



## eXtra Botany

### Special Issue Editorial

# Untangling chromatin interactions

**The plant nucleus contains myriad subdomains that define and are defined by the composition of their chromatin. On a whole nucleus scale, this includes regions of active euchromatin and inactive heterochromatin, although the boundaries between these states are blurred. Different loci constantly enter and exit nuclear structures including the nucleolus and transient regulatory nuclear bodies. Chromatin is defined by its complex combinations of epigenetic modifications and variation in its constituent histone proteins. Here we preview articles that describe many of the mechanisms that regulate this dynamic chromatin.**

The COST-Action CA16212 ‘Impact of Nuclear Domains on Gene Expression and Plant Traits’ (INDEPTH) (<https://www.brookes.ac.uk/indepth/>) includes >170 participants from 32 countries, each of whom are interested in the mechanisms through which nuclear domains influence plant phenotypes. INDEPTH participants span disciplines from physicists interested in image analysis through to plant breeders who aim to understand the contribution of chromatin organization to plant traits and identify novel genetic loci that may benefit breeding programmes. This special issue on ‘Impact of Chromatin Domains on Plant Phenotypes’ coincided with a *JXB*-supported meeting co-organized by the Society of Experimental Biology and INDEPTH that took place in San Lorenzo del Escorial, Spain in December 2019.

## Dynamic regulation across scales

Uncovering the impact of nuclear domains on chromatin dynamics is a research area that stretches across scales, which range from whole-genome organization down to the influence of individual proteins and genetic loci. (Fig. 1)

On the whole-genome scale, Dong *et al.* (2020) review the use of next-generation sequencing-based chromatin conformation capture technologies such as Hi-C to differentiate between large-scale organization of the mammalian and plant genomes. Hi-C provides a low-resolution overview of the relationships between genomic regions and can now be paired with other techniques, such as ChIP, to increase its resolution. Dong *et al.* (2020) also consider the enormous variation found

within 3D genomic organization in plants, which is perhaps unsurprising given the >1000-fold differences in genome size between, for example, *Arabidopsis thaliana* (135 Mb) and *Triticum aestivum* (17 Gb) (Pellicer and Leitch, 2020) and the variation in the percentage and distribution of repetitive and transposable elements in these genomes.

Both Dong *et al.* (2020) and Huang *et al.* (2020) discuss that despite the absence of CCCTC-binding factors (CTCFs), most tested plant genomes, notably except *Arabidopsis*, form topologically associated domains (TADs) as described in mammalian genomes. Genes within TADs interact more strongly with each other than with those outside TADs. In the wheat genome, other structures called intergenic condensed spacers (ICONS) have been described that are enriched in transposable elements in the interior, isolating these elements from the actively transcribed parts of the genome. ICONS appear to support the looped interaction of co-regulated genes, which is confirmed by these regions often exhibiting the same epigenetic marks. One accepted caveat with the data generated by Hi-C and related techniques is that they tell the story of a collage of interactions from thousands of cells across different tissues. Therefore, in the future, analysing the genomic interactions in single cells will provide greater insights into what is occurring in cells that are dynamically responding to changing growth requirements.

## Evaluating the function of nuclear subdomains

The plant nucleus contains a large number of functional subdomains, each of which is defined by both their constituent chromatin and the signalling events that determine their formation. Fernández-Jiménez and Pradillo (2020) focus on the nuclear envelope (NE), which is a dynamic double lipid bilayer that separates the nucleoplasm and cytoplasm. In evolutionary terms, although the proteins that reside in either the outer or inner nuclear membranes (ONM or INM) have little similarity between plants, mammals, and yeast, they have a similar function that is to connect the cytoskeleton, the nucleoskeleton and the nuclear membranes. Even though very few plant NE proteins have been identified, the physical linkages between the INM and ONM are critical for the bi-directional communication between the cytoplasm, nucleoplasm, and its chromatin. The originality of the review of Fernández-Jiménez and Pradillo (2020) is that they discuss the

role of NE components during the breakdown and subsequent reassembly of the NE during mitosis and meiosis. During mitosis, NE proteins can either associate with the cell plate or surround the chromatin, in the latter case presumably facilitating the correct reassembly of NE–chromatin interactions following cell division. During meiosis, the telomeres assemble at the NE in a bouquet structure, the precise formation of which differs between plant species. [Fernández-Jiménez and Pradillo \(2020\)](#) compare these processes in maize, Arabidopsis, wheat, and rice.

