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Chapter 1

Nuclear Architecture and Chromatin Dynamics in Interphase Nuclei of *Arabidopsis thaliana*

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Abstract

The interphase cell nucleus is an extraordinarily complex, ordered, and dynamic organelle. In the last decade, remarkable progress has been made in deciphering the functional organisation of the cell nucleus, which have already highlighted intricate relationships between the genome functions (transcription, DNA repair or replication) and various nuclear compartments. In this review, we describe the architecture of the *Arabidopsis thaliana* interphase cell nucleus and discuss the dynamic nature of its organisation.

Introduction

The linear dimension of eukaryotic genomes is nowadays readily analysed with the development of various high-throughput techniques allowing genome-wide approaches. Thus, their sequences have hardly no mystery, it is easier to question their evolution and increasing studies aim to paint their dynamic epigenomes. This progress has given rise to new challenges, namely to put the genome back in its tridimensional nuclear framework, to examine the interplay between the main functions of the genomes and the architecture of the interphase cell nucleus, and thus to decipher the relationships between nuclear structure and function. Thus, there is a renewed interest in nuclear compartments, some of which were described about two centuries ago, and in the 3D nuclear architecture. The extraordinary complexity of the interphase cell nucleus, its ordered structure, and the dynamics of this organelle at different scales are thus being actively investigated in both animal and plant cells. Much has been learnt about the composition and fine structure of the nucleus, and the mechanism of formation and dynamics of its various functional compartments. A better understanding of the structural and functional interplay between chromatin and the other nuclear compartments is emerging. These studies have been accompanied by the development of specific 3D approaches and tools, such as 3D imaging and modelling, and methods that capture chromosome conformation. Numerous reviews have been published on diverse aspects of nuclear organisation (de Wit and de Laat 2012; Dekker et al., 2013; Delgado et al., 2010; Dion and Gasser 2013; Rajapakse and Groudine 2011; Taddei and Gasser 2012; Towbin et al., 2013). However, much remains to be learnt about chromatin dynamics in plants. In this review, we summarize our current knowledge on nuclear compartments of the interphase nucleus in the model plant *Arabidopsis thaliana*, with a special emphasis on heterochromatin. Indeed, this compartment is highly plastic, exhibiting large-scale reorganisations and contributes to genome organisation, whereas euchromatin dynamics at the scale of the nucleus remain scarcely studied. We also discuss 3D modelling and quantitative techniques for analysing the architecture of the interphase nuclei, which are still in their infancy in *A. thaliana*.

Components of Plant Heterochromatin

In 1928, Emil Heitz classified chromatin into two types: heterochromatin and euchromatin. Whereas the former remains highly condensed throughout the cell cycle, the latter decondenses during interphase (Heitz 1928). This binary classification system, which was originally based on cytological observations in mosses, is still widely used to describe chromatin in all eukaryotes. However, it has evolved tremendously in the past fifteen years and central dogmas, such as the inertness and transcriptional inactivity of heterochromatin, have been challenged. The classification system has been expanded to include molecular and biochemical characteristics, such as 5-cytosine DNA methylation in symmetric or asymmetric contexts, post-translational histone modifications, nucleosome composition and arrangement, and transcriptional status, as determined by specialized polymerases. However, chromatin states at the scale of the nucleus are difficult to determine, due to limitations in resolution, and only the relatively large-scale heterochromatin compartments of interphase nuclei have been analysed using cytological approaches.

The main heterochromatic regions of *A. thaliana*, which are visible by microscopy after DNA counterstaining, occur at the **centromeres**, **pericentromeric regions**, **telomeres**, and **nucleolar organiser regions (NORs)** (Figures 1 and 2). These regions are referred to as constitutive heterochromatin, whereas chromatin that occasionally acquires heterochromatin characteristics and is dispersed throughout the genome is known as facultative chromatin. The cytological appearance of plant heterochromatin varies depending on genome size, ranging from ~63 to ~149 000 Mb (Heslop-Harrison and Schwarzacher 2011) and chromosomal organisation (ranging in dicotyledonous species from $2n=4$, such as in *Haplopappus gracilis*, to $2n\sim 640$ in *Sedum suaveolens*, <http://www.tropicos.org/Project/IPCN>). Plant heterochromatin is either located in discrete and well-defined subnuclear regions that exhibit intense labelling with DNA stain, also called chromocentres (CCs) in some species, e.g., *Arabidopsis thaliana* and *Oryza sativa* (rice), or is distributed throughout the genome in less defined substructures, for instance, in *Zea mays* (maize). The heterochromatin fraction (HF) of *A. thaliana* is estimated to account for 7.1% of the total chromosome length at pachytene (~330 μm), based on a cytological

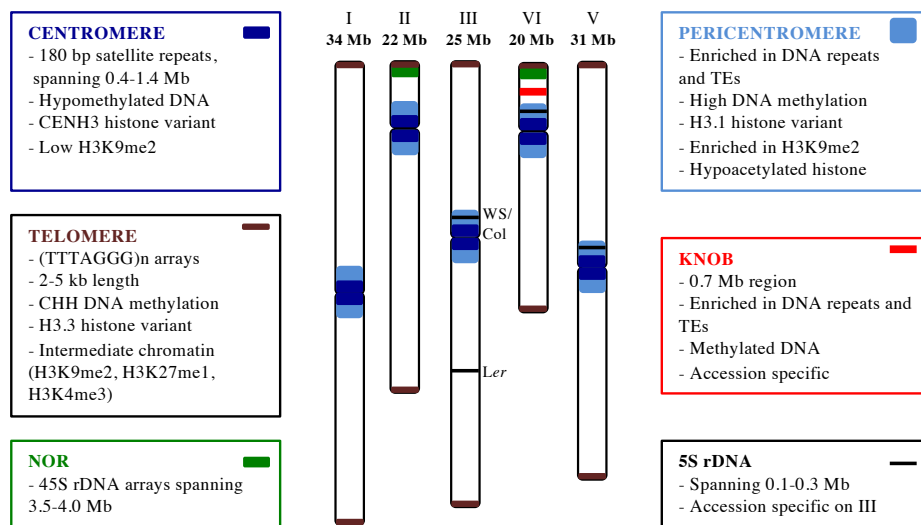


Figure 1: Heterochromatin compartments in *A. thaliana*.

