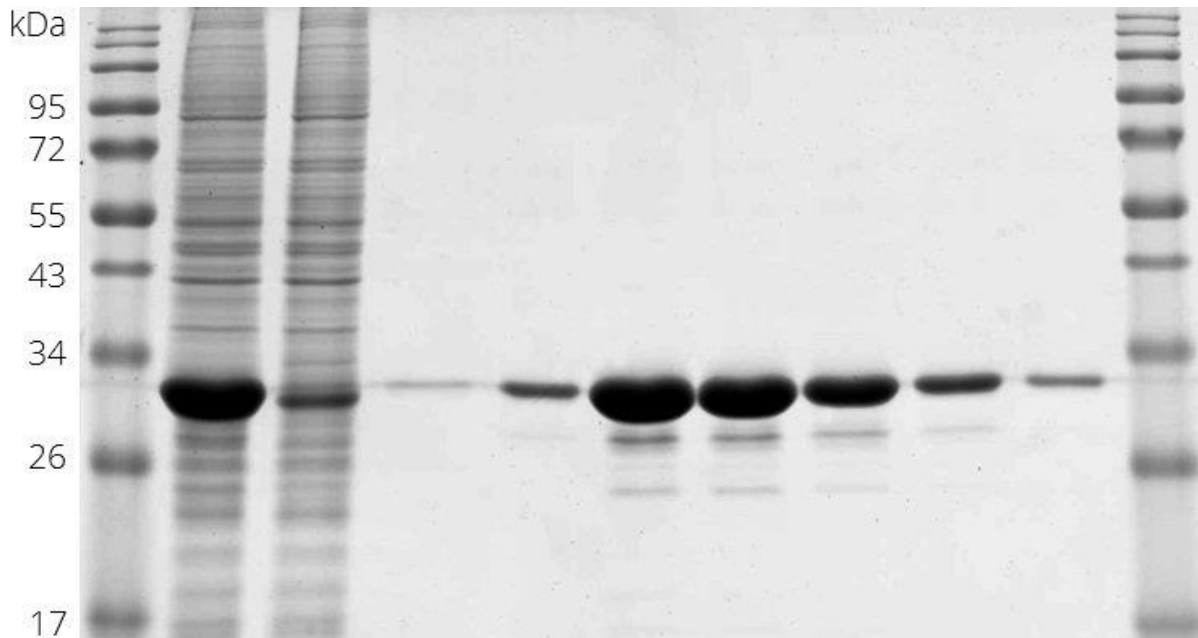
Genes widely used as markers for dehydration-inducible genes

RD29: responsive to desiccation

The homologous *RD29A* and *RD29B* genes are exquisitely sensitive to various abiotic stressors. Therefore, *RD29A* and *RD29B* gene sequences have potential to confer abiotic stress resistance in crop species grown in arid and semi-arid regions.

COR15A:

A cold-regulated gene whose product is targeted to the chloroplast. COR15A **protects stromal proteins from aggregation under various stress conditions**. Constitutive expression increases freezing tolerance in protoplasts in vitro and chloroplasts in vivo.



Dehydrin
rab-related (responsive to ABA) gene, rab18

Abstract Abiotic stresses have adverse effects on plant growth and productivity. The homologous *RD29A* and *RD29B* genes are exquisitely sensitive to various abiotic stressors. Therefore, *RD29A* and *RD29B* gene sequences have potential to confer abiotic stress resistance in crop species grown in arid and semi-arid regions. To our knowledge, no information on the physiological roles of the proteins encoded by *RD29A* and *RD29B* are available in the literature. To understand how these proteins function, we used reverse genetic approaches, including identifying *rd29a* and *rd29b* T-DNA knockout mutants, and examining the effects of complementing transgenes with the genes under control of their native promoters and chimeric genes with the native promoters swapped. Four binary vectors with the *RD29A* and *RD29B* promoters upstream of the cognate *RD29A* and *RD29B* cDNAs and as chimeric genes with noncognate promoters were used to transform *rd29a* and *rd29b* plants. Cold, drought, and salt induced both genes; the promoter of *RD29A* was found to be more responsive to drought and cold stresses, whereas the promoter of *RD29B* was highly responsive to salt stress. Morphological and physiological responses of *rd29a* and *rd29b* plants to salt stress were further investigated. Root growth, and photosynthetic properties declined significantly, while solute concentration ($\Psi\pi$), water use efficiency (WUE) and $\delta^{13}\text{C}$ ratio increased under salt stress. Unexpectedly, the *rd29a* and *rd29b* knockout mutant lines

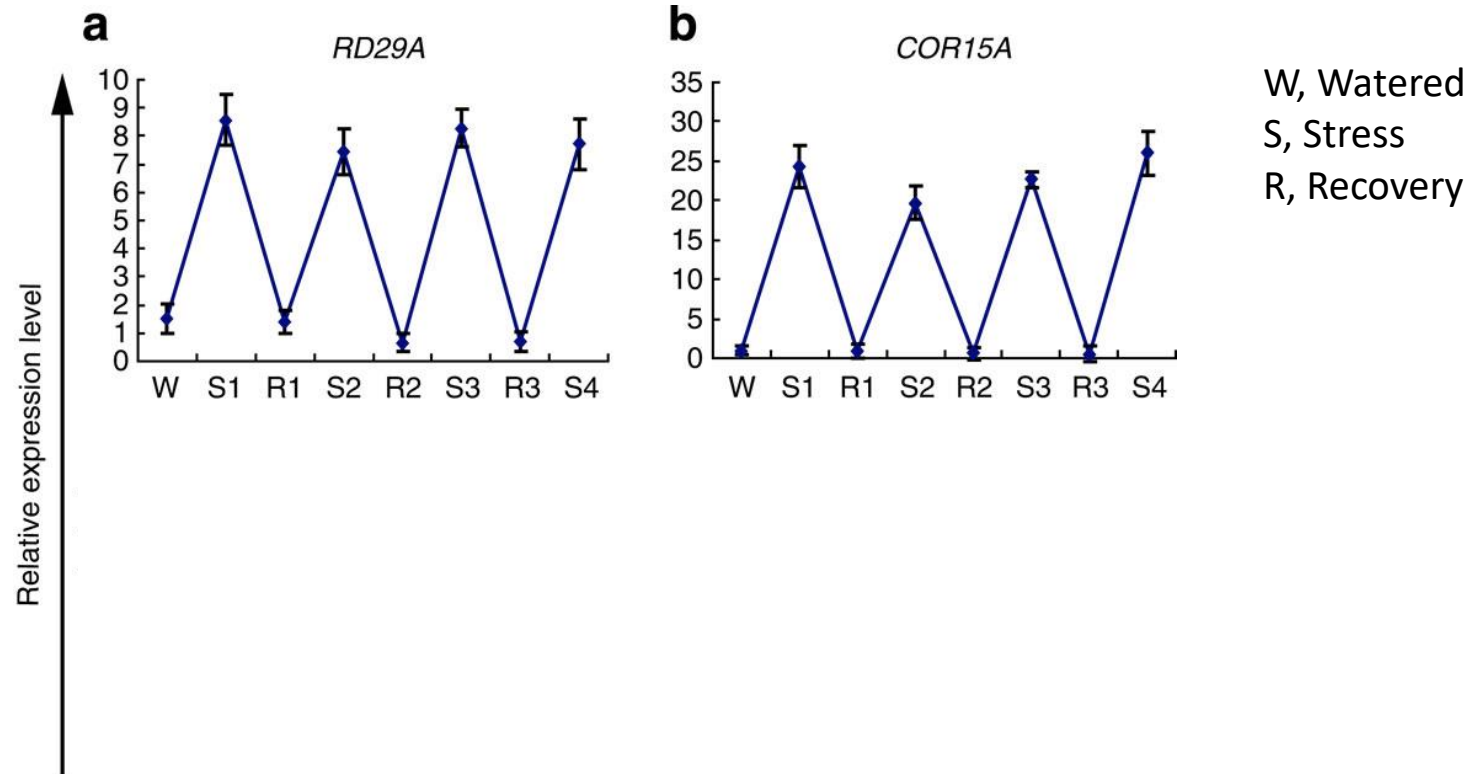
Characterization of abiotic stress-responsive *Arabidopsis thaliana* *RD29A* and *RD29B* genes and evaluation of transgenes

Joseph Msanne · Jiusheng Lin · Julie M. Stone ·
Tala Awada

maintained greater root growth, photosynthesis, and WUE under salt stress relative to control. We conclude that the *RD29A* and *RD29B* proteins are unlikely to serve directly as protective molecules.

Transcript levels of non-trainable and trainable genes in plants before and after single or multiple dehydration stresses.

