



**HAL**  
open science

# Maintenance and dynamic reprogramming of chromatin organization during development

Lauriane Simon, Aline V Probst

► **To cite this version:**

Lauriane Simon, Aline V Probst. Maintenance and dynamic reprogramming of chromatin organization during development. *The Plant Journal*, 2023, 10.1111/tpj.16119 . hal-04269286

**HAL Id: hal-04269286**

**<https://hal.science/hal-04269286>**

Submitted on 3 Nov 2023

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

# **Maintenance and dynamic reprogramming of chromatin organization during development**

Running head: Chromatin maintenance and reprogramming

Lauriane Simon<sup>1</sup> and Aline V. Probst<sup>1</sup>

<sup>1</sup> iGReD, CNRS, Inserm, Université Clermont Auvergne, 63000 Clermont-Ferrand, France

Corresponding author: Probst, Aline V. (aline.probst@uca.fr)

## *Abstract*

Controlled transcription of genes is critical for cell differentiation and development. Gene expression regulation therefore involves a multilayered control from nucleosome composition in histone variants and their post-translational modifications to higher-order folding of chromatin fibers and chromatin interactions in nuclear space. Recent technological advances have allowed gaining insight into these mechanisms, the interplay between local and higher-order chromatin organization and the dynamic changes that occur during stress response and developmental transitions. In this review, we will discuss chromatin organization from the nucleosome to its three-dimensional structure in the nucleus and consider how these different layers of organization are maintained during the cell cycle or rapidly reprogrammed during development.

## *Significance Statement*

Chromatin organization contributes to gene expression control. In this review we examine the interplay between local and higher-order chromatin organization and the dynamic changes that occur during stress response and developmental transitions.

## *Introduction*

In eukaryotes, the genome is organized in the nucleus, the functional control center of the cell. During cellular and organismal life, specific sets of genes need to be transcribed in a particular cell type and others have to be repressed, while transposable elements require continuous control to avoid unscheduled transposition events and deleterious mutations. The organization of the genome into chromatin contributes substantially to this transcriptional control, as access of the transcriptional machinery might be facilitated or prevented by looser or tighter compaction of chromatin. At chromatin's most fundamental level of organization, DNA wraps around an octamer of histone proteins (Luger *et al.*, 1997) forming the nucleosome. Nucleosomes can be bound by linker histones that attach to the nucleosome dyad and linker DNA, thereby forming the chromatosome and locking in the nucleosome at a specific position by restricting linker DNA flexibility (Rudnizky *et al.*, 2021). Chains of nucleosomes arranged as 'pearls on the string' then fold into higher order chromatin fibers that adopt specific structures within the three-dimensional (3D) space of the nucleus. Higher-order folding of chromatin fibers can next help to restrain access for transcription factors and the transcription machinery or favor transcription by allowing enhancer-promoter contacts. Without being exhaustive, we highlight here some recent studies that shed light on local and higher-order chromatin features in the model species *Arabidopsis thaliana*, illustrating how these are maintained during DNA replication or challenged to achieve transcriptome reprogramming during development.

### *1. Establishing chromatin states through histone variants and their modifications*

The nucleosome consists of basic histone proteins, an H3-H4 tetramer and two H2A-H2B dimers around which wrap ~146bp of DNA. Histones are evolutionary highly conserved proteins, comprising histone fold domains that assemble to form a histone octamer and mainly non-structured N- and C-terminal tails that protrude from the nucleosome core (Luger *et al.*, 1997). Most eukaryotes express different non-allelic variants of the core histones H3, H2A, H2B and the linker histone H1 (Talbert and Henikoff, 2021). These histone variants can differ in their primary amino-acid sequence only by a few residues or larger domains, can show tissue or cell-cycle specific expression patterns as well as alternative deposition modes (Borg, Jiang, *et al.*, 2021; Probst, 2022). Given the critical role of histones in structuring nuclear DNA and regulating access to specific DNA sequences, their expression, transport and deposition but also their eviction, recycling or degradation are highly controlled through a network of specific sets of histone chaperones (Probst *et al.*, 2020). The direct structural consequences on nucleosome structure conferred by histone variants and their modifications influence chromatin compaction, higher-order chromatin organization and the transcriptional read-out of the genome.

As in other eukaryotes, *Arabidopsis* histone proteins are abundantly post-translationally modified by methylation, phosphorylation, ubiquitination among others (Leng *et al.*, 2020), both in their histone fold domains and their N- or C-terminal tails. These post-translational modifications (PTMs) can directly modulate histone-histone or histone-DNA interactions as it is exemplified by reduction in the positive charge of histones upon lysine acetylation (Tessarz and Kouzarides, 2014). PTMs can also be subsequently interpreted by reader proteins, thereby contributing to specify transcriptionally permissive or repressive chromatin states (Roudier *et al.*, 2011; Sequeira-Mendes *et al.*, 2014; Liu *et al.*, 2018; Jamge *et al.*, 2022). For example, constitutive heterochromatin, chromosomal regions mainly consisting of repetitive sequences and transposable elements that are constantly transcriptionally repressed, is highly enriched in H3K9me2 and H3K27me1 (Mathieu *et al.*, 2005; Jacob *et al.*, 2009; Jackson *et al.*, 2002). Instead, in euchromatin that comprises most of the genes, transcriptional activity correlates with enrichment in H3K4me3, H3K9ac and/or H2Bubiquitination (Leng *et al.*, 2020), while gene repression is achieved by H3K27me3 deposition by the Polycomb Repressive complex 2 (PRC2) (Mozgova and Hennig, 2015) (**Figure 1**). The importance of these histone modifications, especially the Polycomb mark H3K27me3, for plant development has been revealed by genetic approaches either removing histone modifiers (Goodrich *et al.*, 1997), or more recently expressing histone proteins that cannot be post-translationally modified at specific sites (Fal *et al.*, 2022; Xu *et al.*, 2022; Corcoran *et al.*, 2022). Corcoran *et al.* probed systematically the importance of modifiable histone H4 residues by replacing endogenous *H4* genes by transgenes carrying different point mutations, revealing many residues critical for plant survival or development, including correct flowering time (Corcoran *et al.*, 2022). Interfering specifically with modifications set on H3K27 by replacing lysine 27 by alanine in a transgene-encoded H3 resulted in a substantially altered transcriptome when assessed in calli and strong developmental abnormalities partly reminiscent of those found in mutants of histone methyltransferases of the PRC2 complex (Fal *et al.*, 2022). While interpretation of these observations is complicated by the fact that lysine residues can undergo several modifications, these phenotypes confirm the critical role for H3K27me3 in plant development. Deposition of histone modifications or binding of reader proteins could also be influenced by modifications of adjacent residues. For example, expressing H3 proteins, in which the serine at position 28 is replaced by alanine led to reduced S28 phosphorylation (Xu *et al.*, 2022). Subtle changes in H3K27me3 levels were also observed, even though they are likely the indirect consequence of altered expression of *CURLY LEAF (CLF)* and *SWINGER (SWN)* coding for histone methyltransferase subunits of the PRC2 complex. Interestingly, whether the K27A mutation was introduced in the H3.1 or the H3.3 variant, affected gene expression and plant development in a different manner (Xu *et al.*, 2022; Fal *et al.*, 2022). In both studies, the

expression of a mutated version of H3.3 caused more severe developmental defects. Potential explanations are the distinct genomic enrichment of the two variants, their expression at different cell cycle stages or in specific cell types. Indeed, even though H3.1 and H3.3 histone variants differ by only four amino-acids, they are differently expressed during the cell cycle and employ distinct deposition pathways: H3.1, expressed in S-phase (Okada *et al.*, 2005; Otero *et al.*, 2016) is deposited by CHROMATIN ASSEMBLY FACTOR 1 (CAF-1) at the replication fork (Jiang and Berger, 2017; Benoit *et al.*, 2019). In contrast, H3.3 deposition requires HISTONE REGULATOR A (HIRA) (Nie *et al.*, 2014; Layat *et al.*, 2021; Duc *et al.*, 2015) and ALPHA THALASSEMIA-MENTAL X-LINKED (ATRX) (Duc *et al.*, 2017). These deposition modes contribute to the preferential enrichment of H3.1 at silent genes and at repetitive elements (Ingouff *et al.*, 2010; Stroud *et al.*, 2012; Wollmann *et al.*, 2012), whereas the H3.3 variant occupies predominantly the 3' end of active genes (Duc *et al.*, 2017; Stroud *et al.*, 2012; Wollmann *et al.*, 2012). While the differences in primary amino acid sequences between the two variants likely do not substantially alter nucleosome structure as shown for the mammalian nucleosome containing either H3.1 or H3.3 (Tachiwana *et al.*, 2011), they are thought to determine deposition, eviction and modifications. Differences in the histone fold are crucial to direct deposition mode of the H3 molecule by the respective chaperones (Shi *et al.*, 2011; Jiang and Berger, 2017) and dissimilarities at position 41 (phenylalanine (F) in H3.1 and tyrosine (Y) in H3.3) impact histone eviction. Indeed, H3.141F contributes to restrict H3.1 to silent genes (Lu *et al.*, 2018) and replacement of Y by F in H3.3 (H3.3Y41F) prevents H3.3 removal from rRNA gene repeats upon inhibition of Polymerase I transcription (Shi *et al.*, 2011), suggesting that H3F41 precludes histone eviction or replacement. While the exact mechanism is unresolved, it may implicate interactions between histone and DNA, as H3F41 is critically situated where the histone tail emerges between the DNA helices. Finally, differences at position 31 between H3.1 and H3.3 are known to direct H3K27 monomethylation by ARABIDOPSIS TRITHORAX-RELATED PROTEIN 5 (ATXR5) and ATXR6 specifically to H3.1 (Jacob *et al.*, 2014). Taken together, small differences in the primary amino acid sequences of H3 and H4 histones may interfere with the setting of post-translational modifications or directly affect octamer assembly or nucleosome structure and stability.

Similar to H3 variants, H2A variants also show differential genomic distribution, with H2A.X present all along the chromosome, while H2A and H2A.Z are depleted from heterochromatin and enriched at chromosome arms (Yelagandula *et al.*, 2014). H2A.Z deposition involves the SWI/SNF chromatin remodeling complex SWR1c that can be recruited to certain genes by the DNA-binding protein SWC4 that recognizes AT-rich DNA elements in their promoters (Gómez-Zambrano *et al.*, 2018). *In vitro*, nucleosomes comprising H2A.Z are more unstable compared to nucleosomes containing other H2A variants (Osakabe *et al.*, 2018). How this

difference in nucleosome stability impacts gene transcription is less clear, as H2A.Z can exert both a repressive effect when incorporated along gene bodies and facilitate transcription by contributing to rapid eviction of the +1 nucleosome in response to heat and other environmental factors (Kumar and Wigge, 2010; Sura *et al.*, 2017). In contrast to H2A and H2A.Z, H2A.W that is specifically deposited at heterochromatic regions by the chromatin remodeling factor DECREASE IN DNA METHYLATION (DDM1) (Osakabe *et al.*, 2021), where it promotes chromatin fiber-fiber interactions and heterochromatin condensation (Yelagandula *et al.*, 2014). The characteristic C-terminal tail of H2A.W can contact linker DNA (Osakabe *et al.*, 2018) and influences chromatin accessibility by modulating the binding of the linker histone H1 at these domains (Bourguet *et al.*, 2021).

Taken together, the genomic distribution of specific variants and their modifications contribute to establish specific chromatin states, to regulate DNA accessibility to the transcriptional machinery and have the potential to affect 3D chromatin organization.