Map of the five metacentric (1 and 5), submetacentric (3) and acrocentric (2 and 4) chromosomes. Polymorphic cytological markers (5S rDNA and knob) are indicated by the names of the accessions: Columbia-0 (Col), Landsberg erecta (Ler), Wassilewskija (WS). Transposable elements (TEs).

approach (Fransz et al., 1998); for 10-15% of the genome, based on the genome sequence (AGI 2000); and for 16% of the genome (22 Mb out of the ~135 of the genome), based on DNA accessibility analysed by DNase I chip (Shu et al., 2012). The relative HF (RHF), defined as the area and fluorescence intensity of CCs in relation to the area and fluorescence intensity of the entire nucleus in DAPI counterstaining, is estimated to be ~15% (Schonrock et al., 2006; Soppe et al., 2002), with variations depending on cell type and developmental and environmental cues. Heterochromatin is rich in repetitive DNA sequences and transposable elements, has few genes, and exhibits little or no transcriptional activity. Furthermore, heterochromatin exhibits distinct molecular and biochemical variations according to localisation and functions.

Centromeres are the primary constrictions along mitotic/meiotic chromosomes. The relative location of the centromere differs for each type of chromosome (Figure 1) (for a detailed review, see (Ma et al., 2007)). The centromere directs the assembly of the proteinaceous kinetochore, which interacts with spindle microtubules and facilitates the segregation of sister

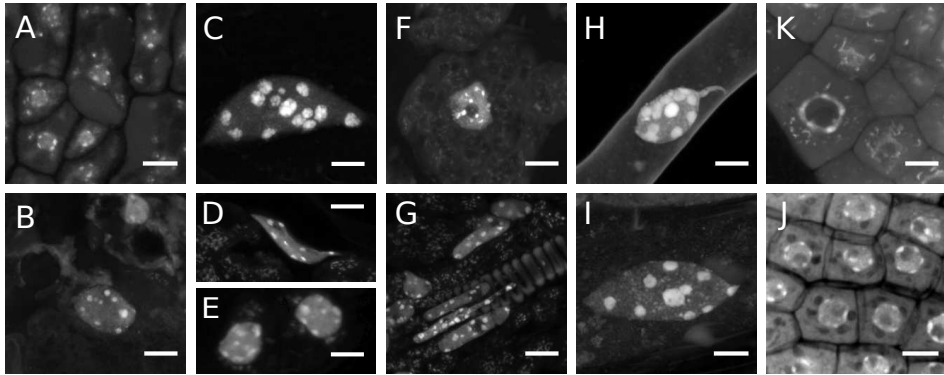


Figure 2: Nuclear diversity in *A. thaliana*.

Cell nuclei were observed in different cell types, either using cryosections (A-G) or whole-mount tissues (H-K), after DAPI staining. The pictures highlight the diversity in shape, size of the nuclei but also in the number and size of chromocenters. Pictures correspond either to a single confocal section of the nucleus (A, K, J) or to the maximum z-projection of an image stack (B-I), for optimal 2D visualisation. A. Nuclei of cotyledon cells of a mature embryo. B. Nucleus of a seed coat cell in a mature embryo. C-G. Three-week-old seedlings. C. Trichome nucleus. D. Leaf epidermal cell nucleus. E. Stomata nuclei. F. Nucleus of a leaf mesophyll cell. G. Nuclei of leaf vascular tissues. H-K. Young root. H. Nucleus of root hair cell. I. Nucleus of a root epidermis cell. J. Nuclei of root meristem. K. Nuclei of the root cap. Scale bars, 5 μ m.

chromatids during mitosis (Delgado et al., 2010). Centromeres of *A. thaliana* are composed of arrays of a 178-bp satellite repeat, ranging from 0.4 to 1.4 Mb, in different chromosomes (Copenhaver et al., 1999; Fransz et al., 1998; Heslop-Harrison et al., 2003; Ma et al., 2007; Zhang et al., 2008). Substantial variation in the copy number of the satellite repeat was reported in different ecotypes (Hall et al., 2006). The DNA sequences of centromeric satellite repeats differ markedly even among closely related species (Heslop-Harrison et al., 1999; Heslop-Harrison and Schwarzacher 2011; Lysák 2009). The centromeric chromatin region has low levels of DNA methylation and of the H3K9me2 epigenetic mark (Zhang et al., 2008). Independent of DNA sequence, the location of the centromere is epigenetically specified by the presence of a histone H3 variant, CENH3 (also named HTR12 in *A. thaliana*). Despite an essential role in mitosis and meiosis, CENH3 is rapidly evolving and participates in the formation of centromeric nucleosomes with unique properties, thereby allowing the centromere to fulfil essential roles in kinetochore formation and genome partitioning (Lermontova et al., 2011; Tachiwana et al., 2011; Tachiwana and Kurumizaka 2011). In *A. thaliana*, the