Genes widely used as markers for dehydration-inducible genes

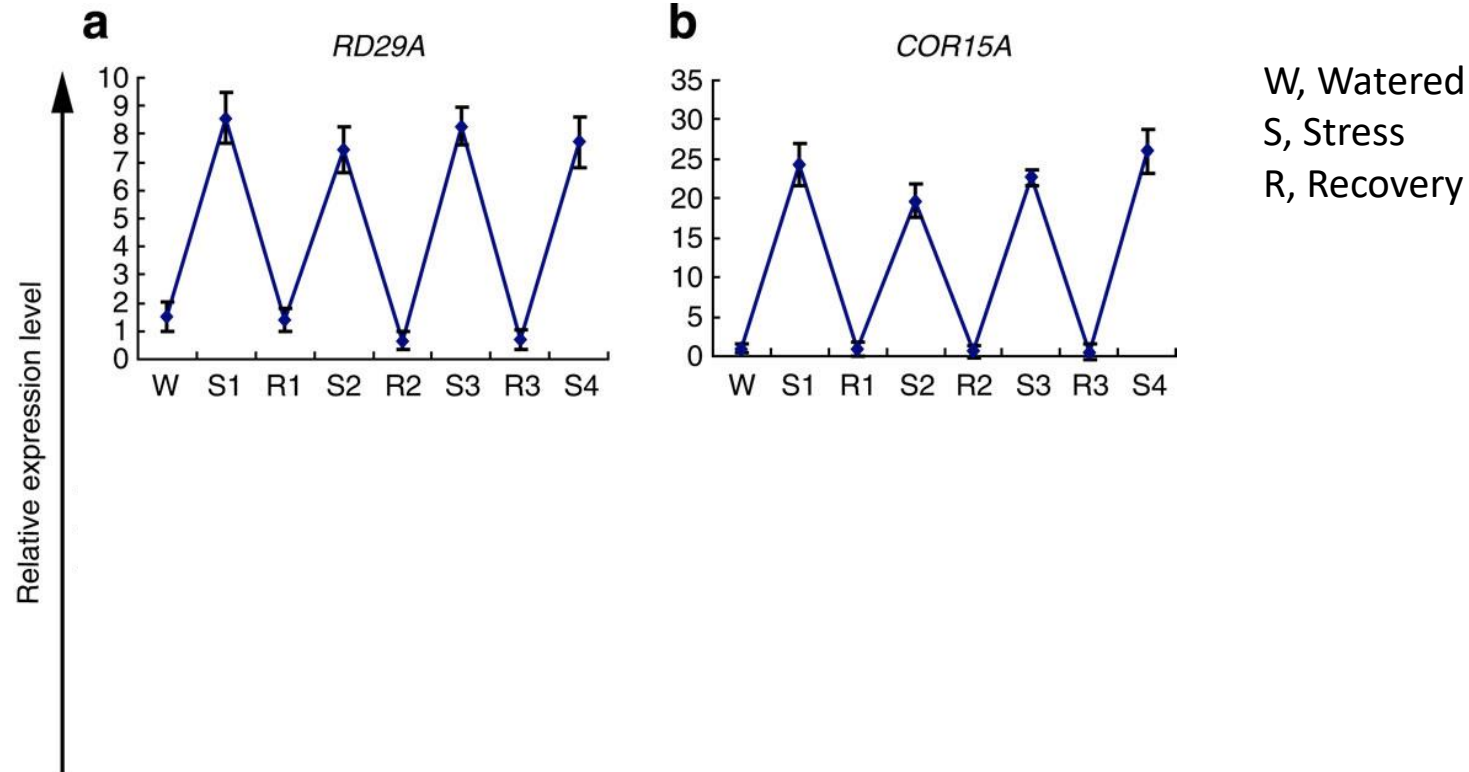


Transcript levels of non-trainable and trainable genes in plants before and after single or multiple dehydration stresses.

Genes widely used as markers for dehydration-inducible genes



NO
'memory'



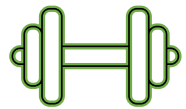
Transcript levels of non-trainable and trainable genes

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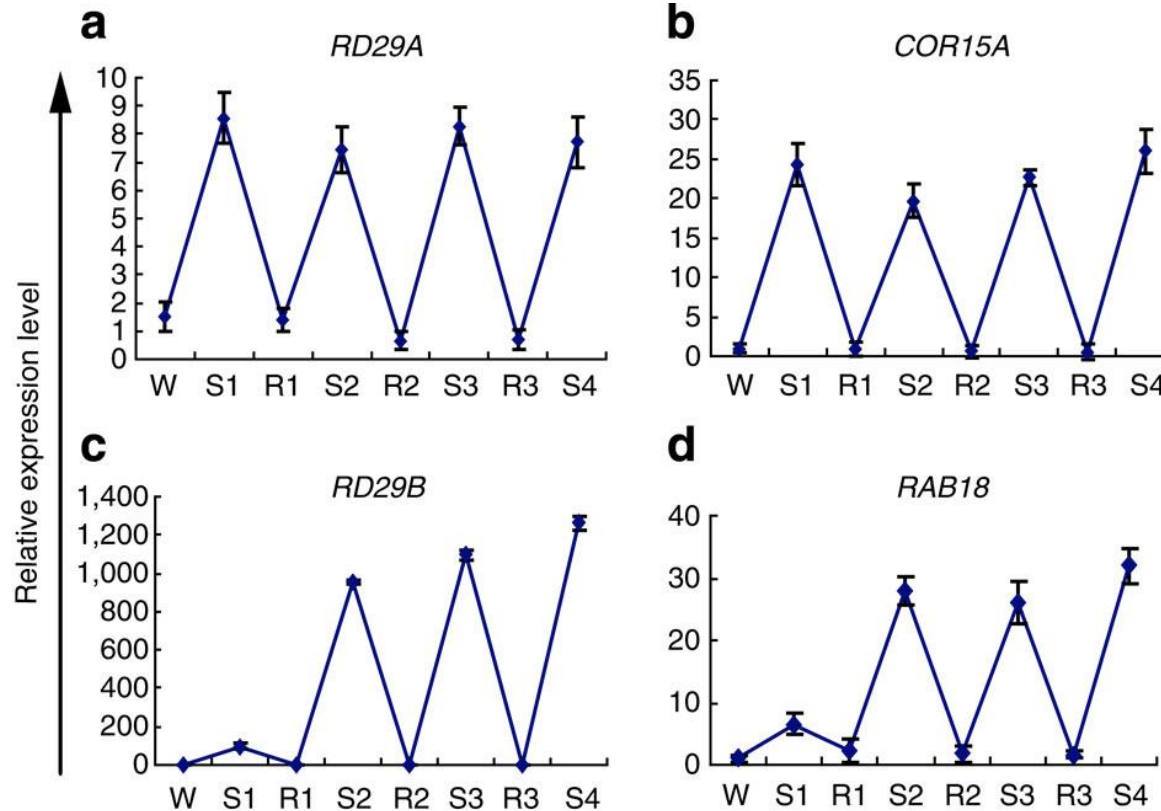
Genes widely used as markers for dehydration-inducible genes



NO
'memory'



'memory',
trainable



W, Watered
S, Stress
R, Recovery

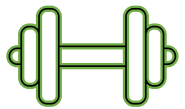
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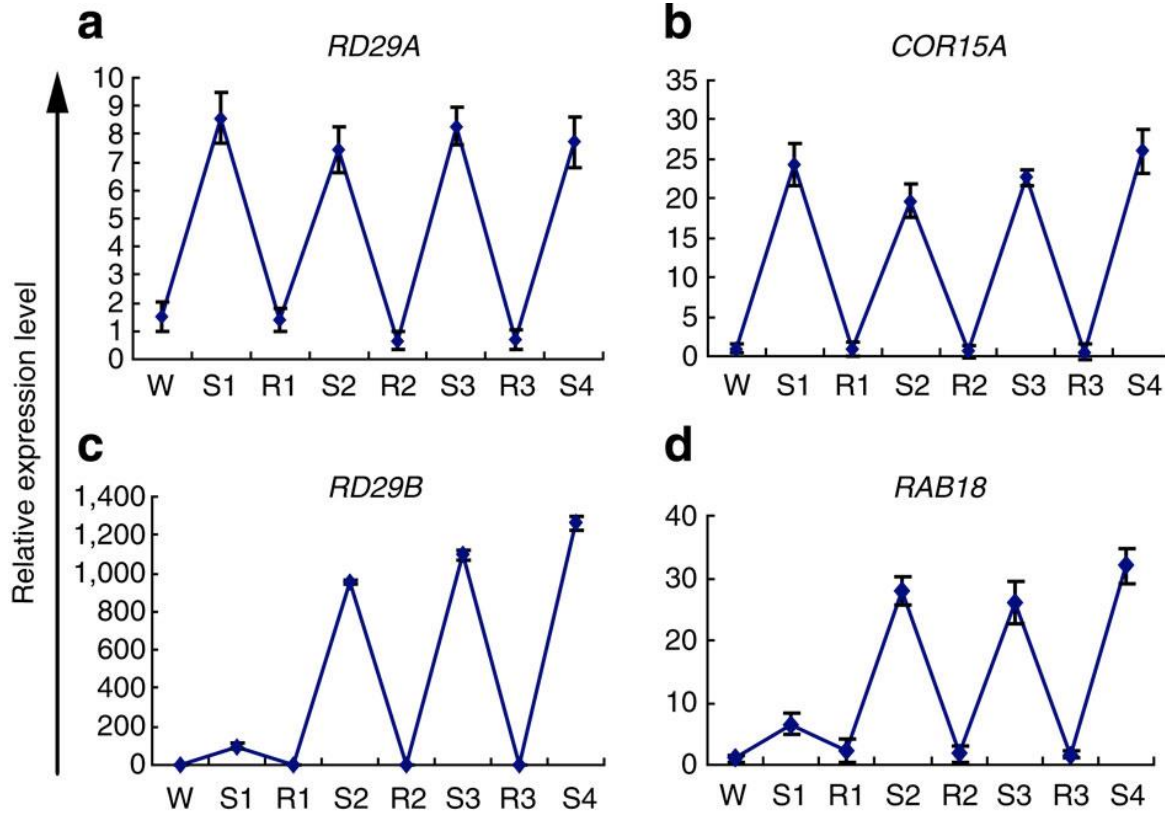
Genes widely used as markers for dehydration-inducible genes