## 2. 3D organization of the *Arabidopsis* nucleus

When observing nuclei stained with DNA intercalating agents such as 4',6-diamidino-2-phenylindole (DAPI), several strongly stained spots, the chromocenters, are visible (**Figure 1**, (Fransz *et al.*, 2002; Probst *et al.*, 2003)). Chromocenters consist of the pericentromeric regions from each of the ten chromosomes and localize preferentially at the nuclear periphery (Fang and Spector, 2005; Poulet *et al.*, 2017). Due to the interaction between homologous pericentromeric regions, resulting in the fusion of 2-3 chromocenters per nucleus, on average eight distinct and well-defined chromocenters are detectable in mesophyll cells. Fluorescence *in situ* hybridization subsequently revealed that each V-shaped chromosome fills a specific chromosome territory (CT) between the nuclear envelope and the nucleolus, around which telomeres are clustered (Schubert *et al.*, 2012; Probst *et al.*, 2003). Most of these chromosome territories are randomly distributed inside the nucleus (Pecinka *et al.*, 2004; Schubert and Shaw, 2011; Di Stefano *et al.*, 2021; Grob *et al.*, 2014; Fransz *et al.*, 2002), except the short arms of chromosomes 2 and 4 bearing the rRNA gene clusters known as the nucleolus-organizing regions (NORs) that tend to associate with their homologous short arms next to the nucleolus (Pontvianne *et al.*, 2016; Pecinka *et al.*, 2004; Di Stefano *et al.*, 2021). Chromatin conformation capture (3C) experiments coupled to sequencing (Hi-C) that inform about interactions between distant chromatin regions later confirmed the existence of CTs, by revealing more frequent interactions between chromatin regions belonging to the same chromosome. Hi-C further showed peculiar inter-chromosomal interactions between pericentromeric regions in good agreement with the possible fusion between chromocenters observed in cytology (Feng *et al.*, 2014; Grob *et al.*, 2014). Telomeres also engage in frequent inter-chromosomal interactions, while no contacts

are observed between pericentromeres and telomeres again supporting the distinct position of chromocenters and telomeres observed in cytology (**Figure 1**). While most information on 3D organization is available from whole leaf tissue therefore averaging organization from different nuclei within this tissue, this organization likely differs from cell type to cell type. For example, in the endosperm (a triploid nutritive tissue surrounding the embryo) CTs were suggested to adopt a non-random arrangement with frequent pairwise associations (Baroux *et al.*, 2017) in agreement with more frequent contacts revealed by Hi-C between chromosome arms compared to leaves (Yadav *et al.*, 2021). Furthermore, Hi-C experiments showed fewer contacts between pericentromeric regions in the endosperm, correlated with the presence of endosperm-specific interspersed (ESI) heterochromatin observed by microscopy (Baroux *et al.*, 2007) and consistent with the endosperm's hypomethylated state and global chromatin decondensation (Hsieh *et al.*, 2009; Moreno-Romero *et al.*, 2016; Yadav *et al.*, 2021).

As in animals (Lieberman-Aiden *et al.*, 2009), Hi-C interaction maps revealed further details such as interactions within Arabidopsis chromosomes that can be partitioned in two classes named A and B compartments with a preference for interactions between regions in the same compartment (Grob *et al.*, 2014; Feng *et al.*, 2014). The A compartment is associated with euchromatin and contains mainly chromosome arms while the B compartment is associated with heterochromatin and comprises mainly pericentromeric and centromeric regions (Grob *et al.*, 2014). Many genomes, including those of certain plants, organize in addition into Topologically-Associated Domains (TADs) (Santos *et al.*, 2020; Domb *et al.*, 2022; Liu *et al.*, 2017; Dong *et al.*, 2017). Although TADs are not a dominant feature for the Arabidopsis genome organization, approximately 1,000 TAD-like structures have been identified (Liu *et al.*, 2017; Wang *et al.*, 2015). TADs may provide a way to co-regulate genes within a given TAD as illustrated by the recent discovery of large enhancers called super-enhancers that coordinate gene expression in a concerted manner to ensure organ development and tissue identity (H., Zhao *et al.*, 2022). Special kinds of TADs are the Lamina associated domains (LADs) also called PLADs in Arabidopsis (Bi *et al.*, 2017; Hu *et al.*, 2019). PLADS have been identified by ChIP against the nucleoskeleton protein CROWDED NUCLEI 1 (CRWN1) (Hu *et al.*, 2019). These PLADs strongly overlap with the chromatin regions identified by a particular restriction enzyme mediated Chromatin Immunoprecipitation (RE-ChIP) directed against the nuclear pore basket protein NUP136 that localizes predominantly at the nuclear periphery (Bi *et al.*, 2017) and correlate with the repressive B-compartment identified by Hi-C (Hu *et al.*, 2019). About 10-20% of the genome, mainly transcriptionally repressed and enriched in the histone modifications H3K9me2 and H3K27me3 has thus been identified to localize at the nuclear periphery (Bi *et al.*, 2017; Hu *et al.*, 2019).

### 3. Chromatin loops and long-range chromatin contacts in gene expression regulation

In addition to the TAD-like structures, about 20,000 chromatin loops have been described (Liu *et al.*, 2016; Zhao *et al.*, 2021; Crevillén *et al.*, 2013; B., Zhao *et al.*, 2022). Chromatin loops can form between enhancers and promoters and small loops in a range of a few kilobases have been found to form between 5' and 3' regions of genes. The latter are globally positively correlated with gene transcription level, however no obvious correlation with specific histone marks was found for high and moderately expressed genes, while silent or low expressed genes were enriched in the histone variant H3.3 (Liu *et al.*, 2016). A well-known example for a locus engaged in gene loops is the floral repressor gene *FLOWERING LOCUS C (FLC)* for which intragenic loop formation correlates with gene expression (Crevillén *et al.*, 2013; Kim and Sung, 2017; Zhao *et al.*, 2021). Several factors have been involved in the formation of a loop connecting the promoter and 3' end of *FLC*, such as the presence of GH1-HMGA1 proteins, which prevent *FLC* loop formation and thereby contribute to *FLC* repression (B., Zhao *et al.*, 2022). In contrast to a general correlation that low expressed genes, engaged in loop formation, show enrichment in the histone variant H3.3 (Liu *et al.*, 2016), H3.3 occupancy or the act of its deposition seem to favor loop formation and expression of the *FLC* locus (Zhao *et al.*, 2021). FRIGIDA (Choi *et al.*, 2011) plays an active role in H3.3 deposition, as it recruits the H3.3 histone chaperone HIRA to the *FLC* locus and thereby directly increases H3.3 occupancy (Zhao *et al.*, 2021). During vernalization, cold-induced transcriptional repression of *FLC* correlates with disruption of the gene loop suggesting that interruption of the loop could be a first step in *FLC* repression (Crevillén *et al.*, 2013). During vernalization, another intragenic loop comprising the first large intron of the *FLC* gene is formed and its establishment requires PRC2 and two long non-coding RNAs (Kim and Sung, 2017). During Polycomb mediated silencing the *FLC* locus also makes long-range contacts, as alleles on homologous chromosomes cluster together (Rosa *et al.*, 2013). On top of *FLC* in its repressed and K27me3-enriched state, additional contacts between regions highly enriched in H3K27me3 were revealed by Hi-C (**Figure 1**) (Feng *et al.*, 2014; Liu *et al.*, 2016). Recently, a Hi-ChIP analysis (Hi-C combined with immunoprecipitation) allowed to identify many more regions enriched in H3K27me3 that are engaged in long-range interactions thereby spatially segregating inactive chromatin domains from transcriptionally active genes (Huang *et al.*, 2021). The H3K27me3 marked genes involved in these long-range interactions differ between tissues, reflecting the role of H3K27me3 in silencing of tissue-specific genes. The long-distance contacts identified by Hi-ChIP depend on the presence of the H3K27me3 mark, as ectopic deposition of H3K27me3 in the *relative of early flowering (ref6)* mutant, lacking one of the H3K27me3 demethylases, induces novel chromatin loops. In contrast, chromatin loops are destabilized in the *cif* mutant,



indicating a global reconfiguration of chromatin architecture and a major role for H3K27me3 in structuring repressive regions in euchromatin (Huang *et al.*, 2021).

While we have here focused on the Arabidopsis genome organization, recent studies also allowed insight into the formation of chromatin loops in species with larger and more transposon-rich genomes such as rice, maize and wheat (Y., Sun *et al.*, 2020; Concia *et al.*, 2020; Deng *et al.*, 2022). For example, the formation of loops between genes with similar chromatin marks and expression level is a characteristic feature of the hexaploid wheat genome (Concia *et al.*, 2020) and diurnally expressed genes in rice were found to group together with RNA polymerase II in clusters facilitating coordinated transcription (Deng *et al.*, 2022).

In addition to long-range interactions between repressed genes, contacts between heterochromatic regions characterize higher-order organization in Arabidopsis. The knob region, present on the short arm of chromosome 4 that initially derived from the pericentromere interacts with the pericentromeric region of the same chromosome, forming an euchromatic loop (Fransz *et al.*, 2000; Fransz *et al.*, 2016; Fransz *et al.*, 2002). Other long-range interactions in so called KNOTs have been observed between transposon hotspots from different chromosomes termed KNOT Engaged Elements (KEEs) (**Figure 1**, (Grob *et al.*, 2014)) or interactive heterochromatin islands (IHIs, (Feng *et al.*, 2014)). KNOTs have later been shown to be involved in regulating invasive DNA elements such as transgenes, however so far the mechanisms remain to be resolved as KNOT formation does correlate with neither DNA methylation, sRNA production (Grob and Grossniklaus, 2019; Grob *et al.*, 2014), nor with position at the nuclear periphery (Bi *et al.*, 2017) and KNOTs still exist in the *su(var)3-9 homolog (suvh) 4 suvh5 suvh6* triple mutant with strongly reduced H3K9me2 levels (Feng *et al.*, 2014).

#### *4. Linking local chromatin changes to 3D genome organization*

Does interfering with histone variants and their modifications affect higher-order chromatin organization? Plants lacking METHYLTRANSFERASE 1 (MET1) or DDM1, mutants with decreased DNA methylation and H3K9me2 levels (Gendrel *et al.*, 2002; Tariq *et al.*, 2003), show reduced contacts between pericentromeric regions and increased interactions between chromosome arms (Feng *et al.*, 2014), in agreement with changes observed in cytology in these mutants (Mathieu *et al.*, 2007; Probst *et al.*, 2003). Instead, depleting H3K9me2 in the *suvh4 suvh5 suvh6* mutant has more subtle effects on heterochromatin organization (Feng *et al.*, 2014; Stroud *et al.*, 2014). Interestingly, the incorporation of the H2A.W histone variant can lead to chromocenter formation when ectopically expressed (Yelagandula *et al.*, 2014) and is required for chromocenter formation in cotyledons during early seedling development

(Benoit *et al.*, 2019). Surprisingly, however, H2A.W deletion causes only subtle defects in chromocenter organization as detectable by microscopy (Yelagandula *et al.*, 2014; Bourguet *et al.*, 2021). In contrast, depletion of the linker histone H1 reduces nucleosome density at repetitive sequences and disturbs their organization in 3D since chromocenters, except those containing NORs, are nearly completely abolished (Rutowicz *et al.*, 2019). In agreement, Hi-C studies revealed a strong decrease in intra-pericentromeric chromatin interactions in *2h1* mutants lacking the linker histone variants H1.1 and H1.2 (Teano *et al.*, 2022). The role of H1 is, however, not restricted to heterochromatin, as linker histones are also abundant in euchromatin, where H1 loss leads to more relaxed and mobile chromatin (Rutowicz *et al.*, 2019). Interestingly, loss of H1 also affects H3K27me3 homeostasis, causing reduced H3K27me3 at genes and H3K27me3 accumulation at certain hot spots shedding light on the important role of linker histones in controlling recruitment of PRC complexes to specific sequences within the genome (Rutowicz *et al.*, 2019; Teano *et al.*, 2022). Taken together, differences at the nucleosome level in particular incorporation of specific histone variants and their modifications together with linker histones have the potential to influence higher-order organization. This is particularly visible at the level of heterochromatin, where deficient heterochromatin marks affect inter-chromosomal interactions. In euchromatin, recent evidence suggests an important role for the repressive H3K27me3 mark in both short and long-range interactions and in structuring the repressive chromatin domains within nuclear space.