rapidly evolving N-terminal tail domain of CENH3 is specifically required for centromeric loading in meiotic nuclei, suggesting different CENH3 loading mechanisms in mitosis and meiosis (Lermontova et al., 2011; Lermontova et al., 2006; Ravi and Chan 2010; Ravi et al., 2011). These data have key functional implications for genome maintenance. A recent study reported that KINETOCHORE NULL2 (KNL2) participates in loading CENH3 at centromeres (Lermontova et al., 2013). KNL2 contains a SANT-associated (SANTA) domain, which is present in chromatin remodelling proteins, and is associated with centromeres during all phases of the mitotic cell cycle, except from metaphase to mid-anaphase. KNL2 inactivation affects both mitotic and meiotic division, without abolishing CENH3 assembly at centromeres (Lermontova et al., 2013). In the *A. thaliana* cell nucleus, centromeres can be visualised by fluorescent *in situ* hybridization (FISH) using a centromeric satellite repeat probe (Fransz et al., 1998), immunocytochemistry using an antibody against HTR12 (Talbert et al., 2002) or AtMSI12, which colocalises with HTR12 (Sato et al., 2005), or live cell imaging using fluorescently tagged HTR12 (Fang and Spector 2005). These approaches have facilitated studies of the dynamics of the centromeric sub-compartment (see below).

The flanking **pericentromeric heterochromatin** is enriched in repetitive DNA sequences and transposable elements (TEs) (Copenhaver et al., 1999). It is also characterized by a high level of 5-cytosine DNA methylation, with some strand-specific bias (Luo and Preuss 2003), and increased methylation of lysine 9 of histone H3 (H3K9me) and of the histone H3.1 variant (Stroud et al., 2012). Recently, pericentromeric heterochromatin was shown to be the least accessible chromatin to DNase I, and blocks of accessible chromatin are progressively more abundant with increasing distance from the centromere (Shu et al., 2012). Thus, there is not a sharp boundary between pericentromeric heterochromatin and euchromatin, but rather a gradual transition to chromatin with an increased protein-coding gene density and a decreased TE density (Shu et al., 2012). The assembly of H3K9me₂-marked heterochromatin requires the transcription of repetitive sequences by specific RNA polymerases and RNA-directed DNA methylation (RdDM) (for reviews, (Beisel and Paro 2011; Castel and Martienssen 2013; Verdell et al., 2009; Zhang and Zhu 2011)).

Telomeres are protective nucleoprotein structures at the extremities of linear chromosomes that stabilize chromosome termini and prevent chromosome fusion and degradation by exonucleases (Lamb et al., 2007; Watson and Riha 2010; Zellinger and Riha 2007). They consist of relatively short tandem repeat arrays (2- to 5-kb in *A. thaliana*) of a conserved short motif (TTTAGGG in most plant species) and associated telomere proteins. Interestingly, non-functional telomere-like repeats have been identified in interchromosomal regions (named interstitial telomeric repeats (ITRs)), some being in close proximity of centromeres (Uchida et al., 2002), whereas other short interstitial telomere motifs (named *telo* box) were preferentially observed in the 5' flanking regions of genes (Gaspin et al., 2010; Regad et al., 1994). The existence of these interspersed telomeric repeats strongly challenge the structural and functional analysis of terminal telomeric repeats but also open interesting perspectives on regulatory mechanisms. The length of telomeres, which is related to lifespan, is under genetic control and varies among species. Although telomeres were originally thought to consist of heterochromatin, a recent molecular analysis of epigenetic marks in *A. thaliana* telomeres revealed that telomeric chromatin has some unexpected and unique features that are characteristic of intermediate heterochromatin (Vrbsky et al., 2010) or even euchromatin (Vaquero-Sedas and Vega-Palas 2013). Indeed, *A. thaliana* telomeres are enriched in H3K9me2 and H3K27me1 heterochromatic marks, but still retain the euchromatic H3K4me3 mark (Vaquero-Sedas et al., 2012; Vrbsky et al., 2010). Furthermore, the *A. thaliana* telomeres are also relatively enriched in the H3.3 histone variant (which is usually associated with transcriptionally active regions) in comparison to centromeres, whereas the centromere is enriched in H3.1 in comparison to telomeres (Vaquero-Sedas and Vega-Palas 2013). Interestingly, subtelomeres and ITRs are of heterochromatic nature (Vaquero-Sedas et al., 2012). The telomeric enrichment in histone H3.3 variant is probably related to the unique juxtapositioning of telomeres and transcriptionally active genes in *A. thaliana*. Furthermore, as in other eukaryotes, *A. thaliana* telomeres are transcribed into non-coding Telomeric Repeat-containing RNAs (named TERRA) (Vrbsky et al., 2010). Telomeric repeats are methylated at asymmetric cytosine sites via an RNA-dependent DNA methylation pathway and small RNAs are derived from TERRAs produced from telomeres and from ITRs located near centromeres (Vrbsky et

al., 2010). Telomeric methylation was shown to be dependent on the activity of the activity of DNA methyltransferase MET1 and the remodelling factor DDM1 (Ogrocka et al., 2013).