NO
'memory'



'memory',
trainable



both the non-trainable and the trainable genes return to their initial (non-stressed) transcript levels



response genes' mRNAs were not persisting

Transcription rates

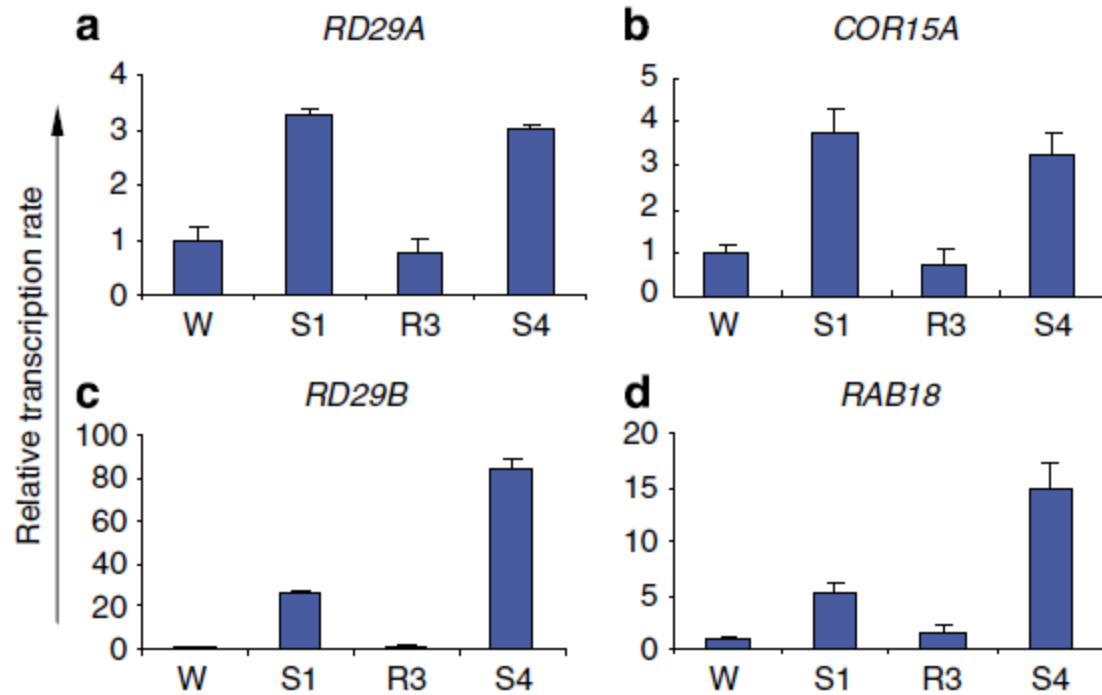
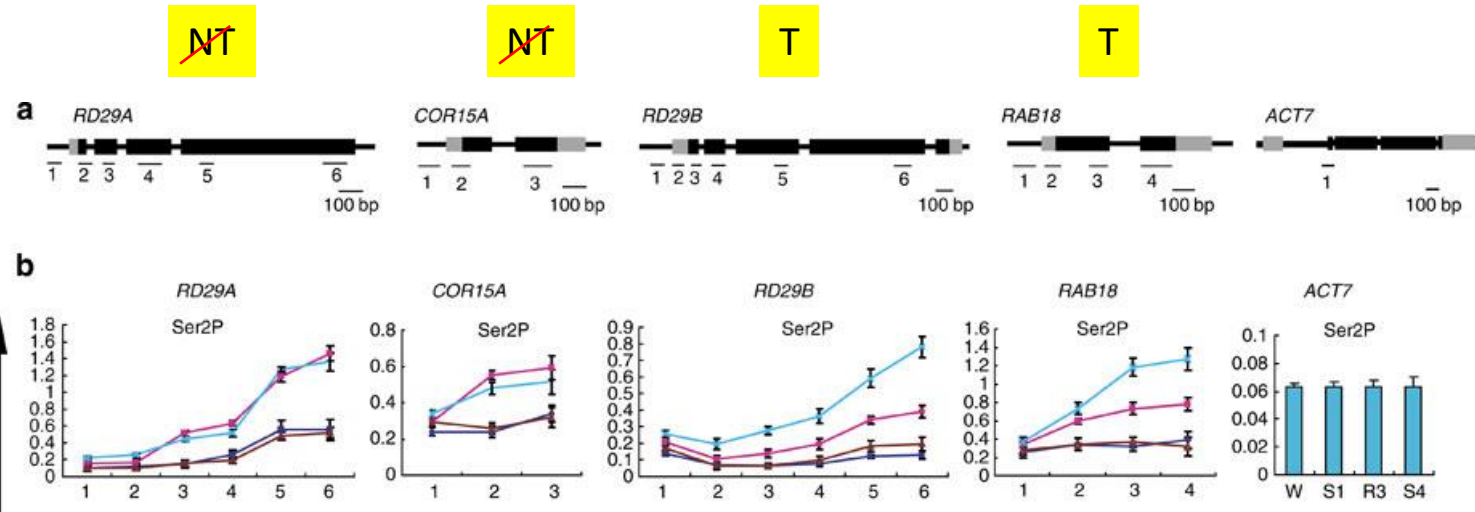


Figure 3 | Nuclear run on assays of non-trained or trained plants. Nuclei were isolated from non-stressed watered (W), singly (S1) or repetitively stressed plants. The repetitively stressed plants were dehydration stressed 3 times and then nuclei isolated before (recovery R3) or during a fourth dehydration stress (S4). Isolated nuclei were used in run on transcription reactions containing biotin-UTP to label newly synthesized transcripts. The nascent biotin-labelled transcripts were purified by binding to streptavidin beads and quantitated by quantitative PCR (qPCR) for **(a)** *RD29A*; **(b)** *COR15A*; **(c)** *RD29B*; **(d)** *RAB18* genes. Labelling experiments were repeated at three times, each with three reverse transcription-qPCR measurements, and the representative experiment shown indicates the mean + s.e.m., $n = 3$ replicates. *UBQ10* was used as internal control.



Schematic diagram of the genes, with the promoter region

Ser2P Pol II = elongation

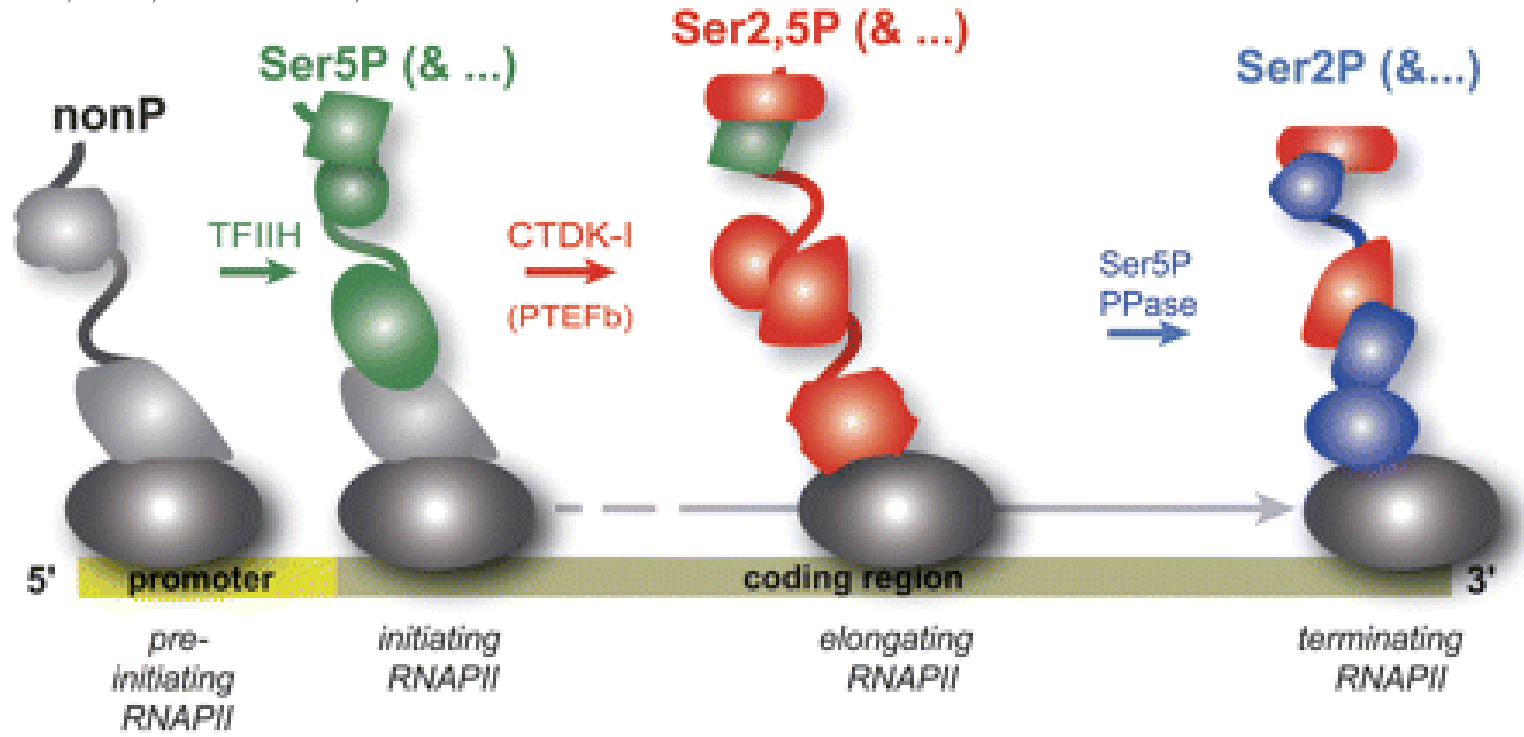
Active transcription elongation is associated with high Ser2P levels accumulating towards the 3'-ends of actively transcribed genes.