##### *5. Maintenance of chromatin states through DNA replication*

During the cell cycle and the life of an organism, chromatin organization is constantly challenged to permit DNA sequence information to be read during transcription, reconstructed during DNA repair or duplicated during DNA replication. All these processes may require changes in post-translational modifications of histones such as phosphorylation of H2A.X to signal DNA damage (Friesner *et al.*, 2005), partial or complete eviction of histones, which carry modifications, and deposition of new histones devoid of these modifications (Stewart-Morgan *et al.*, 2020). During each of these DNA-based cellular activities, there is therefore a tradeoff between the need to reconstitute epigenetic information encoded in the position of nucleosomes, their content in histone variants and their modifications, or to seize the opportunity to modify the chromatin state.

##### *5.1 Maintenance of H3 histone modifications*

During transcription, it has been suggested that the RNA polymerase II machinery can read DNA when only an H2A-H2B dimer is removed (Kireeva *et al.*, 2002). Therefore, H3-H4 histone modifications could be maintained during transcription at least at lowly expressed

genes (Kulaeva *et al.*, 2010). In case of histone eviction, histone chaperones such as FACILITATES CHROMATIN TRANSCRIPTION (FACT) and HIRA recycle parental histones (Torné *et al.*, 2020; Jeronimo *et al.*, 2019). The Arabidopsis FACT complex associates with the RNA polymerase II and elongation factors (Antosz *et al.*, 2017) and immuno-precipitates with transcriptionally active chromatin (Duroux *et al.*, 2004). In yeast, the absence of FACT abolishes faithful and local re-deposition of evicted histones at a given gene and instead leads to random incorporation of these histones (Jeronimo *et al.*, 2019). Arabidopsis mutants in CAF-1 (Kaya *et al.*, 2001), HIRA (Ingouff *et al.*, 2010; Duc *et al.*, 2015) and ATRX (Duc *et al.*, 2017) are viable assuming a partial redundant function in histone deposition. Instead, mutants lacking one of the two FACT subunits are lethal (Lolas *et al.*, 2010) suggesting a critical role for this histone chaperone complex that cannot be compensated by the others.

During replication, every nucleosome is disrupted and here again it is important to reestablish existing chromatin environments by histone recycling. In yeast and mammals there is little if no splitting of the parental H3-H4 tetramers into dimers (Xu *et al.*, 2010), therefore information carried by a parental H3-H4 tetramer is only found on one of the two daughter strands after replication. While distribution of H3-H4 tetramers is mainly random, a slight bias towards the leading strand in mammals (Petryk *et al.*, 2018) or the lagging strand in yeast (Yu *et al.*, 2018) has been observed. Whether such a bias exists in plants, needs still to be determined. To replenish the nucleosomal histone pool, the CAF-1 complex, highly conserved through evolution, is recruited via PCNA to the replication fork and realizes *de novo* histone deposition of H3-H4 tetramers (Verreault *et al.*, 1996). In mammals and plants, CAF-1 interacts preferentially with histone H3.1 and deposits this variant in a replication coupled manner (Tagami *et al.*, 2004; Jiang and Berger, 2017). Histone deposition is therefore closely coupled to DNA replication, ensuring immediate reconstitution of chromatin. Very recently, POL2A, the catalytic subunit of Arabidopsis DNA polymerase epsilon (POL  $\epsilon$ ) required for leading strand elongation, has been shown to bind FASCIATA1 (FAS1), the largest subunit of the CAF-1 complex, and also to exhibit preferential binding to the H3.1 histone variant (Wang *et al.*, 2022). Similar to mammals, where histones can be pre-modified when coupled to CAF-1 before their assembly into chromatin (Loyola *et al.*, 2009), H3.1 can be mono-methylated by ATXR5 and ATXR6 during deposition (Jacob *et al.*, 2014). ATXR proteins only mono-methylate the H3.1 histone variant as the threonine at position 31 in H3.3 causes steric hindrance in the catalytic SET domain preventing mono-methylation of lysine 27 in H3.3 (Jacob *et al.*, 2014). Together with the recruitment of ATXR5 and 6 by PCNA to the replication fork (Jacob *et al.*, 2009), this ensures the exclusive deposition of the repressive mark H3K27me1 on H3.1 by these enzymes coupling assembly of new histones and maintenance of H3K27me1. In a similar manner, maintenance of H3K27me3 can take place concomitantly with DNA replication, as some PRC1 and PRC2 components are directly

recruited to the replication fork via PCNA or through interaction with FAS1 (Jiang and Berger, 2017). This way, newly deposited histones can be modified to maintain H3K27me3 levels. POL2A also interacts genetically and physically with PRC2 components and is required to maintain H3K27me3 at flowering genes (del Olmo *et al.*, 2016). This reinforces the functional link between DNA replication and H3K27me3 maintenance. Therefore, similar to H3K27me1, modification of newly incorporated histones, faithful recycling of parental histones carrying H3K27me3 together with sequence dependent *de novo* targeting of H3K27me3 through recruitment of PRC2 complexes (Zhou *et al.*, 2018) allow maintenance of this silencing mark through the cell cycle. Indeed, the role of cis-regulatory DNA elements such as Polycomb Repressive elements (PREs) in maintenance of H3K27me3 should not be underestimated as, in *Drosophila*, removal of a PRE leads to rapid loss of H3K27me3 from the locus in cycling cells (Laprell *et al.*, 2017). Furthermore, other specific cis-binding factors could help to trap or retain PRC2 complexes as recently reported for the VEL proteins that contribute to *FLC* silencing during vernalization (Fiedler *et al.*, 2022).

## 5.2 Maintenance of H2A-H2B

The described mechanisms ensure propagation of histone modifications situated on the H3-H4 tetramer. Are there similar mechanisms operating to maintain H2A-H2B variants at the replication fork? H2A-H2B dimers are more rapidly exchanged throughout the cell cycle independently of ongoing DNA replication (Jamai *et al.*, 2007), which led to the conclusion that they are less good candidates to carry heritable epigenetic information. POL2A for example does not seem to play a role in H2A.W maintenance (Bourguet *et al.*, 2020). Nevertheless, parental H2A-H2B dimers can be maintained during DNA replication or transcription through the action of the FACT complex that binds not only H3-H4 but also H2A-H2B dimers (Liu *et al.*, 2020). Whether and how *de novo* assembly of H2A variants is coordinated with replication in *Arabidopsis* also remains to be determined. H2A.W deposition at heterochromatin involves the chromatin-remodeling factor DDM1 (Osakabe *et al.*, 2021). DDM1 maintains nucleosome density and remodels chromatin to facilitate access of the methylation machinery to DNA (Zemach *et al.*, 2013) and can directly interact with H2A.W (Osakabe *et al.*, 2021). DDM1 could operate outside S-phase to restore H2A.W occupancy that was diluted during replication, or may function directly at the replication fork like its mammalian homologue Lsh (Han *et al.*, 2020). In contrast, not much is known whether linker histones could be retained during DNA replication or when H1 binding is restored during chromatin maturation following replication. H1 is extremely mobile within chromatin (Rutowicz *et al.*, 2015) suggesting that it can dissociate and re-associate rapidly with newly replicated chromatin. Till now, the lack of efficient synchronization methods for *Arabidopsis*

cell cultures, has prohibited a detailed analysis of the chromatin maintenance events taking place specifically in plant S-phase cells.

### *5.3 Maintenance of 3D chromatin organization during replication*

Do the need to gain access to DNA during replication and the possible transient dilution of epigenetic information during replication impact higher order chromatin organization? How does the 3D organization of chromatin replicate? In general, no global changes in higher-order organization such as chromocenter structures were observed during S phase (Dvořáčková *et al.*, 2018). 3D organization is therefore globally maintained. Furthermore, as in animals, DNA replication in *Arabidopsis* is temporally and spatially organized (Dvořáčková *et al.*, 2018; Concia *et al.*, 2018). Detailed analysis of replication timing showed that replication events mainly occur first at distal arms of the chromosomes (early) before proximal arms (mid), while centromeric and pericentromeric regions replicate late during S-phase (Concia *et al.*, 2018). The replication timing broadly correlates with euchromatin (early and mid) and heterochromatin (late), however a certain portion of the genome was replicating through all phases, suggesting heterogeneity between cells (Concia *et al.*, 2018). One appealing hypothesis is that regrouping replication of chromatin domains with similar chromatin states could help to concentrate specific histone modifiers and chaperones at these locations, facilitating accurate replication of chromatin features at these domains.

Taken together, specific mechanisms exist to faithfully restore patterns of certain histone modifications, in particular H3K27me<sub>3</sub>, rapidly following passage of the replication fork. These mechanisms may have evolved due to the critical role of this histone modification in repressing developmentally regulated genes and therefore ensuring proper development and differentiation (Mozgova and Hennig, 2015). Another reason may be the ancestral role of H3K27me<sub>3</sub> in ensuring transposon silencing and therefore genome maintenance (Délérís *et al.*, 2021). Much remains to be understood how other histone modifications are faithfully replicated; in particular those marks or histone variants that only occupy one or few nucleosomes for example H3K4me<sub>3</sub> methylation and the H2A.Z histone variant. For these marks, restoration cannot rely on recruitment of histone modifiers by neighboring nucleosomes with similar modifications. Maintenance of epigenetic information could also be reinforced by interaction between the DNA methylation and histone modification maintenance machinery (Probst *et al.*, 2009) such as through the interaction of HISTONE DEACETYLASE 6 (HDA6) that interacts with MET1 to reinforce silencing of transposable elements (Liu *et al.*, 2012). Future experiments will show to what extent the 3D genome structure including long-range interactions of H3K27me<sub>3</sub> enriched domains (Huang *et al.*,

2021) are maintained during replication or how they are restored to maintain organization and functionality of the genome.

### 6. Epigenome reprogramming during development

While during the mitotic cell cycle genome organization is preserved during interphase, developmental phase transitions evidence remarkable changes in the epigenome and higher-order chromatin organization associated with transcriptome reprogramming. One of the first observations of global alterations in nuclear organization were made during the generation of protoplasts that show a dramatic decrease in both size and number of chromocenters compared to the mesophyll tissue they are derived from (Tessadori, Chupeau, *et al.*, 2007). Similarly, exposure to low light stress causes dispersion of pericentromeric repeats, a phenotype that is reversible upon return to standard light conditions (van Zanten *et al.*, 2010; Tessadori *et al.*, 2009). Instead, decondensation of heterochromatin in differentiated cells is long-lasting after a prolonged heat stress (Pecinka *et al.*, 2010). Genome wide assessment by Hi-C, although using another experimental setup, confirmed that heat stress causes global changes in 3D genome organization as it increases contacts between pericentromeric regions and distal chromosome arms while inter-chromosomal interactions decrease (L., Sun *et al.*, 2020).