Interstitial blocks of heterochromatin, called **knobs**, occur on the chromosome arms of maize and related species (Albert et al., 2010; Poggio et al., 2005). Knobs vary in size and composition, but are highly enriched in DNA repeats and TEs. Some knobs are visible throughout the cell cycle and are used as cytological markers (Ghaffari et al., 2013). Knobs are associated with low gene density and low transcriptional and recombinational activity. Some *A. thaliana* accessions, such as Wassilewskija (WS) and Columbia-0 (Col-0), bear a ~0.7-Mb knob on the short arm of chromosome 4 (hk4S), which does not colocalise with the CC of chromosome 4 (CC4) and is not visible during interphase (Figure 1) (Fransz et al., 1998; Fransz et al., 2000; Koornneef et al., 2003). hk4S is enriched in centromeric and pericentromeric repeats and has few expressed genes. hk4S was proposed to originate from an inversion event that moved DNA sequences from the pericentromeric outer domain to a distal euchromatin region of the 4S chromosome arm (Fransz et al., 2000). Maize knobs do not have such a pericentromeric origin.

The **nucleolar organiser region** (McClintock 1934) consists of tandem arrays of 45S rRNA-encoding DNA (rDNA), and is another major functional genomic region with heterochromatic characteristics. *A. thaliana* contains two NORs of similar size (each spanning 3.5-4.0 Mb of tandem repeat arrays), located at the subtelomeric regions of the acrocentric chromosomes 2 and 4 (Copenhaver and Pikaard 1996) (Figure 1). The 5S rDNA loci are also organised in tandem arrays (of ~1000 copies), which span 0.1-0.3 Mb and are located at pericentromeric regions of chromosomes 3, 4, and 5 in the Col-0 accession (Campbell et al., 1992; Murata et al., 1997). The presence, location and size of the 5S rDNA cluster on chromosome 3 are accession specific (Figure 1), with some possible intra-accession polymorphisms such as in the Cape Verde Islands (Cvi) accession (Fransz et al., 1998; Lopez et al., 2012; Sanchez-Moran et al., 2002). It was shown that in Col-0 accession, only the 5S rDNA clusters located on chromosomes 4 and 5 participate to the 5S RNA pool (Cloix et al., 2002).

Arabidopsis model of chromosome organisation centred on heterochromatin

In *A. thaliana*, CCs correspond to the coalescence of centromeric and pericentromeric regions of a chromosome and of the NOR, if the chromosome bears a NOR. These heterochromatic structures function as genome organiser centres. Indeed, euchromatic chromosomal regions form loops that span 0.2-2 Mb long and are anchored to CCs (Fransz et al., 2002). This organisation contributes to the overall structure of chromosome territories, as described in the chromocentre-loop model (Fransz et al., 2002), also named the rosette-like model (de Nooijer et al., 2009; van Driel and Fransz 2004). Furthermore, it was shown that highly repetitive elements and TEs located in euchromatic chromosomal arms colocalise with CCs and remain associated with CCs despite extensive demethylation of the genome (Soppe et al., 2002). This suggests that TEs both anchor the euchromatin loops and organise the pericentromeric regions (Soppe et al., 2002).

Variations in the number, size, and shape of centromeric foci and CCs as well as the cell-type specific organisation of heterochromatin have been reported in a number of studies. The nuclei of most cells (e.g., parenchyma cells, epidermal guard cells, and root cells) exhibit a “classical CC” pattern, with 4 to 10 (mean, ~8) conspicuous CCs (Figure 2) (Fang and Spector 2005; Fransz et al., 2002). The heterochromatin index (HX), defined as the percentage of nuclei showing the classical CC pattern was thus calculated in numerous studies to quantify heterochromatin distribution (Fransz et al., 2003). However, conspicuous CCs are absent in some nuclei presenting a rather uniform DAPI fluorescent nucleoplasm, such as the diploid interphase tapetal cell nuclei of premeiotic anthers (Talbert et al., 2002; Weiss and Maluszynska 2001). In the root tip, centromeric foci exist in a variety of shapes, from dots of 0.5 μm in diameter to discontinuous strings (1.0 to 2.0 μm in length) of smaller bead-like dots, suggesting that centromeres have a range of compaction ratios (Talbert et al., 2002). Given that the root tip is actively dividing, this range in centromeric foci shape might be, at least partially, cell cycle dependent. Interestingly, nuclei of the triploid endosperm tissue also have a peculiar heterochromatin

organisation, with small CCs and additional heterochromatic foci interspersed in euchromatin, which is likely linked to parental dosage (Baroux et al., 2007).

In plants, endoreduplication cycles occur in differentiated cells, leading to $\geq 4C$ cell nuclei. A positive correlation between CC association and ploidy levels was reported for a number of plant species (Ceccarelli et al., 1998). In *A. thaliana*, endoreduplicated sister centromere associations have also been reported using live cell imaging (Fang and Spector 2005). These associations are cell-type dependent, being for instance more frequent in root epidermal cells than in leaf epidermal cells (Fang and Spector 2005). Similar results were observed in fixed cell nuclei with an alignment of the majority of the sister centromeres up to 16C (Schubert et al., 2006) but, surprisingly, a much dispersed pattern was reported in 32C nuclei (Schubert et al., 2006).

Distribution of Heterochromatin in the Nuclear Space

In some species, chromosomes exhibit a polarized orientation, with all centromeres clustered at one pole of the interphase nucleus and all telomeres at the other. This peculiar interphase nuclear organisation, originally observed in salamander cell nuclei, was named the Rab1 configuration (Rab1 1885), and has been described in *Allium cepa* (onion), *Hordeum vulgare* (barley), *Triticum aestivum* (wheat), *Secale cereale* (rye), and *Avena sativa* (oats) (Dong and Jiang 1998; Roberts et al., 2009; Santos and Shaw 2004; Schwarzacher et al., 1989; Stack and Clark 1974). The Rab1 configuration is possibly a remnant of the preceding mitotic event. Indeed, during mitosis, the chromosomes condense, separate, and move to opposite poles, with the centromeres being pulled by kinetochore microtubules and leading the way, and the telomeres lagging behind.