In agreement, the Ser2P distribution profiles showed a peak towards the 3'-ends of both the non-trainable and the trainable genes when induced by stress

Phosphorylation and functions of the RNA polymerase II CTD

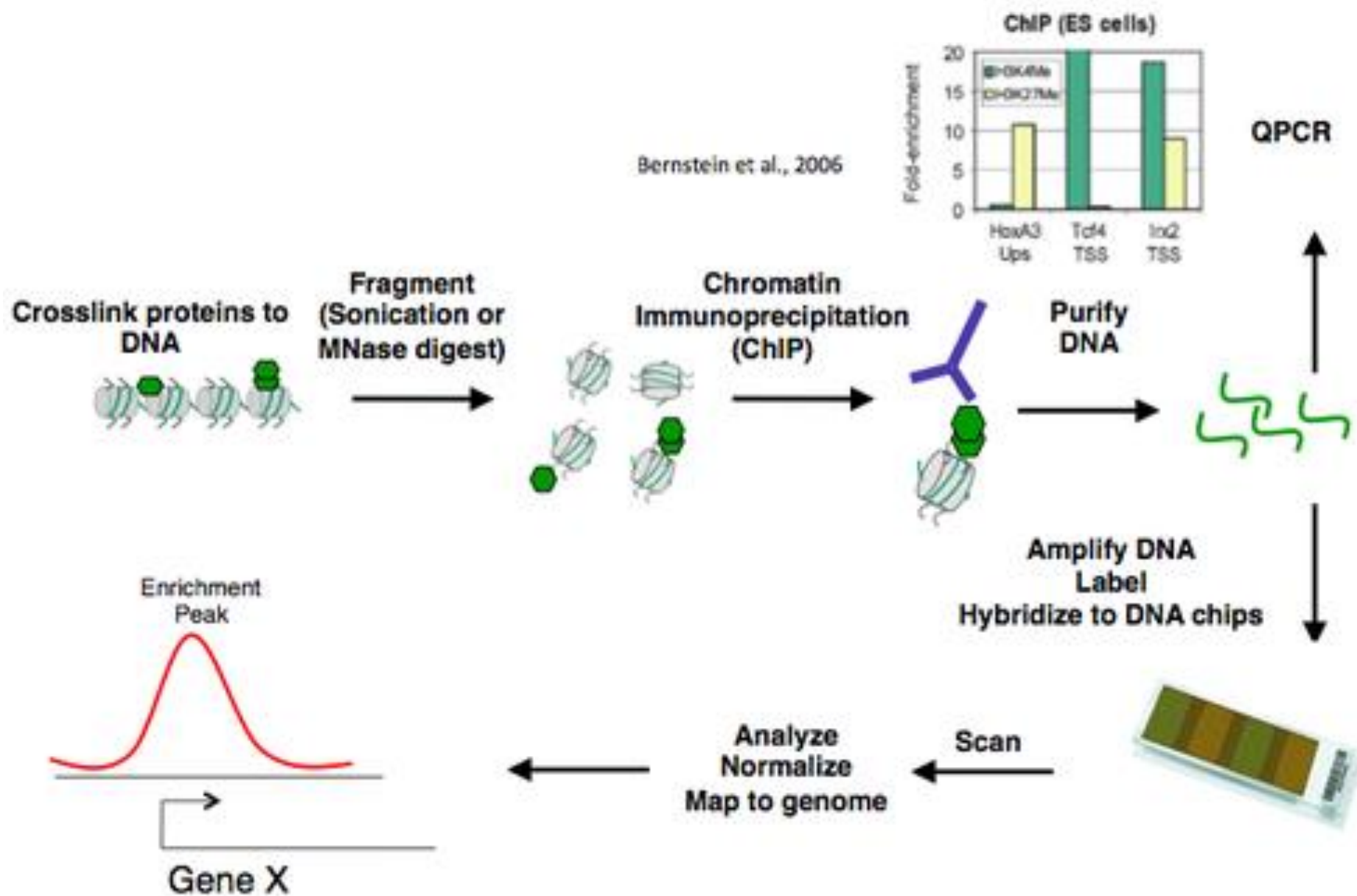
Hemali P. Phatnani¹ and Arno L. Greenleaf²

Department of Biochemistry, Duke University Medical Center, Durham, North Carolina 27710, USA



As the operational definition of memory marks is that they must last longer than the stimulus, we conclude that Ser2P does not function as a memory mark.

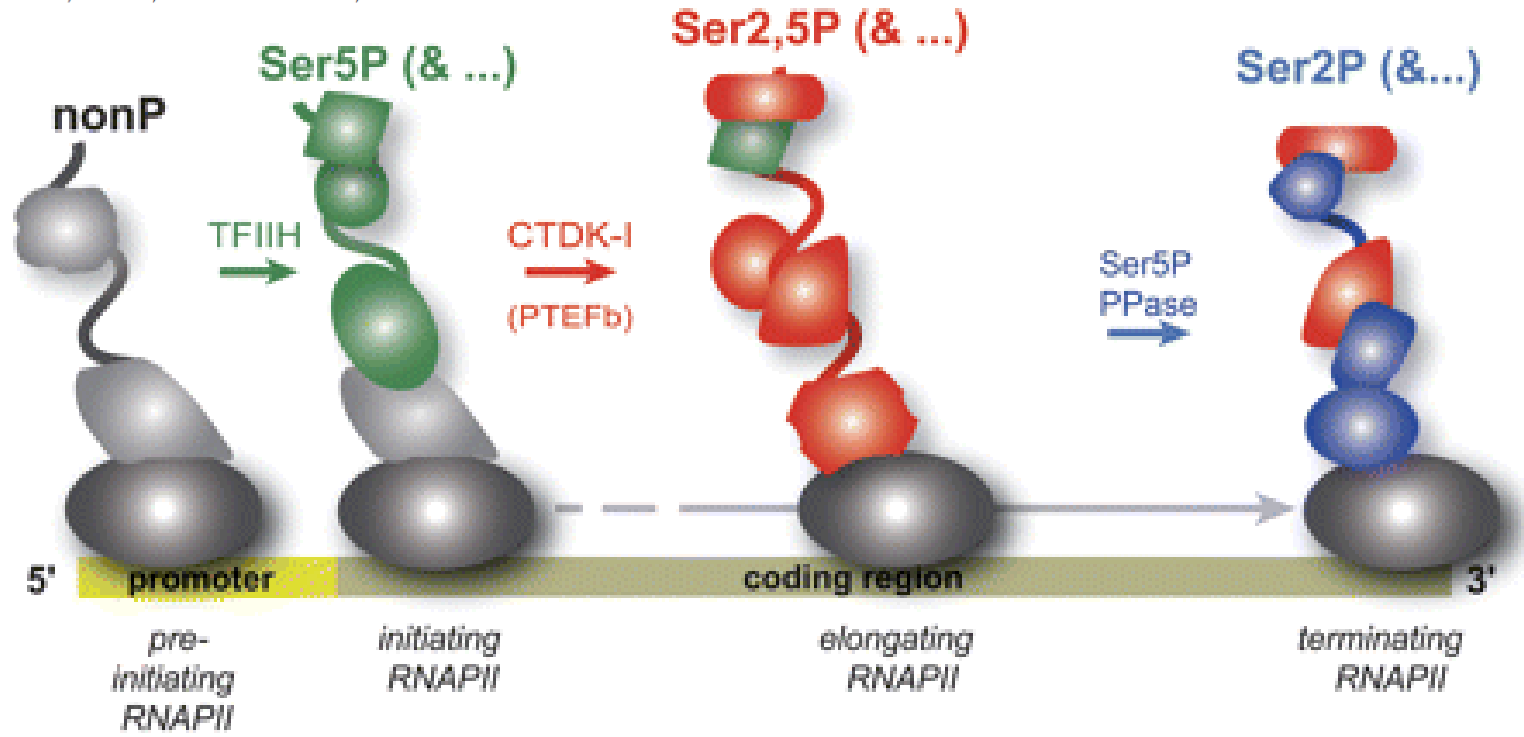
How can you analyse these specific subset of transcripts?