Not only stress situations impact 3D genome reorganization, but dynamic change in higher-order organization and the epigenome have also been reported during development. During the floral transition from vegetative to reproductive growth, which is associated with considerable changes in gene expression, leaf nuclei undergo changes in 3D organization with a transient decondensation of pericentromeric and euchromatic regions (Tessadori, Schulkes, *et al.*, 2007). Important changes in higher order chromatin organization also occur during the switch from skoto- to photomorphogenesis when de-etiolated seedlings are exposed to light for the first time (Bourbousse *et al.*, 2015). While some information is available on the role of light signaling components such as DE-ETIOLATED 1 (DET1) (Bourbousse *et al.*, 2015), CRYPTOCHROME 2 and PHYTOCHROME B in controlling heterochromatin compaction (van Zanten *et al.*, 2010; Snoek *et al.*, 2017), we still know little about the changes at the level of the nucleosome fiber occurring during those higher-order chromatin changes.

Another remarkable developmental transition, seed germination, is likewise associated with important changes in nuclear organization. In the dry seed, the embryo rests in a quiescent state. Embryonic nuclei are small (**Figure 2**) with highly condensed chromatin (van Zanten *et al.*, 2011; van Zanten *et al.*, 2012) that has a peculiar composition, highly enriched in the replacement histone variant H3.3 (Layat *et al.*, 2021; T., Zhao *et al.*, 2022) and a specific H2B variant, H2B.8 (Jiang, Borg, Lorković, *et al.*, 2020; Buttress *et al.*, 2022). H2B.8 is

characterized by a long N-terminal tail that induces formation of phase separated chromatin condensates contributing to chromatin compaction (Buttress *et al.*, 2022). New H3.1 deposition occurs only during imbibition when replication restarts and genes encoding H3.1 are becoming expressed (Masubelele *et al.*, 2005). During seed germination, nuclear size increases, heterochromatin content decreases, and chromocenters disorganize (van Zanten *et al.*, 2011). Here again the cytological chromatin changes correlate with massive alterations in gene expression occurring during seed germination (Narsai *et al.*, 2017; Kawakatsu *et al.*, 2017). Intriguingly, despite the important role of H3K27me3 in cell fate control, gene expression changes precede variations in H3K27me3 methylation (Pan *et al.*, 2022). More details therefore remain to be discovered how gene expression, chromatin structure and higher-order chromatin organization are functionally coupled during this developmental transition. Cytological studies suggested that chromocenter structures are consolidated during seedling establishment and that this process involves local chromatin changes (Mathieu *et al.*, 2003; Benoit *et al.*, 2019). Despite not fully clustered into chromocenters shortly after germination, repetitive sequences are already enriched in the repressive mark H3K9me2 and the linker histone H1. Instead, chromocenter consolidation during the next few days correlates with a progressive increase in H3.1 and H2A.W occupancy (Benoit *et al.*, 2019). Both, rise in H3.1 and H2A.W occupancy and chromocenter formation depend on an operative replication-coupled histone deposition pathway (Benoit *et al.*, 2019) pointing towards a functional link between setting of local chromatin features during replication and heterochromatin organization.

Another striking example of a developmental time frame, during which the epigenome is reprogrammed, is the differentiation of the pollen (PMCs) and spore mother cells (SMCs). PMC and SMC differentiation correlates with a decrease in heterochromatin content and chromocenter number. These changes in higher-order chromatin organization are linked to dynamic alterations in epigenetic marks with an enrichment in H3K4me3, eviction of H2A.Z and the linker histone variants H1.1 and H1.2 as well as the depletion of the repressive mark H3K27me3 (She *et al.*, 2013; She and Baroux, 2015). After meiosis, the SMC will give rise to an ovule that contains an egg and a central cell. The nucleus of the egg cell that after fertilization will give rise to the zygote, contains numerous small H3K9me2 foci rearranged into large chromocenters, but is devoid of H3.1 and the centromeric H3 variant CenH3 (Ingouff *et al.*, 2010; Pillot *et al.*, 2010). Correlating with high levels of LIKE HETEROCHROMATIN PROTEIN1 (LHP1), the H3K27me3 reader (Nakahigashi *et al.*, 2005), no active RNA polymerase II is detected in the egg cell (Pillot *et al.*, 2010). In contrast, the central cell that preserves transcriptional activity, still expresses genes encoding CenH3, H3.1 and the H3.1 deposition machinery, however is strongly depleted in H3K9me2 and lacks chromocenters (Ingouff *et al.*, 2010; Pillot *et al.*, 2010). The PMC, following meiotic

division, will give rise to the mature male gametophyte that contains one vegetative cell and two sperm cells (**Figure 2**). The vegetative nucleus harbors decondensed chromatin devoid of heterochromatin with low level of DNA methylation, H3K9me2, H3K4me2 and H3K9ac (Schoft *et al.*, 2009; Houben *et al.*, 2011; Slotkin *et al.*, 2009). Loss of H3K9me2 and DNA methylation correlates with increased accessibility of pericentromeric chromatin regions correlating with increased transcription of these regions and production of small interfering RNAs from the vegetative nucleus (Slotkin *et al.*, 2009; Borg, Papareddy, *et al.*, 2021). The two sperm cells on the contrary have highly condensed chromatin, strongly reduced H3K27me3 levels, are completely depleted of the histone variant H3.1, but enriched in H3.10 and H2B.8 variants (Ingouff *et al.*, 2010; Borg *et al.*, 2020; Buttress *et al.*, 2022). H2B.8 via its capacity to form phase separated condensates compacts silent euchromatic regions in sperm cells and contributes to the small size of these nuclei. Loss of H2B.8 does not affect the sperm transcriptome, but reduces transmission of the mutant male gamete, revealing a role for sperm nuclear organization in fertility (Buttress *et al.*, 2022). The other sperm enriched histone variant, H3.10, varies from H3.1 and H3.3 in the primary amino acid sequence around lysine 27 making it a bad substrate for H3K27 methylases. H3.10 incorporation contributes to H3K27me3 reprogramming and in turn to transcription of genes essential for sperm differentiation (Borg *et al.*, 2020). Upon fertilization, the histone variant repertoire is again dynamically changed with the eviction of several histone variants (Ingouff *et al.*, 2010) pointing towards further epigenome reprogramming events during early embryonic development.

Taken together, developmental transitions in plants involve important dynamics at the level of nucleosome composition and 3D genome organization. The changes may concern heterochromatin domains such as in the vegetative nucleus or euchromatic regions through incorporation of specific variants like H3.10 that contribute to reprogramming of the Polycomb mark H3K27me3. Scaling down RNA-seq, ChIP-seq and Hi-C analyses to a few specific cells using key technologies such as INTACT (Deal and Henikoff, 2011), nuclear sorting (Buttress *et al.*, 2022) or single cell approaches (Dorrity *et al.*, 2021) coupled to microscopy analysis (She *et al.*, 2013) will allow dissecting the mechanisms operating during chromatin maintenance or reprogramming.

## 7. Perspectives

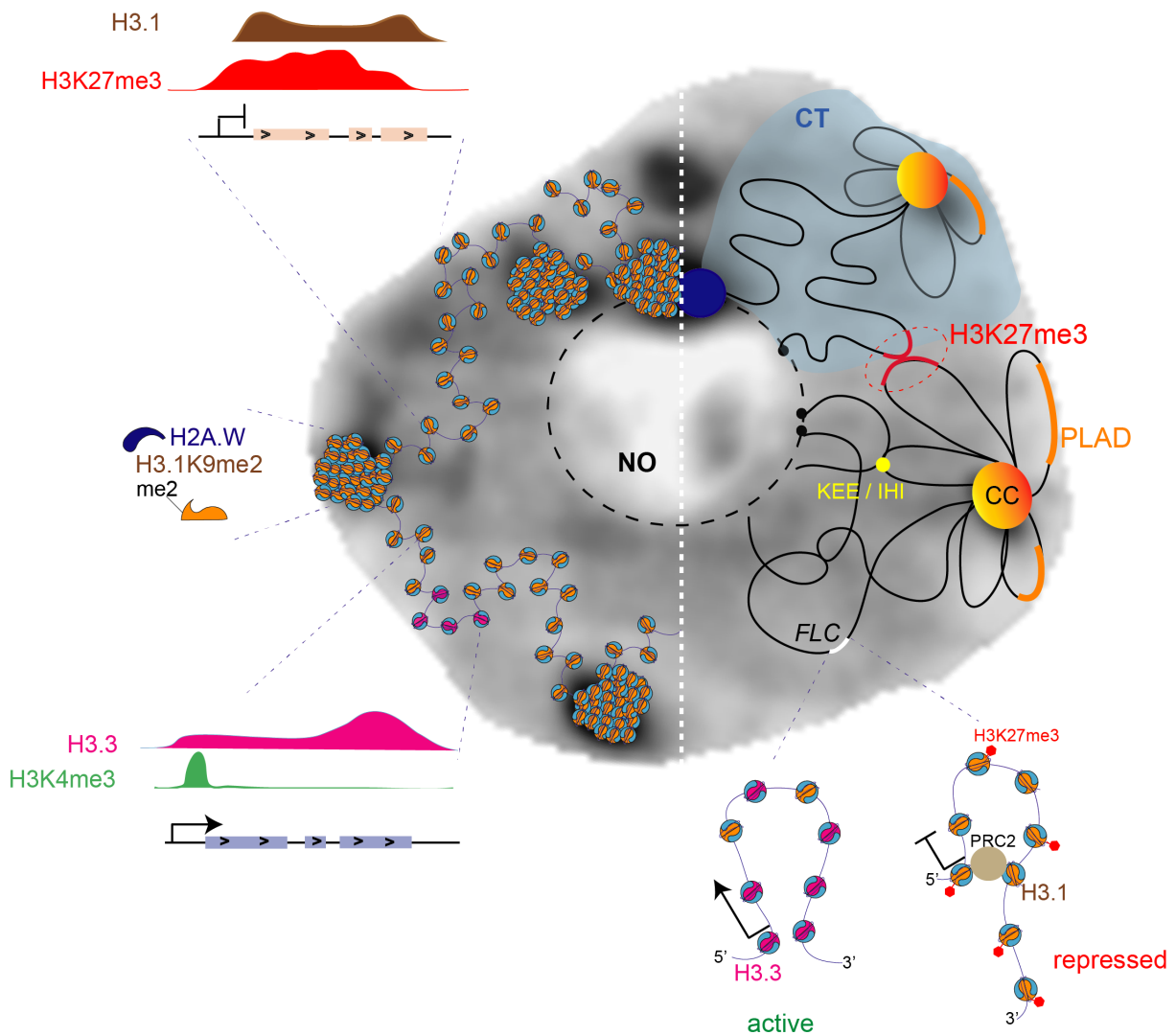
Chromatin organization is essential for gene expression control. Therefore, sophisticated mechanisms ensure maintenance of chromatin states during replication or allow plasticity to remodel chromatin during developmental phase transitions. While we have here concentrated on maintenance and reprogramming of histone variants and modifications and their link with 3D nuclear organization, these dynamics are often associated with both



maintenance of DNA methylation during DNA replication or substantial methylation reprogramming. Furthermore, changes in chromatin marks and higher-order structures can be linked to the expression of non-coding RNAs as shown for the *FLC* locus that expresses several non-coding RNAs (Swiezewski *et al.*, 2009; Kim and Sung, 2017) or *APOLO* (*AUXIN-REGULATED PROMOTER LOOP*) that regulates auxin-responsive genes (Ariel *et al.*, 2020). Such RNAs can even make the link between DNA methylation and histone modifications through the Polycomb machinery (Fonouni-Farde *et al.*, 2022).