The Rab1 configuration is not present in *A. thaliana* interphase nuclei. Rather, the centromeres are located at CCs, which occupy preferentially peripheral positions, and the telomeres are preferentially associated with the nucleolus (Armstrong et al., 2001; Fransz et al., 2002; Schubert et al., 2012).

Interestingly, it was observed that plants with large genomes, e.g. *A. cepa*, ~149 000 Mb, tend to exhibit the Rabl pattern, whereas those with smaller genomes, e.g., *A. thaliana*, ~135 Mb, tend to exhibit a non-Rabl pattern. These data suggest a correlation between the Rabl configuration and genome size; however, the non-Rabl configuration was also reported in *Sorghum bicolor* (sorghum) and maize (Dong and Jiang 1998), two species with quite large genomes. Thus, other determinants of the Rabl configuration may exist. Interestingly, the non-Rabl configuration appears to be tissue-specific in diploid rice; whereas the Rabl configuration is present in root xylem vessels, it is absent in other root tissues (Prieto et al., 2004). Endoreduplication may occur in the large nuclei of vascular tissues and induce these changes in chromatin distribution, in agreement with the previously described correlation, or the large nucleolus of xylem cells might underlie the redistribution of centromeres and telomeres. In *A. thaliana*, endopolyploidy (Schubert et al., 2012)

The preferential locations of telomeres at the nucleolus and the dispersed peripheral distribution of centromeres were also observed during meiotic interphase in *A. thaliana* (Armstrong et al., 2001). In meiotic prophase of most species, (e.g. *A. thaliana* and maize), the ends of chromosomes cluster together on the inner surface of the nuclear envelope, forming a structure called the “bouquet” (for reviews, see (Cowan et al., 2001; Franklin and Cande 1999; Tiang et al., 2012)). Thus, in maize, a Rabl configuration is observed prior to the last premeiotic cell division, is lost during the following interphase (Bass et al., 1997) and a bouquet is formed in meiotic prophase. These observations demonstrate that the distribution of chromosomes in the nuclear volume is tightly regulated.

Many studies have reported that *A. thaliana* centromeres tend to preferentially localise to the nuclear periphery and telomeres to the nucleolus using fixed nuclei. This centromere distribution was confirmed by measuring the distances between centromeres and the nuclear envelope in 3D images of various diploid living cells from transgenic *A. thaliana* plants expressing HTR12-GFP (Fang and Spector 2005). However, this pattern might be more complex. Live cell imaging also revealed that centromere clusters transiently formed at opposite poles at the end of mitosis in root meristematic cells (Fang

and Spector 2005) and in root tip cells (Lindhout et al., 2007). Lastly, in *A. thaliana* and *A. lyrata* interphase nuclei, CCs from chromosomes 2 and 4, which bear NORs, are more frequently located in close proximity to the nucleolus (Berr et al., 2006; Fransz et al., 2002; Schubert et al., 2012). Using spatial statistics, a recent study showed that the 3D intra-nuclear distribution of CCs in leaf cell nuclei was not completely random and further demonstrated that this repartition was more regular than a completely random one (Andrey et al., 2010). This finding was observed in both round and elongated nuclei of plant cells, which differ in differentiation stage and ploidy level. This repulsive trend is based on the global analysis of the CC population. Therefore, it is not incompatible with some frequent associations of specific CCs, such as CC2s and CC4s. Observation of CCs in close proximity (CC clusters) has also been reported in de Nooijer et al. (2009). However, in this study the frequency and the intensity of the phenomenon remains elusive as no quantification was provided. Therefore, the spatial distribution of CCs seems to obey to a global apparent repulsive tendency with some attractive trends for specific CCs. It remains to be determined whether this regular distribution of CCs can be fully explained by peripheral positioning, or if additional constraints have to be invoked to explain the apparent mutual repulsion between CCs. For example, the existence of euchromatin loops anchored at CCs, as proposed by the rosette model of chromosome organisation (Fransz et al., 2002), could prevent CCs from coming into close proximity. Specific proteins may also be involved, as recently demonstrated by the clustering of centromeres in CAP-D protein mutants (Schubert et al., 2013). Interestingly, the global centromere patterning is not transmitted through mitosis and asymmetric centromeric patterns were reported in daughter cells by tracking centromere movements in a few mitosis events in root meristematic diploid cells (Fang and Spector 2005).

Dynamics of the Heterochromatin Compartment during Development

The plant life cycle is punctuated by major developmental phase transitions and the reiterative production of plant phytomers, but also by diverse adaptations to environmental changes. These events require transcriptional

reprogramming events that modulate the expression of specific sets of genes. Recent studies showed that these transcriptional reprogramming events are accompanied by reorganisation of heterochromatin compartments, illustrating that the nucleus is highly plastic (Baroux et al., 2011; Schubert and Shaw 2011; van Zanten et al., 2012b). Whether this reorganisation participates in or is a consequence of gene regulation remains to be elucidated.

The female spore mother cell (or megaspore mother cell, MMC) differentiates from somatic cells within ovules and ultimately gives rise to female gametes. Large-scale chromatin reprogramming occurs during the specification of the MMC, and this probably contributes to the acquisition of the gametophyte fate (for a review see, (Baroux et al., 2011)). During this nuclear reorganisation, the nucleolus and nucleus expand, the RHF and CC undergo a reduction in number, and the heterochromatin decondenses (She et al., 2013). MMC chromatin reprogramming may be divided into two distinct phases: an early and rapid phase, during which the composition of the nucleosome changes, followed by a late phase, during which histone modifications undergo important changes (She et al., 2013).