Phosphorylation and functions of the RNA polymerase II CTD

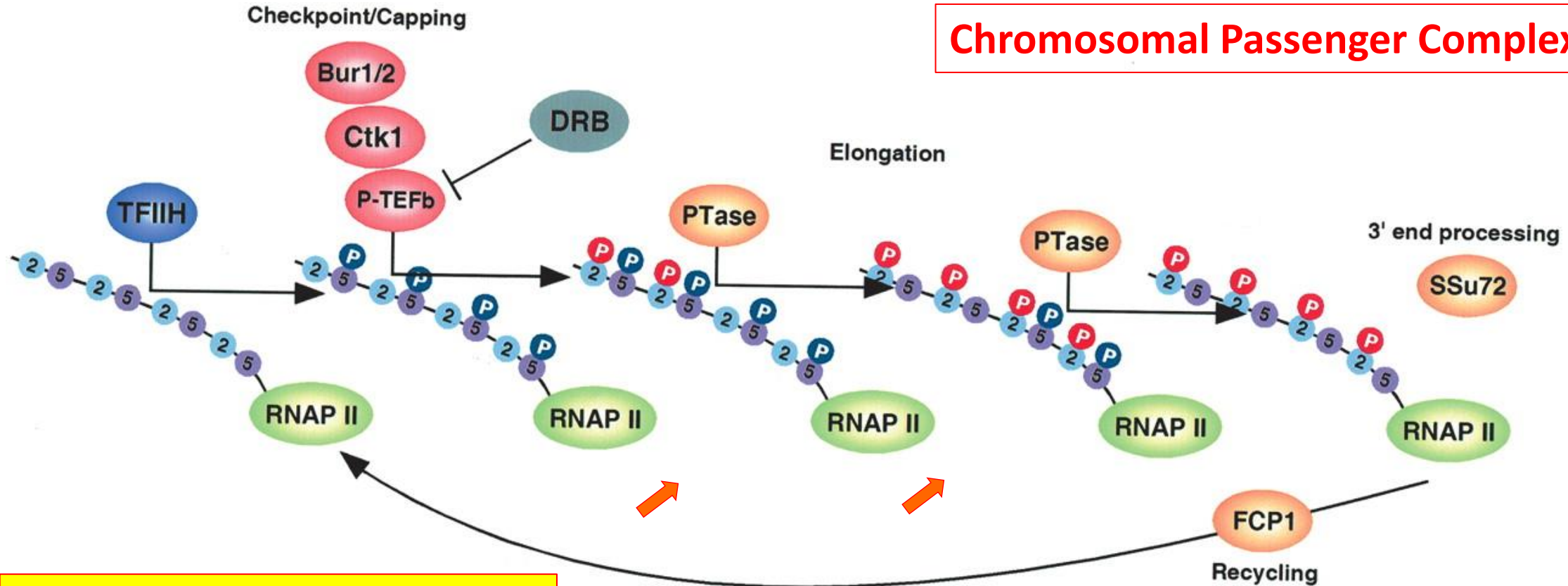
Hemali P. Phatnani¹ and Arno L. Greenleaf²

Department of Biochemistry, Duke University Medical Center, Durham, North Carolina 27710, USA



RNA Pol II and the chromatin histone H3K4me3 modification

Pol II has consensus repeats $(Y_1S_2P_3T_4S_5P_6S_7)_{34}$ at its C-terminal Domain (CTD)

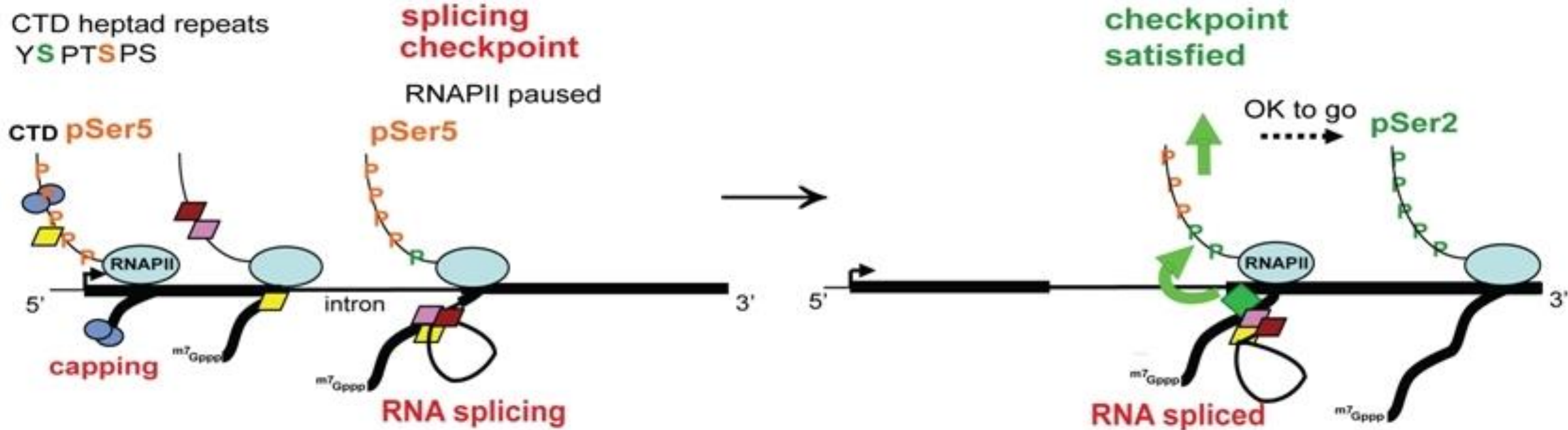


Chromosomal Passenger Complex (CPC)

Ser5P Pol II = initiation
Ser2P Pol II = elongation

Post-translational modifications of the CPC are very important for the transcription, and interact with chromatin changes

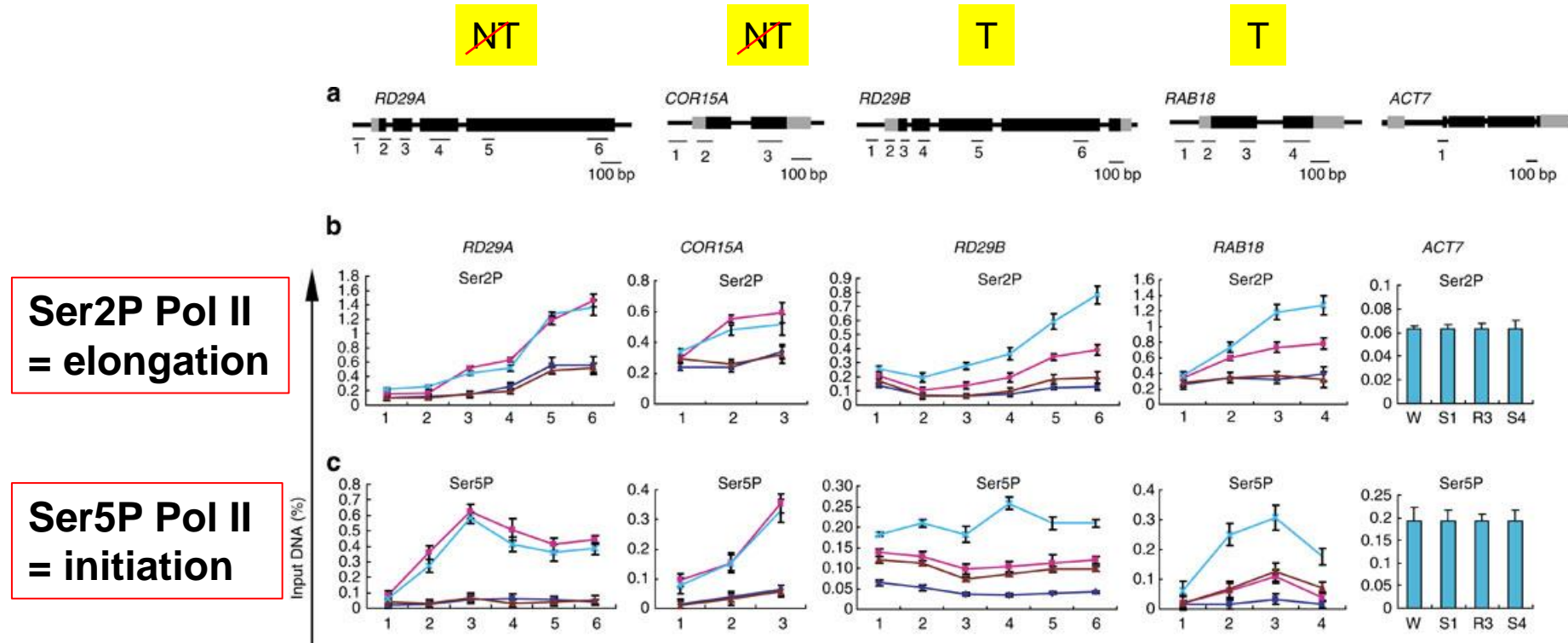
RNA Pol II and the chromatin histone H3K4me3 modification