Further investigation will also show whether and how 3D chromosome organization is actively maintained during DNA replication and how it is quickly reformed after mitosis. Finally, more questions remain to be answered such as to what extent chromatin marks determine 3D chromosome organization or how far specific localization of loci for example in PLADs close to the nuclear periphery favors setting of repressive marks. More exciting data will certainly emerge with the development of new and innovative technologies that will allow manipulating the epigenome in a dynamic and cell-specific manner.

Figures and legends:



**Figure 1:** Schematic representation of chromatin organization in an Arabidopsis nucleus. Left: Heterochromatin in interphase nuclei is highly condensed and organizes into DAPI-bright chromocenters, with repressive chromatin marks (H3K9me2 enrichment) and a different nucleosome composition (H2A.W and H3.1) than the surrounding euchromatin that is characterized by a more relaxed chromatin fiber. A representative repressed gene with high H3.1 occupancy and H3K27me3 enrichment and active genes with an H3K4me3 methylation peak at the transcription start site and H3.3 occupancy in the 3' end are shown. Right: 3D chromatin organization within the nuclear space. Arabidopsis chromosomes within their chromosome territory (CT, light blue, (Pecinka *et al.*, 2004)) adopt a rosette-like organization (Fransz *et al.*, 2002), with intrachromosomal interactions taking place between the centromere proximal regions, while centromere distal regions interact preferentially with each other. Telomeres (black dots) and nucleolus organizer regions (NORs, blue) cluster at

the nucleolar periphery. Certain chromatin regions termed plant lamina-associated domains (PLADs, orange) situate at the nuclear periphery. Interchromosomal interactions have been observed between H3K27me3 enriched genes (red) and between specific heterochromatic sequences situated on chromosome arms termed KEEs (KNOT Engaged Elements) or interactive heterochromatic islands (IHIs, yellow) (Grob *et al.*, 2014; Feng *et al.*, 2014). Certain genes form gene loops exemplified here for the *FLC* locus that engages either in a loop between the promoter and the 3' end that is associated with transcriptional activity (Crevillén *et al.*, 2013; Zhao *et al.*, 2021) or another loop including the first intron that requires the PRC2 complex and is associated with transcriptional repression (Kim and Sung, 2017). Drawings are superposed on an Arabidopsis nucleus stained with a DNA intercalating-agent (DAPI). Euchromatin appears as light grey, chromocentres as dark grey foci and the nucleolus (NO) as a white region at the center of the nucleus.

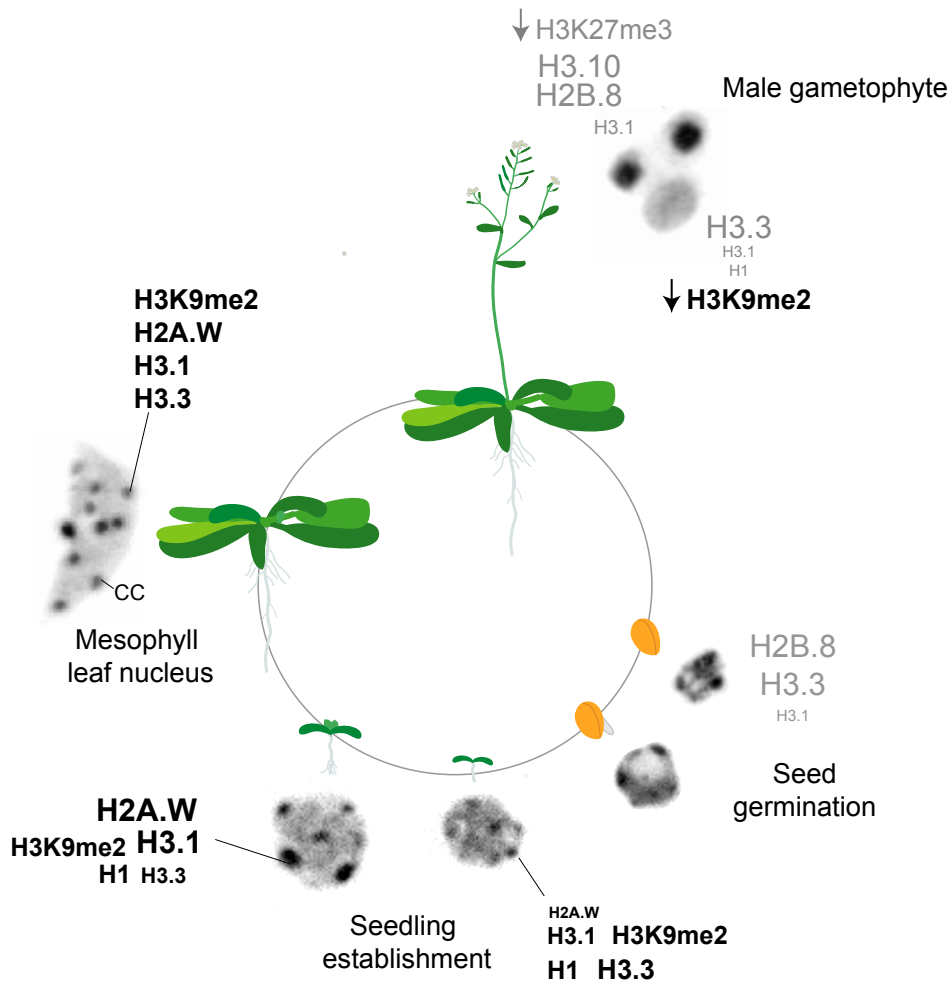


Figure 2: Illustration of the chromatin dynamics during certain developmental phase transitions.

The mesophyll leaf nucleus is characterized by light grey euchromatin and black (DAPI-bright) chromocenters (CC). In the male gametophyte, sperm nuclei (SN) are small and highly condensed, while the vegetative nucleus (VN) is bigger, lacks H3K9me2 and shows no visible chromocenter structures (Slotkin *et al.*, 2009; Borg, Papareddy, *et al.*, 2021). Sperm chromatin is enriched in a specific H3 (H3.10) and H2B (H2B.8) variant (Borg *et al.*, 2020; Buttress *et al.*, 2022). H2B.8 is also enriched in the small and condensed nuclei in the dry seed embryo (Jiang, Borg, Lorkovi, *et al.*, 2020). During germination, nuclear size increases and heterochromatin becomes more relaxed before being reformed during seedling establishment. During chromocenter formation, repetitive sequences gain H3.1 and H2A.W (Benoit *et al.*, 2019). Euchromatic histone variants and modifications are indicated in grey, those in heterochromatin in black. Maximum intensity projections of paraformaldehyde fixed nuclei isolated from the different developmental stages and stained with DAPI (reverse colored) are shown. The size of the letters represents the relative enrichment in histone variants or modifications.

### *Acknowledgements*

We thank C. Tatout and S. Amiard for critical reading of the manuscript and acknowledge funding from ANR grants 4D-HEAT ANR-21-CE20-0036, EpiLinks ANR-22-CE20-0001 and SeedChrom ANR-22-CE20-0028, from European Union's Horizon Europe research and innovation program under the Marie Skłodowska-Curie grant agreement No 101073476 (EpiSeedLink) as well as the CAP20-25 I-site projects Nucleomouv and SEED.

### *References:*

- Antosz, W., Pfab, A., Ehrnsberger, H.F., et al.** (2017) The Composition of the Arabidopsis RNA Polymerase II Transcript Elongation Complex Reveals the Interplay between Elongation and mRNA Processing Factors. *Plant Cell*, **29**, 854–870.
- Ariel, F., Lucero, L., Christ, A., et al.** (2020) R-Loop Mediated trans Action of the APOLO Long Noncoding RNA. *Mol. Cell*, **77**, 1055-1065.e4.
- Baroux, C., Pecinka, A., Fuchs, J., Kreth, G., Schubert, I. and Grossniklaus, U.** (2017) Non-random chromosome arrangement in triploid endosperm nuclei. *Chromosoma*, **126**, 115–124.
- Baroux, C., Pecinka, A., Fuchs, J., Schubert, I. and Grossniklaus, U.** (2007) The triploid endosperm genome of Arabidopsis adopts a peculiar, parental-dosage-dependent chromatin organization. *Plant Cell*, **19**, 1782–1794.
- Benoit, M., Simon, L., Desset, S., Duc, C., Cotterell, S., Poulet, A., Goff, S. Le, Tatout, C. and Probst, A. V** (2019) Replication-coupled histone H3.1 deposition determines nucleosome composition and heterochromatin dynamics during Arabidopsis seedling development. *New Phytol.*, **221**, 385–398.
- Bi, X., Cheng, Y.J., Hu, B., Ma, X., Wu, R., Wang, J.W. and Liu, C.** (2017) Nonrandom domain organization of the Arabidopsis genome at the nuclear periphery. *Genome Res.*, **27**, 1162–1173.
- Borg, M., Jacob, Y., Susaki, D., et al.** (2020) Targeted reprogramming of H3K27me3 resets epigenetic memory in plant paternal chromatin. *Nat. Cell Biol.*, **22**, 621–629.
- Borg, M., Jiang, D. and Berger, F.** (2021) Histone variants take center stage in shaping the epigenome. *Curr. Opin. Plant Biol.*, **61**, 101991.
- Borg, M., Papareddy, R.K., Dombey, R., Axelsson, E., Nodine, M.D., Twell, D. and Berger, F.** (2021) Epigenetic reprogramming rewires transcription during the alternation of generations in Arabidopsis. *Elife*, **10**.
- Bourbousse, C., Mestiri, I., Zabulon, G., et al.** (2015) Light signaling controls nuclear architecture reorganization during seedling establishment. *Proc. Natl. Acad. Sci.*, **112**, E2836-44.

- Bourguet, P., López-González, L., Gómez-Zambrano, Á., et al.** (2020) DNA polymerase epsilon is required for heterochromatin maintenance in Arabidopsis. *Genome Biol.*, **21**, 283.
- Bourguet, P., Picard, C.L., Yelagandula, R., et al.** (2021) The histone variant H2A.W and linker histone H1 co-regulate heterochromatin accessibility and DNA methylation. *Nat. Commun.*, **12**, 2683.
- Buttress, T., He, S., Wang, L., Zhou, S., Saalbach, G., Vickers, M., Li, G., Li, P. and Feng, X.** (2022) Histone H2B.8 compacts flowering plant sperm through chromatin phase separation. *Nature*, **611**, 614–622.
- Choi, K., Kim, J., Hwang, H.-J., Kim, S., Park, C., Kim, S.Y. and Lee, I.** (2011) The FRIGIDA complex activates transcription of FLC, a strong flowering repressor in Arabidopsis, by recruiting chromatin modification factors. *Plant Cell*, **23**, 289–303.
- Concia, L., Brooks, A.M., Wheeler, E., et al.** (2018) Genome-Wide Analysis of the Arabidopsis Replication Timing Program. *Plant Physiol.*, **176**, 2166–2185.
- Concia, L., Veluchamy, A., Ramirez-Prado, J.S., et al.** (2020) Wheat chromatin architecture is organized in genome territories and transcription factories. *Genome Biol.*, **21**, 104.
- Corcoran, E.T., LeBlanc, C., Huang, Y.-C., Arias Tsang, M., Sarkiss, A., Hu, Y., Pedmale, U. V and Jacob, Y.** (2022) Systematic histone H4 replacement in *Arabidopsis thaliana* reveals a role for H4R17 in regulating flowering time. *Plant Cell*, **34**, 3611–3631.
- Crevillén, P., Sonmez, C., Wu, Z. and Dean, C.** (2013) A gene loop containing the floral repressor FLC is disrupted in the early phase of vernalization. *EMBO J.*, **32**, 140–148.
- Deal, R.B. and Henikoff, S.** (2011) The INTACT method for cell type-specific gene expression and chromatin profiling in *Arabidopsis thaliana*. *Nat. Protoc.*, **6**, 56–68.
- Déléris, A., Berger, F. and Duharcourt, S.** (2021) Role of Polycomb in the control of transposable elements. *Trends Genet.*, **37**, 882–889.
- Deng, L., Gao, B., Zhao, L., et al.** (2022) Diurnal RNAPII-tethered chromatin interactions are associated with rhythmic gene expression in rice. *Genome Biol.*, **23**, 7.
- Domb, K., Wang, N., Hummel, G. and Liu, C.** (2022) Spatial Features and Functional Implications of Plant 3D Genome Organization. *Annu. Rev. Plant Biol.*, **73**, 173–200.
- Dong, P., Tu, X., Chu, P.-Y., Lü, P., Zhu, N., Grierson, D., Du, B., Li, P. and Zhong, S.** (2017) 3D Chromatin Architecture of Large Plant Genomes Determined by Local A/B Compartments. *Mol. Plant*, **10**, 1497–1509.
- Dorrity, M.W., Alexandre, C.M., Hamm, M.O., Vigil, A.-L., Fields, S., Queitsch, C. and Cuperus, J.T.** (2021) The regulatory landscape of *Arabidopsis thaliana* roots at single-cell resolution. *Nat. Commun.*, **12**, 3334.