In *A. thaliana*, embryonic development is completed about ten days after pollination (DAP). After a phase of seed maturation, which involves the accumulation of sufficient reserves and desiccation (from 10 DAP to 20 DAP), the seed undergoes a period of dormancy. Seed maturation is accompanied by two independent processes, nuclear shrinkage and chromatin compaction, which occur between 8 and 12 DAP and precede the major dehydration event of the maturing seed (Mansfield and Briarty 1992; van Zanten et al., 2012a; van Zanten et al., 2011). The RHF in embryonic cotyledon nuclei increases sharply during the maturation phase, while the 45S rDNA loci and the centromeric and pericentromeric repeats remain localised to the CCs during seed maturation. Interestingly, the nuclear volume is independent of both the moisture content and dormancy status of the seed, but is developmentally controlled. ABSCISIC ACID INSENSITIVE3 (ABI3), a key transcription factor in seed maturation, participates in nuclear shrinkage, which is thought to be a general adaptive response to desiccation tolerance (van Zanten et al., 2011). During the early events of seed germination (48-72 h after imbibition), the nuclear volume

increases again, and this increase requires the activity of LITTLE NUCLEI1 (LINC1) and LINC2, two lamin-like analogues (Ciska et al., 2013; van Zanten et al., 2012a; van Zanten et al., 2011). Furthermore, chromatin reorganisation accompanies this event. Whereas the 45S rDNA loci remain localised to CCs during germination, the centromeric and pericentromeric repeats are more dispersed at the onset of germination (van Zanten et al., 2012a). These CCs are smaller than those present in mature seeds. The classical conspicuous CC pattern reappears later during seedling growth.

During floral transition, which corresponds to the short developmental switch from the vegetative to the reproductive phase, a transient reduction in both RHF and HX was observed in three accessions (Col-0, *Ler*, *Cvi*), which was accompanied by the decompaction of pericentromeric regions and 5S rDNA chromatin, followed by their subsequent relocation to CCs three days after bolting (Tessadori et al., 2007b).

Dynamics of the Heterochromatin Compartment in response to Environmental Cues

Two recent studies reported a correlation between heterochromatin organisation and ambient light intensity; specifically, the RHF and HX increase with an increase in light intensity (Tessadori et al., 2009; van Zanten et al., 2010; van Zanten et al., 2012b). In the first study, Tessadori et al. (2009) analysed the HX in 21 *A. thaliana* accessions originating from different geographical habitats and identified a significant correlation between geographical latitude, which determines the photon flux density (light intensity) of the region, and the HX. Interestingly, the HX was found to plateau (at 100 $\mu\text{mol m}^{-2} \text{s}^{-1}$ for Col-0; at 200 $\mu\text{mol m}^{-2} \text{s}^{-1}$ for Landsberg *erecta* (*Ler*), a widely-used Central-European accession). The lowest HX was observed in the subtropical Cape Verde Islands-0 (*Cvi*-0) accession, which has smaller and fewer CCs than *Ler*. Furthermore, the *Cvi*-0 accession exhibited dispersed 5S rDNA and pericentromeric repeats, and the centromeric and 45S rDNA sequences remained in the reduced CCs. This chromatin arrangement is reminiscent of the one observed during floral transition. The second study showed that chromatin

compaction progressively decreases after a reduction in light intensity from 200 $\mu\text{mol m}^{-2} \text{s}^{-1}$ to 15 $\mu\text{mol m}^{-2} \text{s}^{-1}$. This heterochromatic event is reversible with return to normal light conditions, and the intensity of the response varies in different accessions (with Col-0 being more sensitive than *Ler*) (van Zanten et al., 2010). Therefore, chromatin plasticity seems to contribute to the plant's adaptation to environmental light conditions.

Alternatively, the heterochromatin response to low light can be viewed as an abiotic stress response. Upon exposure to another abiotic stress, namely, prolonged heat stress, the transcription of centromeric and pericentromeric repeats is reactivated and these regions exhibit a dispersed pattern in FISH (Pecinka et al., 2010). Interestingly, throughout recovery, transcription of centromeric and pericentromeric repeats was progressively silenced, whereas decondensation persisted for up to one week. Therefore, this is another example showing that chromatin condensation status and gene expression can be uncoupled. Furthermore, such alterations did not occur in meristematic cells, or in cells from leaves, which were produced after the period of heat stress. It was proposed that the specific meristematic chromatin response indicates the existence of a safeguard mechanism that minimizes genome damage in the germline (Pecinka et al., 2010). Interestingly, heterochromatin decompaction was not observed after freezing or UV-C treatments (Pecinka et al., 2010). Therefore, decondensation of the heterochromatin compartments is either not a general stress response or each type of stress is associated with chromatin reorganisation in a specific compartment or with a distinctive timing and amplitude pattern. It will be interesting to decipher the signalling mechanisms that induce large-scale chromatin reorganisation in differentiated cells and prevent such reorganisation in rapidly dividing cells. Reorganisation of heterochromatin was also observed in response to biotic stress (Pavet et al., 2006). A drastic reduction in RHF and CC number (with most nuclei having only two small CCs) and loosening of CCs were observed within one day of infection with the bacterial pathogen *Pseudomonas syringae*.

A drastic decondensation involving pericentromeric regions, 5S rDNA, centromeric repeats, and 45S rDNA was described during the isolation of *A. thaliana* protoplasts (Tessadori et al., 2007a). Despite general NOR

decondensation, a fraction remains partially condensed, participating to small CCs close to the nucleolus. The protoplast chromatin reorganisation is accompanied by the acquisition of totipotency and major transcriptional reprogramming that affects, for example, chromatin-associated genes and genes encoding histone variants (Chupeau et al., 2013). It remains to be determined whether the reorganisation of protoplast chromatin results from a stress response due to enzymatic digestion and osmotic and light changes and/or is necessary for totipotency acquisition and major transcriptional reprogramming (Chupeau et al., 2013).