Ser5P Pol II = initiation
Ser2P Pol II = elongation

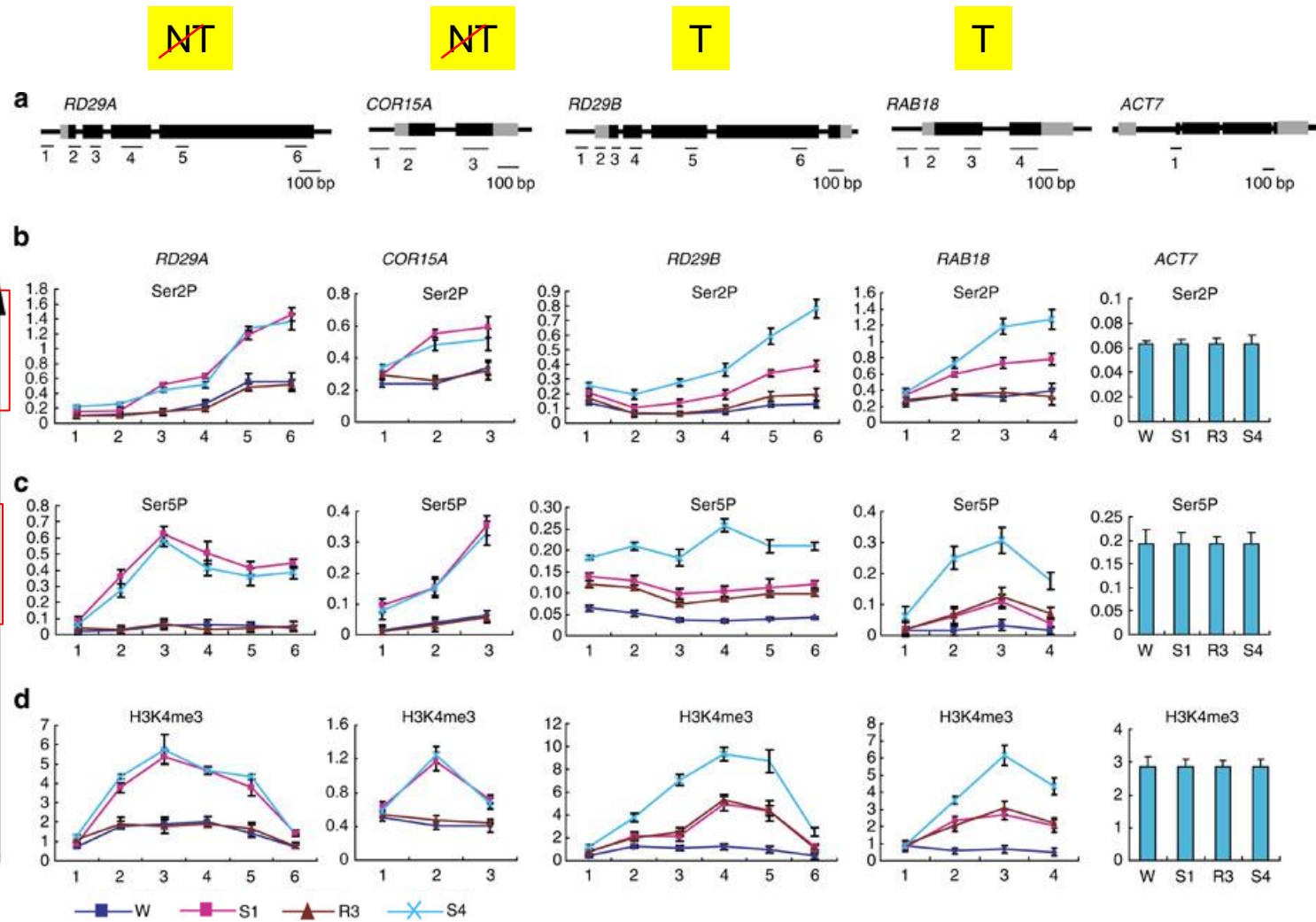
Post-translational modifications of the CPC are very important for the transcription, and interact with chromatin changes

RNA Pol II and the chromatin histone H3K4me3 modification



For the trainable genes, the Ser5P patterns were higher for the repetitively stressed (S4) than for singly stressed (S1) plants, consistent with their transcript levels.

RNA Pol II and the chromatin histone H3K4me3 modification



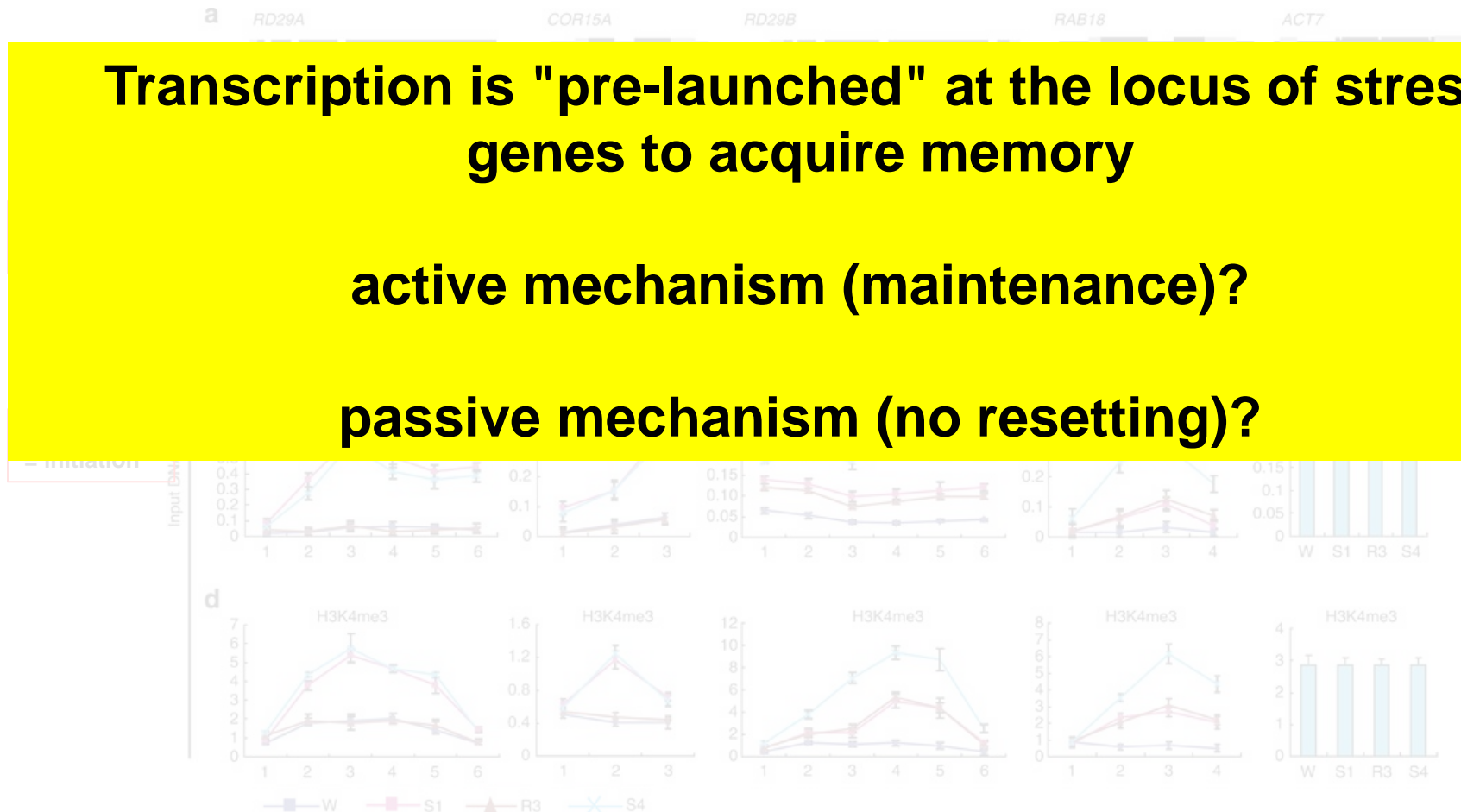
At the non-trainable genes, H3K4me3 acts as a reversible chromatin mark dynamically changing with transcript levels.

At the trainable genes, H3K4me3 acts as a persistent epigenetic mark associated with the transcriptional memory displayed by these genes.

Transcription is "pre-launched" at the locus of stress genes to acquire memory

active mechanism (maintenance)?

passive mechanism (no resetting)?