- Duc, C., Benoit, M., Détourné, G., et al.** (2017) Arabidopsis ATRX Modulates H3.3 Occupancy and Fine-Tunes Gene Expression. *Plant Cell*, **29**, 1773–1793.
- Duc, C., Benoit, M., Goff, S. Le, Simon, L., Poulet, A., Cotterell, S., Tatout, C. and Probst, A. V** (2015) The histone chaperone complex HIR maintains nucleosome occupancy and counterbalances impaired histone deposition in CAF-1 complex mutants. *Plant J.*, **81**, 707–722.
- Duroux, M., Houben, A., Růžička, K., Friml, J. and Grasser, K.D.** (2004) The chromatin remodelling complex FACT associates with actively transcribed regions of the Arabidopsis genome. *Plant J.*, **40**, 660–671.
- Dvořáčková, M., Raposo, B., Matula, P., Fuchs, J., Schubert, V., Peška, V., Desvoyes, B., Gutierrez, C. and Fajkus, J.** (2018) Replication of ribosomal DNA in Arabidopsis occurs both inside and outside the nucleolus during S phase progression. *J. Cell Sci.*, **131**, jcs202416.
- Fal, K., Tomkova, D., Masson, M. Le, et al.** (2022) Lysine 27 of histone H3.3 is a fine modulator of developmental gene expression and stands as an epigenetic checkpoint for lignin biosynthesis in Arabidopsis. *bioRxiv*, 2022.06.08.495374.
- Fang, Y. and Spector, D.L.** (2005) Centromere positioning and dynamics in living Arabidopsis plants. *Mol. Biol. Cell*, **16**, 5710–5718.
- Feng, S., Cokus, S.J., Schubert, V., Zhai, J., Pellegrini, M. and Jacobsen, S.E.** (2014) Genome-wide Hi-C Analyses in Wild-Type and Mutants Reveal High-Resolution Chromatin Interactions in Arabidopsis. *Mol. Cell*, **55**, 694–707.
- Fiedler, M., Franco-Echevarría, E., Schulten, A., Nielsen, M., Rutherford, T.J., Yeates, A., Ahsan, B., Dean, C. and Bienz, M.** (2022) Head-to-tail polymerization by VEL proteins underpins cold-induced Polycomb silencing in flowering control. *Cell Rep.*, **41**, 111607.
- Fonouni-Farde, C., Christ, A., Blein, T., et al.** (2022) The Arabidopsis APOLO and human UPAT sequence-unrelated long noncoding RNAs can modulate DNA and histone methylation machineries in plants. *Genome Biol.*, **23**, 181.
- Fransz, P., Jong, J.H. de, Lysak, M., Castiglione, M.R. and Schubert, I.** (2002) Interphase chromosomes in Arabidopsis are organized as well defined chromocenters from which euchromatin loops emanate. *Proc. Natl. Acad. Sci. U. S. A.*, **99**, 14584–14589.
- Fransz, P., Linc, G., Lee, C.-R., et al.** (2016) Molecular, genetic and evolutionary analysis of a paracentric inversion in *Arabidopsis thaliana*. *Plant J.*, **88**, 159–178.
- Fransz, P.F., Armstrong, S., Jong, J.H. de, Parnell, L.D., Drunen, C. van, Dean, C., Zabel, P., Bisseling, T. and Jones, G.H.** (2000) Integrated cytogenetic map of chromosome arm 4S of *A. thaliana*: structural organization of heterochromatic knob and centromere region. *Cell*, **100**, 367–376.

- Friesner, J.D., Liu, B., Culligan, K. and Britt, A.B.** (2005) Ionizing Radiation – dependent  $\gamma$ -H2AX Focus Formation Requires Ataxia Telangiectasia Mutated and Ataxia Telangiectasia Mutated and Rad3-related. *Mol. Biol. Cell*, **16**, 2566–2576.
- Gendrel, A. V, Lippman, Z., Yordan, C., Colot, V. and Martienssen, R.A.** (2002) Dependence of heterochromatic histone H3 methylation patterns on the Arabidopsis gene DDM1. *Science*, **297**, 1871–1873.
- Gómez-Zambrano, Á., Crevillén, P., Franco-Zorrilla, J.M., et al.** (2018) Arabidopsis SWC4 Binds DNA and Recruits the SWR1 Complex to Modulate Histone H2A.Z Deposition at Key Regulatory Genes. *Mol. Plant*, **11**, 815–832.
- Goodrich, J., Puangsomlee, P., Martin, M., Long, D., Meyerowitz, E.M. and Coupland, G.** (1997) A Polycomb-group gene regulates homeotic gene expression in Arabidopsis. *Nature*, **386**, 44–51.
- Grob, S. and Grossniklaus, U.** (2019) Invasive DNA elements modify the nuclear architecture of their insertion site by KNOT-linked silencing in *Arabidopsis thaliana*. *Genome Biol.*, **20**, 120.
- Grob, S., Schmid, M.W. and Grossniklaus, U.** (2014) Hi-C Analysis in Arabidopsis Identifies the KNOT, a Structure with Similarities to the flamenco Locus of Drosophila. *Mol. Cell*, **55**, 678–693.
- Han, M., Li, Jialun, Cao, Y., et al.** (2020) A role for LSH in facilitating DNA methylation by DNMT1 through enhancing UHRF1 chromatin association. *Nucleic Acids Res.*, **48**, 12116–12134.
- Houben, A., Kumke, K., Nagaki, K. and Hause, G.** (2011) CENH3 distribution and differential chromatin modifications during pollen development in rye (*Secale cereale* L.). *Chromosom. Res.*, **19**, 471–480.
- Hsieh, T., Ibarra, C., Silva, P., Zemach, A., Eshed-Williams, L., Fischer, R. and Zilberman, D.** (2009) Genome-Wide Demethylation of Arabidopsis Endosperm. *Science*, **324**, 1451–1454.
- Hu, B., Wang, N., Bi, X., Karaaslan, E.S., Weber, A.-L., Zhu, W., Berendzen, K.W. and Liu, C.** (2019) Plant lamin-like proteins mediate chromatin tethering at the nuclear periphery. *Genome Biol.*, **20**, 87.
- Huang, Y., Sicar, S., Ramirez-Prado, J.S., et al.** (2021) Polycomb-dependent differential chromatin compartmentalization determines gene coregulation in Arabidopsis. *Genome Res.*, **31**, 1230–1244.
- Ingouff, M., Rademacher, S., Holec, S., et al.** (2010) Zygotic resetting of the HISTONE 3 variant repertoire participates in epigenetic reprogramming in Arabidopsis. *Curr. Biol.*, **20**, 2137–2143.
- Jackson, J.P., Lindroth, A.M., Cao, X. and Jacobsen, S.E.** (2002) Control of CpNpG DNA



- methylation by the KRYPTONITE histone H3 methyltransferase. *Nature*, **416**, 556–560.
- Jacob, Y., Bergamin, E., Donoghue, M.T.A., et al.** (2014) Selective Methylation of Histone H3 Variant H3.1 Regulates Heterochromatin Replication. *Science*, **364**, 1249–1253.
- Jacob, Y., Feng, S., LeBlanc, C.A., et al.** (2009) ATXR5 and ATXR6 are H3K27 monomethyltransferases required for chromatin structure and gene silencing. *Nat. Struct. Mol. Biol.*, **16**, 763–768.
- Jamai, A., Imoberdorf, R.M. and Strubin, M.** (2007) Continuous histone H2B and transcription-dependent histone H3 exchange in yeast cells outside of replication. *Mol. Cell*, **25**, 345–355.
- Jamge, B., Lorković, Z.J., Axelsson, E., Yelagandula, R., Akimcheva, S. and Berger, F.** (2022) Transcriptional activity is shaped by the chromatin landscapes in Arabidopsis. *bioRxiv*, 2022.06.02.494419.
- Jeronimo, C., Poitras, C. and Robert, F.** (2019) Histone Recycling by FACT and Spt6 during Transcription Prevents the Scrambling of Histone Modifications. *Cell Rep.*, **28**, 1206-1218.e8.
- Jiang, D. and Berger, F.** (2017) DNA replication–coupled histone modification maintains Polycomb gene silencing in plants. *Science*, **357**, 1146–1149.
- Jiang, D., Borg, M., Lorkovi, Z.J. and Id, S.A.M.** (2020) The evolution and functional divergence of the histone H2B family in plants. *PLoS Genet.*, 1–22.
- Jiang, D., Borg, M., Lorković, Z.J., Montgomery, S.A., Osakabe, A., Yelagandula, R., Axelsson, E. and Berger, F.** (2020) The evolution and functional divergence of the histone H2B family in plants. *PLoS Genet.*, **16**, e1008964.
- Kawakatsu, T., Nery, J.R., Castanon, R. and Ecker, J.R.** (2017) Dynamic DNA methylation reconfiguration during seed development and germination. *Genome Biol.*, **18**, 171.
- Kaya, H., Shibahara, K.I., Taoka, K.I., Iwabuchi, M., Stillman, B. and Araki, T.** (2001) FASCIATA genes for chromatin assembly factor-1 in arabidopsis maintain the cellular organization of apical meristems. *Cell*, **104**, 131–142.
- Kim, D.-H. and Sung, S.** (2017) Vernalization-Triggered Intragenic Chromatin Loop Formation by Long Noncoding RNAs. *Dev. Cell*, **40**, 302-312.e4.
- Kireeva, M.L., Walter, W., Tchernajenko, V., Bondarenko, V., Kashlev, M. and Studitsky, V.M.** (2002) Nucleosome Remodeling Induced by RNA Polymerase II. *Mol. Cell*, **9**, 541–552.
- Kulaeva, O.I., Hsieh, F. and Studitsky, V.M.** (2010) RNA polymerase complexes cooperate to relieve the nucleosomal barrier and evict histones. *Proc. Natl. Acad. Sci.*, **107**, 11325–11330.
- Kumar, S. V and Wigge, P.A.** (2010) H2A.Z-containing nucleosomes mediate the thermosensory response in Arabidopsis. *Cell*, **140**, 136–147.