[Santos et al. \(2020\)](#) take a broader look at the relationship between nuclear domains and regulation of gene expression. Published reports about so-called ‘nuclear bodies’ are increasing and they are described as the location of enzymatic reactions and also the sequestration, storage, modification, recycling, or degradation of proteins. These can be permanent structures, such as the nucleolus, or can form under particular environmental stresses. Until recently, the mechanism of formation of nuclear bodies was unknown, but [Santos et al. \(2020\)](#) review literature from both mammalian experimental systems and more recently in Arabidopsis that suggests that they may be formed by liquid–liquid phase separation (LLPS) through the interaction of intrinsically disordered domain proteins. Introduction of the potential role of LLPS in mammalian cells was a highlight of the El Escorial meeting as introduced by Adam Klosin from the Max Planck Institute of Molecular Cell Biology and Genetics in Dresden ([Klosin et al., 2020](#)). Future research might reveal that the physical changes mediated by LLPS will define the topological relationships between other nuclear compartments.

## Epigenetic changes in the control of chromatin structure and function

Chromatin is comprised of both DNA and histone proteins. The epigenetic modification of either component can control both chromatin function and its recruitment to specific nuclear domains. [Jiang et al. \(2020\)](#) examine how post-translational modification of histones through cycles of acetylation and deacetylation is involved in signalling cascades that respond to 17 different external and internal stimuli. Whilst there is a growing understanding of the molecular mechanisms of acetylation and deacetylation, the authors report that there remains an enormous amount to understand about why particular signalling components interact and how these interactions occur in a dynamically changing system.

Another source of complexity that regulates chromatin dynamics comes from the different functions of histone variants. [Probst et al. \(2020\)](#) highlight that whilst some of these variants only differ by a few amino acids, their different incorporation within chromatin can have significant functional ramifications on nucleosome stability, higher order chromatin organization, or by indirectly influencing chromatin function through histone variant-specific binding partners.

[Pecinka et al. \(2020\)](#) look more widely at the role of epigenetic modifications in the organization of plant chromatin both during interphase and throughout cell divisions. Importantly, they review how discoveries made in both model and crop plant species have expanded the knowledge on how these modifications

can influence chromatin dynamics. [Varotto et al. \(2020\)](#) address how plant breeders might target epigenetic changes in the development of climate-smart crops. They outline that the discovery of epigenetic changes in several crops (maize, barley, wheat, rice, legumes, rapeseed, and tomato) allow for heritable adaptation to different environmental challenges, therefore opening up a new area of exploitation for plant breeders. Technological advances in genome sequencing and bioinformatic analysis mean that functional epigenetic changes can be identified in crop plants, despite their usually large and complex genomes.

As highlighted by [Probst et al. \(2020\)](#), at the protein level the regulation of chromatin dynamics can be controlled through the recruitment of different histone variants. One specific example is the recruitment of the Centromeric Histone3 (CenH3) variant to centromeres, where it is needed for correct kinetochore establishment and equivalent segregation of the homologous chromosomes during cell division. Of course CenH3 does not function alone, so a large number of interacting partners have been identified in yeast and mammalian systems. [Keceli et al. \(2020\)](#) review the function of plant CenH3 and provide a list of 78 putative CenH3-interacting partner orthologues or functional homologues from Arabidopsis, maize, or rice. This provides a useful resource for researchers interested in addressing the possible function of these proteins.