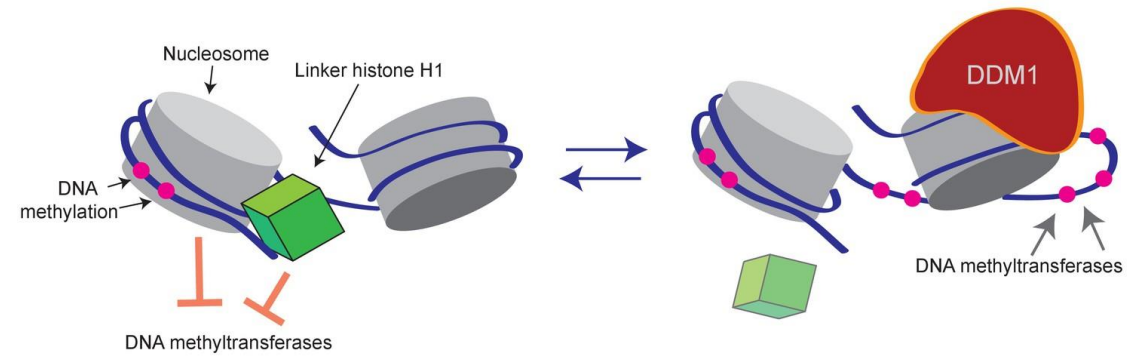
- Priming mechanisms allow plants to respond more effectively to recurrent stress.
- These mechanisms are closely linked to transcriptional memory.
- Examples of trans-generational effects of stress exist but are rare.
- Systematic studies, robust, and people are now essential.

Stress $\xrightarrow{\checkmark}$ Epigenetic modifications

Epigenetic modifications $\xrightarrow{?}$ Inheritable phenotype

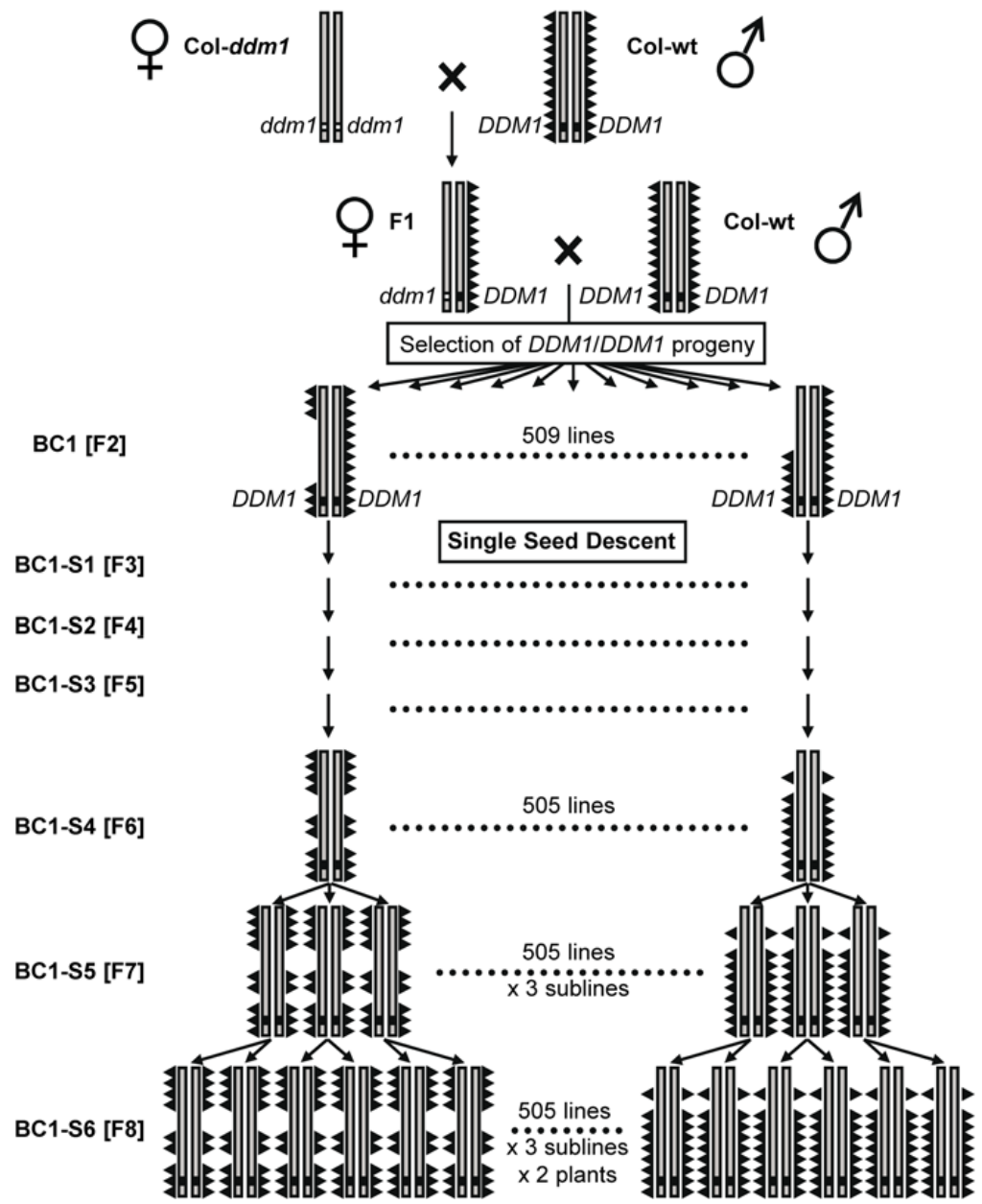
can lead to trans-generational effects? and adaptive?

DDM1 = Deficient in DNA methylation 1 is an ATP-dependent DNA helicase



DDM1 encodes an ATPase chromatin remodeler that is primarily involved in the maintenance of DNA methylation and silencing of repeat elements

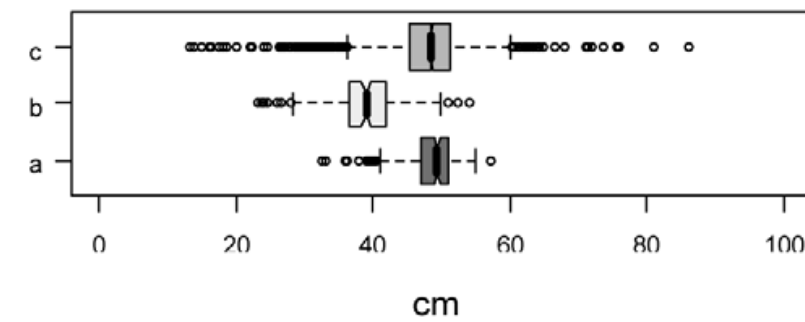
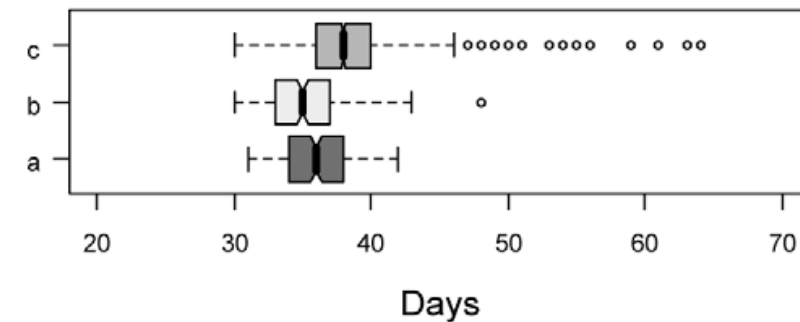
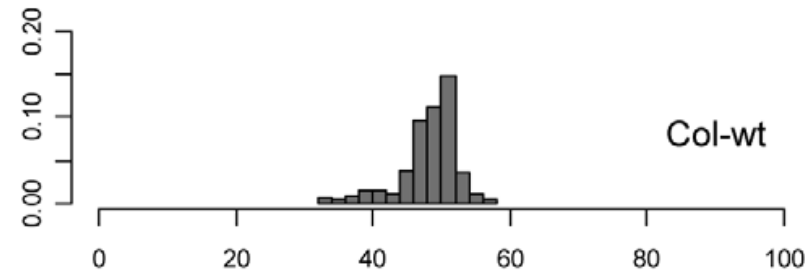
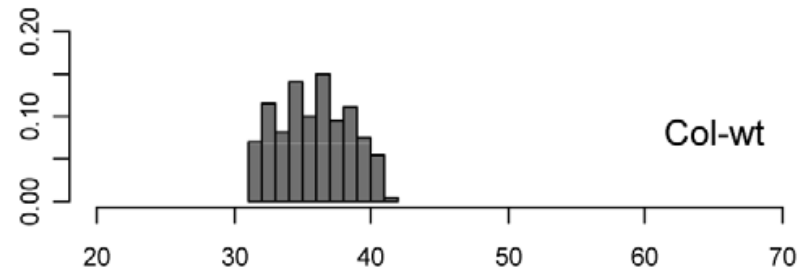
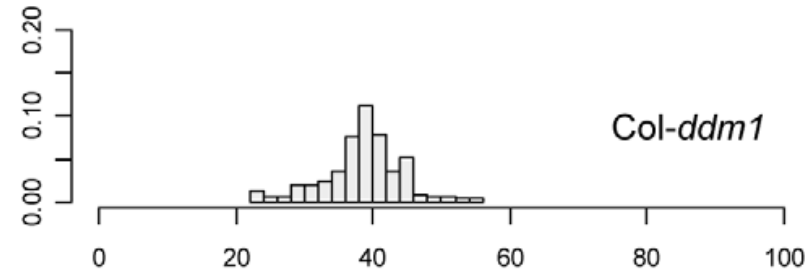
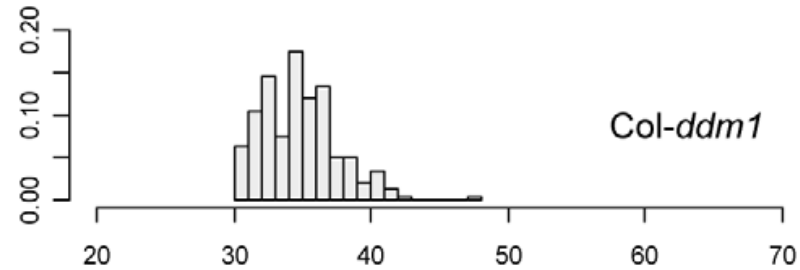
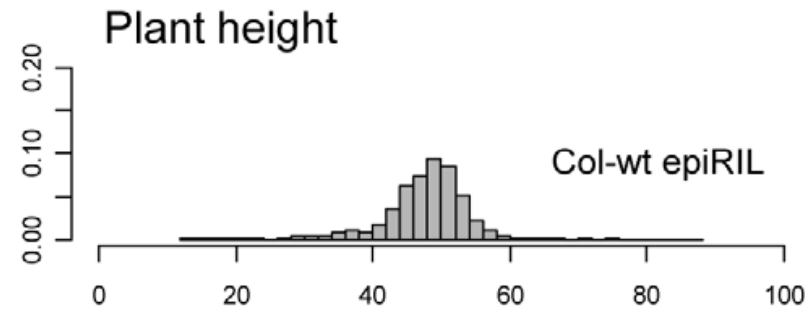
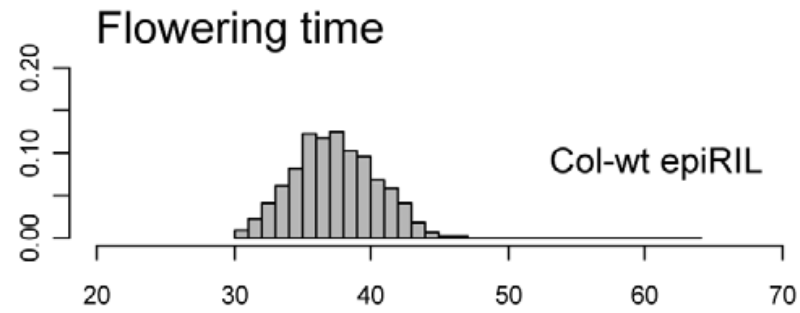
The epiRILs show that epigenetic changes can lead to stable and heritable phenotypes in plants.