- Laprell, F., Finkl, K. and Müller, J.** (2017) Propagation of Polycomb-repressed chromatin requires sequence-specific recruitment to DNA. *Science*, **356**, 85–88.
- Layat, E., Bourcy, M., Cotterell, S., Zdzieszyńska, J., Dasset, S., Duc, C., Tatout, C., Bailly, C. and Probst, A. V** (2021) The Histone Chaperone HIRA Is a Positive Regulator of Seed Germination. *Int. J. Mol. Sci.*, **22**, 4031.
- Leng, X., Thomas, Q., Rasmussen, S.H. and Marquardt, S.** (2020) A G(enomic)P(ositioning)S(ystem) for Plant RNAPII Transcription. *Trends Plant Sci.*, **25**, 744–764.
- Liu, C., Cheng, Y.-J., Wang, J.-W. and Weigel, D.** (2017) Prominent topologically associated domains differentiate global chromatin packing in rice from Arabidopsis. *Nat. plants*, **3**, 742–748.
- Liu, C., Wang, C., Wang, G., Becker, C., Zaidem, M. and Weigel, D.** (2016) Genome-wide analysis of chromatin packing in *Arabidopsis thaliana* at single-gene resolution. *Genome Res.*, **26**, 1057–1068.
- Liu, X., Yu, C.-W., Duan, J., Luo, M., Wang, K., Tian, G., Cui, Y. and Wu, K.** (2012) HDA6 Directly Interacts with DNA Methyltransferase MET1 and Maintains Transposable Element Silencing in Arabidopsis. *Plant Physiol.*, **158**, 119–129.
- Liu, Y., Tian, T., Zhang, K., You, Q., Yan, H., Zhao, N., Yi, X., Xu, W. and Su, Z.** (2018) PCSD: a plant chromatin state database. *Nucleic Acids Res.*, **46**, D1157–D1167.
- Liu, Y., Zhou, K., Zhang, N., et al.** (2020) FACT caught in the act of manipulating the nucleosome. *Nature*, **577**, 426–431.
- Lolas, I.B., Himanen, K., Grønlund, J.T., Lynggaard, C., Houben, A., Melzer, M., Lijsebettens, M. Van and Grasser, K.D.** (2010) The transcript elongation factor FACT affects Arabidopsis vegetative and reproductive development and genetically interacts with HUB1/2. *Plant J.*, **61**, 686–97.
- Loyola, A., Tagami, H., Bonaldi, T., Roche, D., Quivy, J.P., Imhof, A., Nakatani, Y., Dent, S.Y.R. and Almouzni, G.** (2009) The HP1alpha - CAF1 - SetDB1-containing complex provides H3K9me1 for Suv39-mediated K9me3 in pericentric heterochromatin. *EMBO Rep.*, **10**, 769–775.
- Lu, L., Chen, X., Qian, S. and Zhong, X.** (2018) The plant-specific histone residue Phe41 is important for genome-wide H3.1 distribution. *Nat. Commun.*, **9**, 630.
- Luger, K., Mäder, A. and Richmond, R.** (1997) Crystal structure of the nucleosome core particle at 2.8 Å resolution. *Nature*, **389**, 251–260.
- Masubelele, N.H., Dewitte, W., Menges, M., Maughan, S., Collins, C., Huntley, R., Nieuwland, J., Scofield, S. and Murray, J.A.** (2005) D-type cyclins activate division in the root apex to promote seed germination in Arabidopsis. *Proc. Natl. Acad. Sci. U. S. A.*, **102**, 15694–15699.

- Mathieu, O., Jasencakova, Z., Vaillant, I., Gendrel, A. V, Colot, V., Schubert, I. and Tourmente, S.** (2003) Changes in 5S rDNA chromatin organization and transcription during heterochromatin establishment in Arabidopsis. *Plant Cell*, **15**, 2929–2939.
- Mathieu, O., Probst, A. V and Paszkowski, J.** (2005) Distinct regulation of histone H3 methylation at lysines 27 and 9 by CpG methylation in Arabidopsis. *EMBO J.*, **24**, 2783–91.
- Mathieu, O., Reinders, J., Caikovski, M., Smathajitt, C. and Paszkowski, J.** (2007) Transgenerational stability of the Arabidopsis epigenome is coordinated by CG methylation. *Cell*, **130**, 851–862.
- Moreno-Romero, J., Jiang, H., Santos-González, J. and Köhler, C.** (2016) Parental epigenetic asymmetry of PRC2-mediated histone modifications in the Arabidopsis endosperm. *EMBO J.*, **35**, 1298–1311.
- Mozgova, I. and Hennig, L.** (2015) The polycomb group protein regulatory network. *Annu. Rev. Plant Biol.*, **66**, 269–296.
- Nakahigashi, K., Jasencakova, Z., Schubert, I. and Goto, K.** (2005) The Arabidopsis heterochromatin protein1 homolog (TERMINAL FLOWER2) silences genes within the euchromatic region but not genes positioned in heterochromatin. *Plant Cell Physiol.*, **46**, 1747–1756.
- Narsai, R., Gouil, Q., Secco, D., Srivastava, A., Karpievitch, Y. V., Liew, L.C., Lister, R., Lewsey, M.G. and Whelan, J.** (2017) Extensive transcriptomic and epigenomic remodelling occurs during *Arabidopsis thaliana* germination. *Genome Biol.*, **18**, 172.
- Nie, X., Wang, H., Li, J., Holec, S. and Berger, F.** (2014) The HIRA complex that deposits the histone H3.3 is conserved in Arabidopsis and facilitates transcriptional dynamics. *Biol. Open*, **3**, 794–802.
- Okada, T., Endo, M., Singh, M. and Bhalla, P.** (2005) Analysis of the histone H3 gene family in Arabidopsis and identification of the male-gamete-specific variant AtMGH3. *Plant J.*, **44**, 557–568.
- Olmo, I. del, López, J.A., Vázquez, J., Raynaud, C., Piñeiro, M. and Jarillo, J.A.** (2016) Arabidopsis DNA polymerase  $\epsilon$  recruits components of Polycomb repressor complex to mediate epigenetic gene silencing. *Nucleic Acids Res.*, **44**, 5597–5614.
- Osakabe, A., Jamge, B., Axelsson, E., et al.** (2021) The chromatin remodeler DDM1 prevents transposon mobility through deposition of histone variant H2A.W. *Nat. Cell Biol.*, **23**, 391–400.
- Osakabe, A., Lorkovic, Z.J., Kobayashi, W., Tachiwana, H., Yelagandula, R., Kurumizaka, H. and Berger, F.** (2018) Histone H2A variants confer specific properties to nucleosomes and impact on chromatin accessibility. *Nucleic Acids Res.*, **46**, 7675–7685.

- Otero, S., Desvoyes, B., Peiró, R. and Gutierrez, C.** (2016) Histone H3 Dynamics Reveal Domains with Distinct Proliferation Potential in the Arabidopsis Root. *Plant Cell*, **28**, 1361–71.
- Pan, J., Zhang, H., Zhan, Z., Zhao, T. and Jiang, D.** (2022) A REF6-dependent H3K27me3-depleted state facilitates gene activation during germination in Arabidopsis. *J. Genet. Genomics*, **13**:S1673-8527(22)00219–3.
- Pecinka, A., Dinh, H.Q., Baubec, T., Rosa, M., Lettner, N. and Mittelsten Scheid, O.** (2010) Epigenetic regulation of repetitive elements is attenuated by prolonged heat stress in Arabidopsis. *Plant Cell*, **22**, 3118–3129.
- Pecinka, A., Schubert, V., Meister, A., Kreth, G., Klatte, M., Lysak, M.A., Fuchs, J. and Schubert, I.** (2004) Chromosome territory arrangement and homologous pairing in nuclei of *Arabidopsis thaliana* are predominantly random except for NOR-bearing chromosomes. *Chromosoma*, **113**, 258–269.
- Petryk, N., Dalby, M., Wenger, A., Stromme, C.B., Strandsby, A., Andersson, R. and Groth, A.** (2018) MCM2 promotes symmetric inheritance of modified histones during DNA replication. *Science*, **361**, 1389–1392.
- Pillot, M., Baroux, C., Vazquez, M.A., Autran, D., Leblanc, O., Vielle-Calzada, J.P., Grossniklaus, U. and Grimanelli, D.** (2010) Embryo and endosperm inherit distinct chromatin and transcriptional states from the female gametes in Arabidopsis. *Plant Cell*, **22**, 307–320.
- Pontvianne, F., Carpentier, M.-C., Durut, N., et al.** (2016) Identification of Nucleolus-Associated Chromatin Domains Reveals a Role for the Nucleolus in 3D Organization of the *A. thaliana* Genome. *Cell Rep.*, **16**, 1574–1587.
- Poulet, A., Duc, C., Voisin, M., et al.** (2017) The LINC complex contributes to heterochromatin organisation and transcriptional gene silencing in plants. *J. Cell Sci.*, **130**, 590–601.
- Probst, A. V** (2022) Deposition and eviction of histone variants define functional chromatin states in plants. *Curr. Opin. Plant Biol.*, **69**, 102266.
- Probst, A. V, Desvoyes, B. and Gutierrez, C.** (2020) Similar yet Critically Different: The distribution, dynamics and function of Histone Variants. *J. Exp. Bot.*, **71**, 5191–5204.
- Probst, A. V, Dunleavy, E. and Almouzni, G.** (2009) Epigenetic inheritance during the cell cycle. *Nat. Rev. Mol. cell Biol.*, **10**, 192–206.
- Probst, A. V, Fransz, P.F., Paszkowski, J. and Mittelsten Scheid, O.** (2003) Two means of transcriptional reactivation within heterochromatin. *Plant J.*, **33**, 743–749.
- Rosa, S., Lucia, F. De, Mylne, J.S., Zhu, D., Ohmido, N., Pendle, A., Kato, N., Shaw, P. and Dean, C.** (2013) Physical clustering of FLC alleles during polycomb-mediated epigenetic silencing in vernalization. *Genes Dev.*, **27**, 1845–1850.

- Roudier, F., Ahmed, I., Bérard, C., et al.** (2011) Integrative epigenomic mapping defines four main chromatin states in Arabidopsis. *EMBO J.*, **30**, 1928–38.
- Rudnizky, S., Khamis, H., Ginosar, Y., Goren, E., Melamed, P. and Kaplan, A.** (2021) Extended and dynamic linker histone-DNA Interactions control chromatosome compaction. *Mol. Cell*, **81**, 3410-3421.e4.
- Rutowicz, K., Lirski, M., Mermaz, B., et al.** (2019) Linker histones are fine-scale chromatin architects modulating developmental decisions in Arabidopsis. *Genome Biol.*, **20**, 157.
- Rutowicz, K., Puzio, M., Halibart-Puzio, J., et al.** (2015) A specialized histone H1 variant is required for adaptive responses to complex abiotic stress and related DNA methylation in Arabidopsis. *Plant Physiol.*, **169**, 2080–2101.
- Santos, A.P., Gaudin, V., Mozgová, I., et al.** (2020) Tidying-up the plant nuclear space: domains, functions, and dynamics. *J. Exp. Bot.*, **71**, 5160–5178.
- Schoft, V.K., Chumak, N., Mosiolek, M., Slusarz, L., Komnenovic, V., Brownfield, L., Twell, D., Kakutani, T. and Tamaru, H.** (2009) Induction of RNA-directed DNA methylation upon decondensation of constitutive heterochromatin. *EMBO Rep.*, **10**, 1015–1021.
- Schubert, I. and Shaw, P.** (2011) Organization and dynamics of plant interphase chromosomes. *Trends Plant Sci.*, **16**, 273–281.
- Schubert, V., Berr, A. and Meister, A.** (2012) Interphase chromatin organisation in Arabidopsis nuclei: constraints versus randomness. *Chromosoma*, **121**, 369–387.
- Sequeira-Mendes, J., Aragüez, I., Peiró, R., Mendez-Giraldez, R., Zhang, X., Jacobsen, S.E., Bastolla, U. and Gutierrez, C.** (2014) The Functional Topography of the Arabidopsis Genome Is Organized in a Reduced Number of Linear Motifs of Chromatin States. *Plant Cell*, **26**, 2351–2366.
- She, W. and Baroux, C.** (2015) Chromatin dynamics in pollen mother cells underpin a common scenario at the somatic-to-reproductive fate transition of both the male and female lineages in Arabidopsis. *Front. Plant Sci.*, **6**, 294.
- She, W., Grimanelli, D., Rutowicz, K., Whitehead, M.W.J., Puzio, M., Kotlinski, M., Jerzmanowski, A. and Baroux, C.** (2013) Chromatin reprogramming during the somatic-to-reproductive cell fate transition in plants. *Development*, **140**, 4008–19.
- Shi, L., Wang, J., Hong, F., Spector, D.L. and Fang, Y.** (2011) Four amino acids guide the assembly or disassembly of Arabidopsis histone H3.3-containing nucleosomes. *Proc. Natl. Acad. Sci. U. S. A.*, **108**, 10574–10578.
- Slotkin, R.K., Vaughn, M., Borges, F., Tanurdzic, M., Becker, J.D., Feijo, J.A. and Martienssen, R.A.** (2009) Epigenetic Reprogramming and Small RNA Silencing of Transposable Elements in Pollen. *Cell*, **136**, 461–472.
- Snoek, B.L., Pavlova, P., Tessadori, F., Peeters, A.J.M., Bourbousse, C., Barneche, F.,**