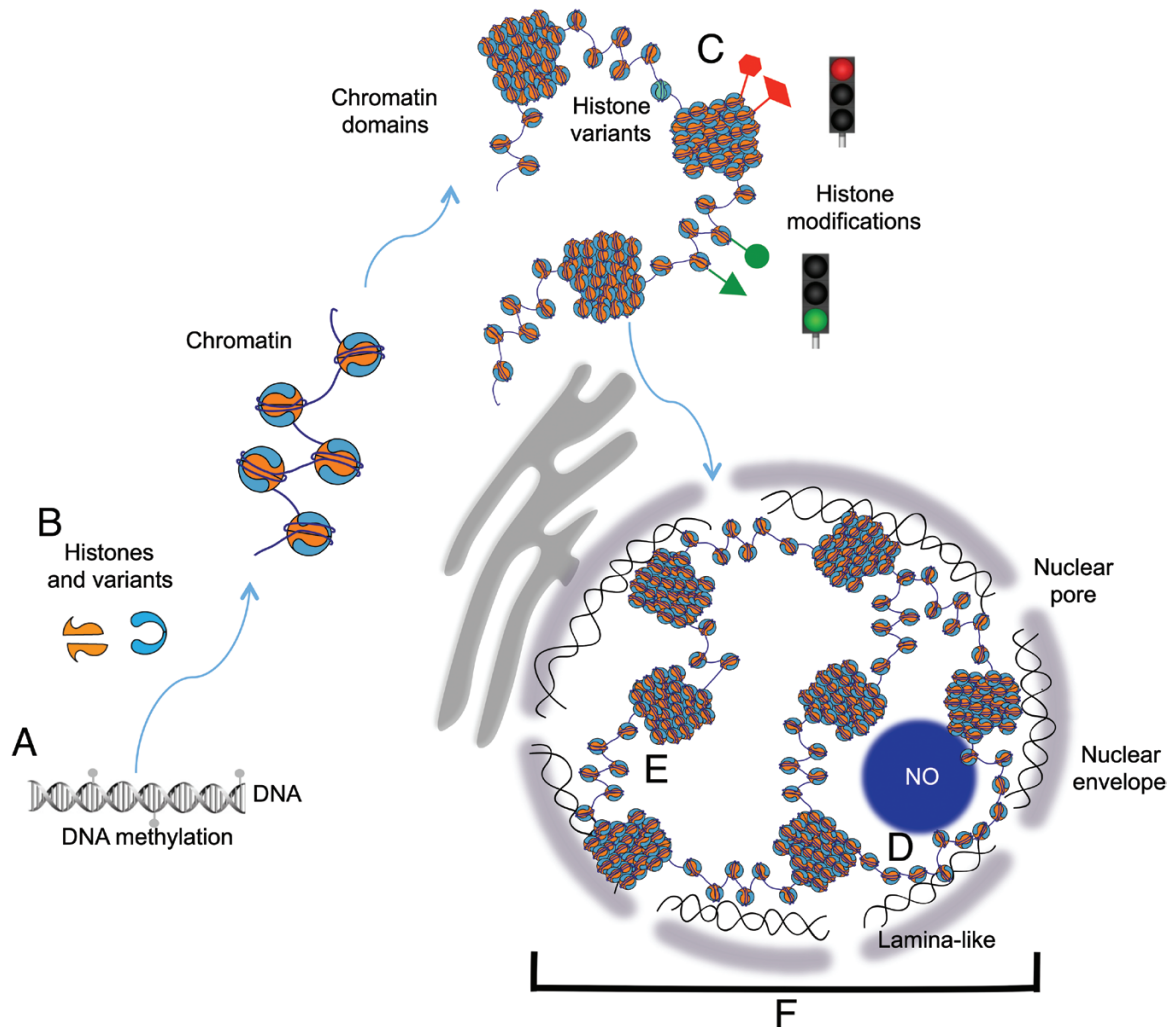
## Linking environment and chromatin dynamics

An ever-present thread that is woven through this special issue concerns the explicit influence that external environmental factors have on the organization and regulation of chromatin dynamics. [Perrella et al. \(2020\)](#) focus on nuclear changes that occur during photomorphogenesis and thermogenesis, while [Chen et al. \(2020\)](#) and [Bäurle and Trindade \(2020\)](#) broadly review how biotic and abiotic stresses, respectively, which induce important and wide transcriptional reprogramming, impact chromatin dynamics from the level of the nucleosome up to higher order organization.

[Raxwal et al. \(2020\)](#) present original research in which they investigate genome-wide changes in chromatin conformations that occur following growth in the presence of four abiotic stresses (heat, cold, salt, or drought). They captured open chromatin using either FAIRE-Seq or DNase-seq, and show that a quarter of the genome changes its conformation following one of these stresses. Although this highlights that the plasticity of plant growth enables them to have a robust genetic response to environmental stimuli, it also confirms that much of the actual business of ‘growing’ occurs irrespective of the external conditions!

## Perspectives

This special issue includes articles that describe how chromatin dynamics are influenced both by changes at the individual protein level and by alterations on a whole-genome level. However, these multiscale processes are inextricably linked, so a major future challenge is to obtain a better understanding of how these interactions are regulated. At the macromolecule level, the challenge is to understand how specific proteins are selected



**Fig. 1.** Chromatin dynamics are controlled across scales. (A) DNA methylation and changes of gene expression at individual loci. (B) Incorporation of histone variants into chromatin. (C) Post-translational modifications of histones. (D) Arrangement of nuclear subdomains. (E) Separation of euchromatin and heterochromatin. (F) Whole-genome organization. NO, nucleolus.

for their functions and what is their mechanism of action; for example, of the 12 nuclear-localized histone acetyltransferases in *Arabidopsis thaliana*, what ultimately determines the specificity of each of their activities (Jiang *et al.*, 2020) or how are different histone variants deposited at specific regions along a gene or a chromosome (Probst *et al.*, 2020)?

On the genome level, there is a growing understanding of higher order chromatin structures, how these interact, and the space they inhabit within the nucleus. The challenge here is to understand the functional significance of these domains and what are the physiological consequences of their alterations. How is chromatin organization remodelled in response to biotic and abiotic stresses? How do changes at the level of the nucleosome and the higher order chromatin arrangements influence the establishment and maintenance of epigenetic memory states?