can lead to trans-generational effects? and adaptive?

Larger phenotypic variation was observed among the Col-wt epiRILs, than among the Col-wt or Col-ddm1 parental lines.

Increased phenotypic variation of this kind is indicative of a component of segregational variance that typically arises in the construction of Recombinant Inbred Lines obtained from parents that differ by numerous DNA sequence polymorphisms.



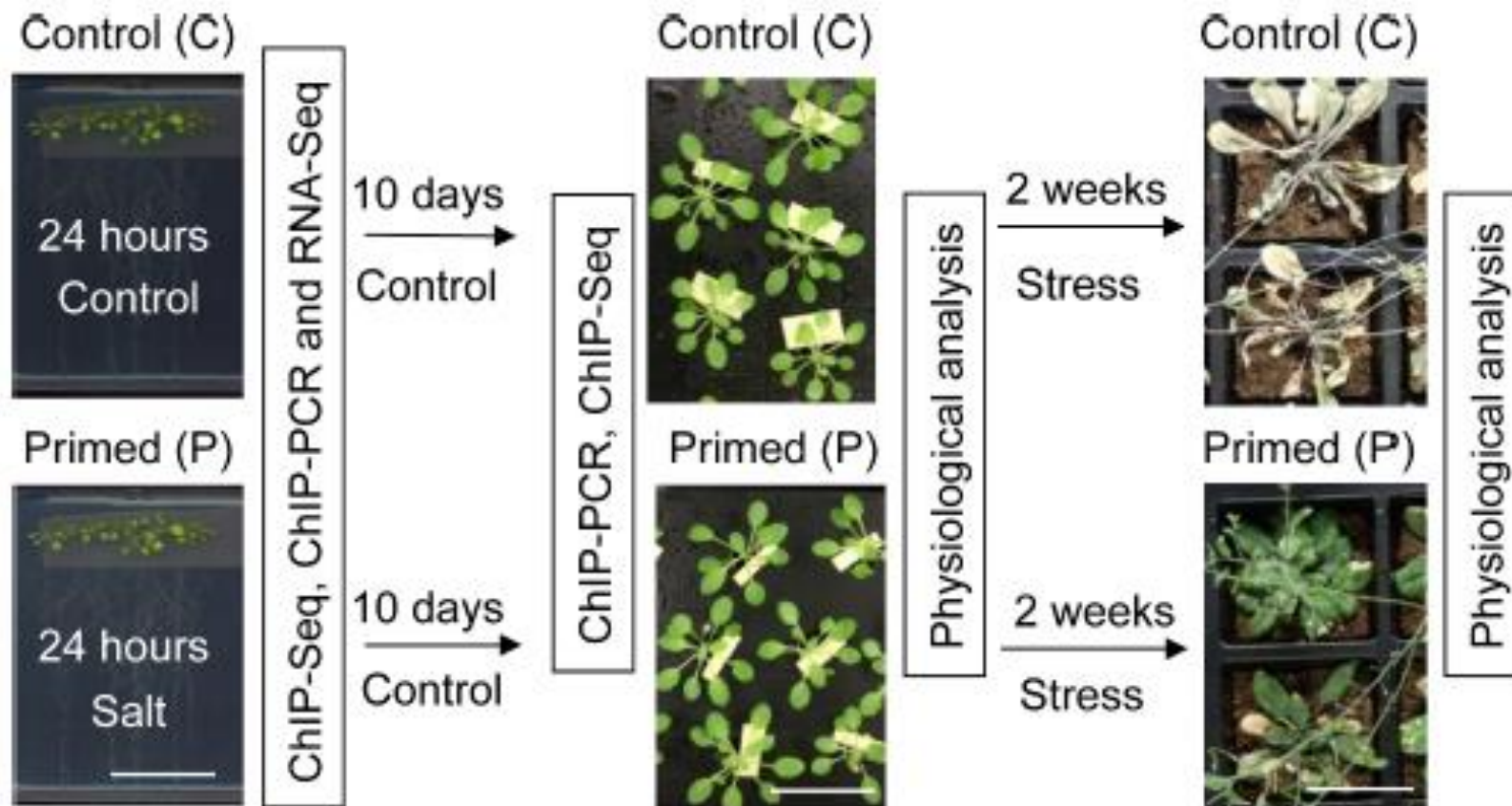
RESEARCH

Open Access

Hyperosmotic priming of *Arabidopsis* seedlings establishes a long-term somatic memory accompanied by specific changes of the epigenome

Emanuela Sani^{1,3}, Pawel Herzyk¹, Giorgio Perrella¹, Vincent Colot² and Anna Amtmann^{1*}

Also hyperosmotic stress induce an adaptative response (intra-generational)



Sani et al. 2013

Stress $\xrightarrow{\checkmark}$ Epigenetic modifications

Epigenetic modifications $\xrightarrow{\checkmark}$ Inheritable phenotype

Stress $\xrightarrow{\checkmark}$ Epigenetic modifications

Epigenetic modifications $\xrightarrow{\checkmark}$ Inheritable phenotype

Stress $\xrightarrow{?}$ Inheritable phenotype

Epigenetic variation contributes to environmental adaptation of *Arabidopsis thaliana*

Rik Kooke^{1,2,3} and Joost J B Keurentjes^{1,3,*}

¹Laboratory of Genetics; Wageningen University; Wageningen, The Netherlands; ²Laboratory of Plant Physiology; Wageningen University; Wageningen, The Netherlands; ³Centre for Biosystems Genomics; Wageningen, The Netherlands

The Plant Cell, Vol. 27: 337–348, February 2015, www.plantcell.org © 2015 American Society of Plant Biologists. All rights reserved.

Epigenetic Basis of Morphological Variation and Phenotypic Plasticity in *Arabidopsis thaliana*

Rik Kooke,^{a,b,c} Frank Johannes,^d René Wardenaar,^d Frank Becker,^a Mathilde Etcheverry,^e Vincent Colot,^e Dick Vreugdenhil,^{b,c} and Joost J.B. Keurentjes^{a,c,1}