Mechanisms involved in the Spatial Heterochromatin Distribution

Two main patterns of heterochromatin distribution emerge from the previous examples: the first involves the partial decondensation of CCs at the 5S and pericentromeric regions and the second affects all heterochromatic compartments of the CCs. A detailed study of the progressive and sequential reformation of CCs during protoplast culture provided complementary information about the highly ordered structure of CCs (Tessadori et al., 2007a). During sequential CC recompaction, the NOR regions (the largest regions, at 3.5-4 Mb) reorganise first followed by the centromeric (0.4-1.4 Mb), 5S rDNA (0.1-0.3 Mb), and dispersed pericentromeric repeats, including transposons, suggesting that the timing and size of the repeat arrays are correlated (Tessadori et al., 2007a). Thus, the 5S and pericentromeric sequences might participate in one core domain of the CCs, first mobilized in chromatin decondensation events, and the centromeric repeats and 45S rDNA in another core domain, more central or with some different properties. Establishing whether this latter core domain decondenses without affecting the other one would provide insight into the structure of CCs. The number of anchoring sites might also be proportional to the size of the arrays, and may thus contribute to the kinetics and formation of sub-compartments of the CCs.

Finally, the underlying biochemical properties of heterochromatin, such as DNA methylation, epigenetic marks, or histone composition, are also expected

to contribute to this sort of “CC breathing”. Heterochromatin dynamics has been considered as either dependent or independent of epigenetic changes, suggesting that several mechanisms, with possible self-reinforcing feedbacks, exist. For instance, by using molecular approaches, the 5S rDNA arrays were shown to be hypomethylated when they loop out of CCs during seed germination (Mathieu et al., 2003) and demethylation of the centromeric and pericentromeric repeats was shown to accompany a biotic-induced chromatin decondensation (Pavet et al., 2006). However, no change in DNA methylation was observed at centromeric repeats during floral transition (Tessadori et al., 2007b), in protoplasts (Tessadori et al., 2007a) and in response to heat stress (Mittelsten Scheid et al., 2002; Pecinka et al., 2010). Despite the large-scale reorganisation, there is no change in H3K9me2 and H3K4me3 contents in protoplasts, as determined by immunoblot analysis of total histones. In heat-stressed cell nuclei, a reduction in nucleosome occupancy with a small reduction in H3K9me2 was observed (Mittelsten Scheid et al., 2002; Pecinka et al., 2010). From these data, it is tempting to speculate that the epigenetic-dependent pathway might contribute to the formation of a putative 5S-pericentromeric core domain, and the independent pathway to that of the other putative core domain. However, it is important to note that most studies used methods with low sensitivity at the global nuclear scale to detect epigenetic changes and did not consider all of the chromatin marks and their combinations (Baubec et al., 2010). Furthermore, all sub-compartments were not simultaneously analysed. Therefore, specific epigenetics variations may not yet have been identified. Alternatively, the “CC breathing” could be seen as a continuous process with various amplitude and timing patterns. Finally, another key missing element is a better understanding of the higher-order structures of chromatin. The existence of 30-nm chromatin fibres is still a matter of debate, and an alternative chromatin model that involves interdigitation of nucleosomal arrays, which is more compatible with rapid conformational changes providing access to DNA, is currently proposed (Fussner et al., 2011; Luger et al., 2012) and might also affect “CC breathing”.

A few mutations with a marked impact on the formation and/or spatial distribution of conspicuous heterochromatin sub-compartments have been described (Table 1). Three main classes of genetic determinants involved in

heterochromatin dynamics can be tentatively distinguished based on their functions (Table 1). The first class (Class I) corresponds to genes involved in the formation of heterochromatin and the maintenance of silencing in *A. thaliana* (*MET1*, *CMT3*, *NRPD2*, *NRPE1*) (Douet et al., 2009; Mittelsten Scheid et al., 2002; Onodera et al., 2005; Soppe et al., 2002; Vaillant et al., 2008). It is important to note that mutations that affect silencing do not necessarily alter nuclear heterochromatin organisation. For instance, the nuclear shape and CC structure of the *morpheus' molecule1* mutant (*mom1*), which is affected in an epigenetic regulator, are normal (Probst et al., 2003). The second class (Class II) includes genes encoding chromatin-associated proteins, such as the ATP-dependent SWI2/SNF2-like chromatin remodeling DDM1 factor (Probst et al., 2003; Soppe et al., 2002), which was shown to have specific functions in heterochromatin remodelling (Zemach et al., 2013); the histone modifying enzyme HDA6 (Probst et al., 2004); and the chromatin assembly subunits FAS1 and FAS2 (Schonrock et al., 2006). The first two classes of genetic determinants may participate in the epigenetic-dependent pathway involved in heterochromatin dynamics. A the third emerging class (Class III), contains genes that encode diverse nuclear structural proteins, such as the two lamin-like proteins *LINC1* and *LINC2* (Dittmer et al., 2007) that might be involved in an epigenetic-independent pathway. Based on the identification of nuclear lamina-associated chromatin domains in *Drosophila* and human (Guelen et al., 2008; Pickersgill et al., 2006), we expect that mutations that affect the plant nuclear envelope (Boruc et al., 2012; Graumann et al., 2010) might have an impact on plant chromatin organisation. Furthermore, some subunits of the cohesion and condensin complexes, such as SYN4 and CAP-D3 proteins, also play important roles in sister chromatid organisation and centromere distribution, thus impacting on the interphase chromatin architecture (Schubert et al., 2013; Schubert et al., 2009).