How does the arrangement of these higher order chromatin structures intersect with the formation of nuclear bodies, which presumably coalesce chromatin from all regions of the genome? It is now relatively trivial to identify which genetic loci and proteins interact, but advances in imaging techniques will allow researchers to more precisely define where these interactions occur and how they will change in response to internal and external stimuli.

In addition, a better understanding of chromatin dynamics throughout cell division, applying new methods based on live-cell imaging, super-resolution microscopy, or even computational data analysis will help to shed light on mechanisms controlling chromosome behaviour.

It is no surprise that the nucleoplasm is a confined yet remarkably complex space for interacting molecules. Over the next decade, the research outputs of plant scientists and the fruits of their interactions with technology developers, physicists, bioinformaticians, and mathematicians will hopefully allow a better understanding of how chromatin is segregated and its epigenetic information functionally integrated in the nuclear space to bring about alterations in plant growth.

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## References

- Bäurle I, Trindade I.** 2020. Chromatin regulation of somatic abiotic stress memory. *Journal of Experimental Botany* **71**, 5269–5279.
- Chen J, Clinton M, Qi G, Wang D, Liu F, Qing Fu Z.** 2020. Reprogramming and remodeling: transcriptional and epigenetic regulation of salicylic acid-mediated plant defense. *Journal of Experimental Botany* **71**, 5256–5268.
- Dong P, Tu X, Liang Z, Kang BH, Zhong S.** 2020. Plant and animal chromatin 3D organization, similar structure but different function. *Journal of Experimental Botany* **71**, 5119–5128.
- Fernandez-Jimenez N, Pradillo M.** 2020. The role of the nuclear envelope in the regulation of chromatin dynamics during cell division. *Journal of Experimental Botany* **71**, 5148–5159.
- Huang Y, Rodriguez-Granados NY, Latrasse D, Raynaud C, Benhamed M, Ramirez-Prado JS.** 2020. The matrix revolutions: towards the decoding of the plant chromatin three-dimensional reality. *Journal of Experimental Botany* **71**, 5129–5147.
- Jiang J, Ding AB, Liu F, Zhong X.** 2020. Linking signaling pathways to histone acetylation dynamics in plants. *Journal of Experimental Botany* **71**, 5179–5190.
- Keçeli BN, Jin C, Van Damme D, Geelen D.** 2020. Conservation of CENH3 interaction partners in plants. *Journal of Experimental Botany* **71**, 5237–5246.
- Klosin A, Oltsch F, Harmon T, Honigmann A, Jülicher F, Hyman AA, Zechner C.** 2020. Phase separation provides a mechanism to reduce noise in cells. *Science* **367**, 464–468.
- Pecinka A, Chevalier C, Colas I, Kalantidis K, Varotto S, Krugman T, Michaelidis C, Vallés MP, Muñoz A, Pradillo M.** 2020. Chromatin dynamics during interphase and cell division: similarities and differences between model and crop plants. *Journal of Experimental Botany* **71**, 5205–5222.
- Pellicer J, Leitch IJ.** 2020. The Plant DNA C-values database (release 7.1): an updated online repository of plant genome size data for comparative studies. *New Phytologist* **226**, 301–305.
- Perrella G, Zioutopoulou A, Headland LR, Kaiserli E.** 2020. The impact of light and temperature on chromatin organization and plant adaptation. *Journal of Experimental Botany* **71**, 5247–5255.
- Probst AV, Desvoyes B, Gutierrez C.** 2020. Similar yet critically different: the distribution, dynamics and function of histone variants. *Journal of Experimental Botany* **71**, 5191–5204.
- Raxwal VK, Ghosh S, Singh S, Agarwal SK, Goel S, Jagannath A, Kumar A, Scaria V, Agarwal M.** 2020. Abiotic stress mediated modulation of chromatin landscape in *Arabidopsis thaliana*. *Journal of Experimental Botany* **71**, 5280–5293.
- Santos AP, Gaudin V, Mozgová I, Pontvianne F, Schubert D, Tek AL, Dvořáčková M, Liu C, Franz P, Rosa S, Farrona S.** 2020. Tidying-up the plant nuclear space: domains, functions, and dynamics. *Journal of Experimental Botany* **71**, 5160–5178.
- Varotto S, Tani E, Abraham E, Pontvianne F, Schubert D, Tek AL, Dvořáčková M, Liu C, Franz P, Rosa S, Farrona S.** 2020. Epigenetics: possible applications in climate-smart crop breeding. *Journal of Experimental Botany* **71**, 5223–5236.