- Jong, H. de, Fransz, P.F. and Zanten, M. van** (2017) Genetic Dissection of Morphometric Traits Reveals That Phytochrome B Affects Nucleus Size and Heterochromatin Organization in *Arabidopsis thaliana*. *G3 (Bethesda)*, **7**, 2519–2531.
- Stefano, M. Di, Nützmann, H.-W., Marti-Renom, M.A. and Jost, D.** (2021) Polymer modelling unveils the roles of heterochromatin and nucleolar organizing regions in shaping 3D genome organization in *Arabidopsis thaliana*. *Nucleic Acids Res.*, **49**, 1840–1858.
- Stewart-Morgan, K.R., Petryk, N. and Groth, A.** (2020) Chromatin replication and epigenetic cell memory. *Nat. Cell Biol.*, **22**, 361–371.
- Stroud, H., Do, T., Du, J., Zhong, X., Feng, S., Johnson, L., Patel, D.J. and Jacobsen, S.E.** (2014) Non-CG methylation patterns shape the epigenetic landscape in *Arabidopsis*. *Nat. Struct. Mol. Biol.*, **21**, 64–72.
- Stroud, H., Otero, S., Desvoyes, B., Ramírez-Parra, E., Jacobsen, S.E. and Gutierrez, C.** (2012) Genome-wide analysis of histone H3.1 and H3.3 variants in *Arabidopsis thaliana*. *Proc. Natl. Acad. Sci.*, **109**, 5370–5.
- Sun, L., Jing, Y., Liu, X., Li, Q., Xue, Z., Cheng, Z., He, H. and Qian, W.** (2020) Heat stress-induced transposon activation correlates with 3D chromatin organization rearrangement in *Arabidopsis*. *Nat. Commun.*, **11**, 1886.
- Sun, Y., Dong, L., Zhang, Y., et al.** (2020) 3D genome architecture coordinates trans and cis regulation of differentially expressed ear and tassel genes in maize. *Genome Biol.*, **21**, 143.
- Sura, W., Kabza, M., Karlowski, W.M., Bieluszewski, T., Kus-Slowinska, M., Pawełszek, Ł., Sadowski, J. and Ziolkowski, P.A.** (2017) Dual Role of the Histone Variant H2A.Z in Transcriptional Regulation of Stress-Response Genes. *Plant Cell*, **29**, 791–807.
- Swiezewski, S., Liu, F., Magusin, A. and Dean, C.** (2009) Cold-induced silencing by long antisense transcripts of an *Arabidopsis* Polycomb target. *Nature*, **462**, 799–802.
- Tachiwana, H., Osakabe, A., Shiga, T., Miya, Y., Kimura, H., Kagawa, W. and Kurumizaka, H.** (2011) Structures of human nucleosomes containing major histone H3 variants. *Acta Crystallogr. Sect. D, Biol. Crystallogr.*, **67**, 578–583.
- Tagami, H., Ray-Gallet, D., Almouzni, G. and Nakatani, Y.** (2004) Histone H3.1 and H3.3 complexes mediate nucleosome assembly pathways dependent or independent of DNA synthesis. *Cell*, **116**, 51–61.
- Talbert, P.B. and Henikoff, S.** (2021) Histone variants at a glance. *J. Cell Sci.*, **134**, jcs244749.
- Tariq, M., Saze, H., Probst, A. V., Lichota, J., Habu, Y. and Paszkowski, J.** (2003) Erasure of CpG methylation in *Arabidopsis* alters patterns of histone H3 methylation in

- heterochromatin. *Proc. Natl. Acad. Sci. U. S. A.*, **100**, 8823–8827.
- Teano, G., Concia, L., Carron, L., et al.** (2022) Histone H1 protects telomeric repeats from H3K27me3 invasion in *Arabidopsis*. *bioRxiv*, 2020.11.28.402172.
- Tessadori, F., Chupeau, M.-C., Chupeau, Y., Knip, M., Germann, S., Driel, R. van, Fransz, P. and Gaudin, V.** (2007) Large-scale dissociation and sequential reassembly of pericentric heterochromatin in dedifferentiated *Arabidopsis* cells. *J. Cell Sci.*, **120**, 1200–1208.
- Tessadori, F., Schulkes, R.K., Driel, R. van and Fransz, P.** (2007) Light-regulated large-scale reorganization of chromatin during the floral transition in *Arabidopsis*. *Plant J.*, **50**, 848–857.
- Tessadori, F., Zanten, M. van, Pavlova, P., et al.** (2009) Phytochrome B and histone deacetylase 6 control light-induced chromatin compaction in *Arabidopsis thaliana*. *PLoS Genet.*, **5**, e1000638.
- Tessarz, P. and Kouzarides, T.** (2014) Histone core modifications regulating nucleosome structure and dynamics. *Nat. Rev. Mol. Cell Biol.*, **15**, 703–708.
- Torné, J., Ray-Gallet, D., Boyarchuk, E., Garnier, M., Baccon, P. Le, Coulon, A., Orsi, G.A. and Almouzni, G.** (2020) Two HIRA-dependent pathways mediate H3.3 de novo deposition and recycling during transcription. *Nat. Struct. Mol. Biol.*, **27**, 1057–1068.
- Verreault, A., Kaufman, P.D., Kobayashi, R. and Stillman, B.** (1996) Nucleosome assembly by a complex of CAF-1 and acetylated histones H3/H4. *Cell*, **87**, 95–104.
- Wang, C., Huang, J., Li, Y., et al.** (2022) DNA polymerase epsilon binds histone H3.1-H4 and recruits MORC1 to mediate meiotic heterochromatin condensation. *Proc. Natl. Acad. Sci. U. S. A.*, **119**, e2213540119.
- Wang, C., Liu, C., Roqueiro, D., Grimm, D., Schwab, R., Becker, C., Lanz, C. and Weigel, D.** (2015) Genome-wide analysis of local chromatin packing in *Arabidopsis thaliana*. *Genome Res.*, **25**, 246.
- Wollmann, H., Holec, S., Alden, K., Clarke, N., Jacques, P. and Berger, F.** (2012) Dynamic deposition of histone variant H3.3 accompanies developmental remodeling of the *Arabidopsis* transcriptome. *PLoS Genet.*, **8**, e1002658.
- Xu, L., Cheng, J. and Jiang, H.** (2022) Mutation of histone H3 serine 28 to alanine influences H3K27me3-mediated gene silencing in *Arabidopsis thaliana*. *Plant Physiol.*, kiac409.
- Xu, M., Long, C., Chen, X., Huang, C., Chen, S. and Zhu, B.** (2010) Partitioning of histone H3-H4 tetramers during DNA replication-dependent chromatin assembly. *Science*, **328**, 94–98.
- Yadav, V.K., Santos-González, J. and Köhler, C.** (2021) INT-Hi-C reveals distinct chromatin architecture in endosperm and leaf tissues of *Arabidopsis*. *Nucleic Acids*

*Res.*, **49**, 4371–4385.

- Yelagandula, R., Stroud, H., Holec, S., et al.** (2014) The Histone Variant H2A.W Defines Heterochromatin and Promotes Chromatin Condensation in Arabidopsis. *Cell*, **158**, 98–109.
- Yu, C., Gan, H., Serra-Cardona, A., et al.** (2018) A mechanism for preventing asymmetric histone segregation onto replicating DNA strands. *Science*, **361**, 1386–1389.
- Zanten, M. van, Carles, A., Li, Y. and Soppe, W.** (2012) Control and consequences of chromatin compaction during seed maturation in *Arabidopsis thaliana*. *Plant Signal. Behav.*, **7**, 338.
- Zanten, M. van, Koini, M.A., Geyer, R., Liu, Y., Brambilla, V., Bartels, D., Koornneef, M., Fransz, P. and Soppe, W.J.J.** (2011) Seed maturation in *Arabidopsis thaliana* is characterized by nuclear size reduction and increased chromatin condensation. *Proc. Natl. Acad. Sci. U. S. A.*, **108**, 20219–24.
- Zanten, M. van, Tessadori, F., McLoughlin, F., Smith, R., Millenaar, F.F., Driel, R. van, Voeselek, L.A., Peeters, A.J. and Fransz, P.** (2010) Photoreceptors CRYPTOCHROME2 and phytochrome B control chromatin compaction in Arabidopsis. *PLANT Physiol.*, **154**, 1686–1696.
- Zemach, A., Kim, M.Y., Hsieh, P., Coleman-Derr, D., Eshed-Williams, L., Thao, K., Harmer, S.L. and Zilberman, D.** (2013) The Arabidopsis Nucleosome Remodeler DDM1 Allows DNA Methyltransferases to Access H1-Containing Heterochromatin. *Cell*, **153**, 193–205.
- Zhao, B., Xi, Y., Kim, J. and Sung, S.** (2022) Chromatin architectural proteins regulate flowering time by precluding gene looping. *Sci. Adv.*, **7**, eabg3097.
- Zhao, F., Zhang, H., Zhao, T., Li, Z. and Jiang, D.** (2021) The histone variant H3.3 promotes the active chromatin state to repress flowering in Arabidopsis. *Plant Physiol.*, **186**, 2051–2063.
- Zhao, H., Yang, M., Bishop, J., et al.** (2022) Identification and functional validation of super-enhancers in *Arabidopsis thaliana*. *Proc. Natl. Acad. Sci.*, **119**, e2215328119.
- Zhao, T., Lu, J., Zhang, H., Xue, M., Pan, J., Ma, L., Berger, F. and Jiang, D.** (2022) Histone H3.3 deposition in seed is essential for the post-embryonic developmental competence in Arabidopsis. *Nat. Commun.*, **13**, 7728.
- Zhou, Y., Wang, Y., Krause, K., Yang, T., Dongus, J.A., Zhang, Y. and Turck, F.** (2018) Telobox motifs recruit CLF/SWN-PRC2 for H3K27me3 deposition via TRB factors in Arabidopsis. *Nat. Genet.*, **50**, 638–644.