Different signalling pathways involved in heterochromatin reorganisation are expected that might converge on key regulators of heterochromatin reorganisation, such as the factors described in Table 1. Indeed, development and environmental processes impact on heterochromatin spatial organisation. These regulatory components might be specific to signalling pathways or shared by different signalling pathways.

Class	Mutant	Protein function	Nuclear phenotype	Reference
I	<i>methyltransferase1 (met1)</i>	DNA methyltransferase	Small CCs (chromocenter) fraction reduced by ~25-30% - Pericentromeric sequences away from the CCs - reduced heterochromatic 5S rDNA fraction - DNA methylation reduced by ~70% - Decreased H3K9 methylation - Transcriptional reactivation of silent genes	Soppe et al. 2002; Vailliant et al. 2008
	<i>chromomethylase 3 (cmt3)</i>	DNA methyltransferase	Reduced heterochromatic 5S rDNA fraction - Decreased symmetrical methylation at 5S rDNA	Vailliant et al. 2008
	<i>nuclear RNA polymerase D2A and D2B (nrd2a nrd2b double mutant)</i>	Second largest subunit of Polymerase IV	Numerous but small CCs - Decondensation of 5S rDNA with less colocalization with CCs - Increased number of NOR signals due to dissociation - H3K9me2 signals are dispersed and colocalize with the numerous small DAPI foci	Onodera et al. 2005; Douet et al. 2008
	<i>Nuclear RNA polymerase E1 (nrpe1)</i>	Largest subunit of Polymerase V	Decondensed 5S rDNA, at chromosome 4 but not for 5S rDNA at chromosomes 3 and 5 - Decondensed NOR4	Douet et al. 2009
	<i>repressor of silencing 1 (ros1)</i>	DNA glycosylase/demethylase	Reduction of the transient decondensation of 5S rDNA loci at 3-day post-germination	Douet et al. 2008
II	<i>decrease in DNA methylation1 (ddm1)</i>	SWI2/SNF2 chromatin remodelling factor	Small and decondensed CCs with looping out of pericentromeric sequences - Smaller heterochromatic 5S rDNA fraction - Reduction of DNA methylation by ~70% and of H3K9 methylation - Transcriptional reactivation of silent loci	Soppe et al. 2002; Probst et al. 2003; Mathieu et al. 2003
	<i>histone deacetylase6 (hda6)</i>	RPD3-like histone deacetylase - involved light response of chromatin	Reduction of RHF and HX - Decondensation of rDNA loci with enrichment of H4ac4 and H3K4me at rDNA loci - Transcriptional reactivation of the 7S1 pericentromeric repeats	Probst et al. 2004; Tessadori et al. 2009
	<i>fasciata1, fasciata2 (fas1, fas2)</i>	Subunits of Chromatin Assembly Factor 1 (CAF-1)	Reduced total heterochromatin fraction - Maintenance of transcriptional silencing at heterochromatic loci	Schönrock et al. 2006
III	<i>little nuclei1 and 2 (linc1 linc2 double mutant)</i>	Lamin-like analogs - related to Nuclear Matrix Constituent Protein1 (NMCP1)	Reduced nuclear size - Altered nuclear morphology - reduction of CC number (4.6±0.1) - Higher DNA packaging ratio - Altered ploidy	Dittmer et al. 2007; Sakamoto et Takagi, 2011
	<i>syn4</i>	alpha-kleisin subunit of the cohesin complex	Decreased sister chromatid alignments along chromosome arms in 4C differentiated leaf nuclei and impaired sister centromere cohesion	Schubert et al. 2009
	<i>cep-D3</i>	HEAT-repeat containing condensin CAP-D subunit	Alterations of centromeric and pericentromeric heterochromatin association - decreased sister chromatid cohesion in 4C nuclei	Schubert et al. 2013

Table 1: Mutations affecting the spatial organisation of heterochromatic compartments in *A. thaliana*.

As described above, light intensity is an important environmental signal that controls chromatin compaction. The light-signalling pathway is mediated by well-described photoreceptors, some of which are localised to the nucleus. Among them, CRYPTOCHROME 2 (CRY2) and PHYTOCHROME B (PHYB) are involved in chromatin reorganisation, whereas others, such as phototropins and CRYPTOCHROME1, are not (Tessadori et al., 2007b; van Zanten et al., 2010). These data suggest that CRY2 and PHYB also participate in the spatial organisation of heterochromatin. Thus, many elements that affect the timing and molecular events of heterochromatin dynamics remain to be identified, and the impact of heterochromatic reorganisation on the 3D organisation of the genome remains to be established.

Chromosome Territories

In plant and animal cell nuclei, each chromosome occupies a discrete portion of the nuclear space, distinct from that of other chromosomes, named chromosome territory (CT) (Boveri 1909; Cremer and Cremer 2010; Tiang et al., 2012). Deciphering the rules and mechanisms governing their spatial nuclear distribution as well as their internal organisation is a highly dynamic and challenging research field, due to its consequences on genome functions (Bickmore and van Steensel 2013; de Graaf and van Steensel 2013). Chromosome conformation capture method (3C) and derived methods, such as high-throughput chromosome conformation capture (HiC), have been developed in animal to provide maps of interaction frequencies between genomic regions at the locus, chromosome or whole genome scales (de Wit and de Laat 2012). Tri-dimensional conformations of the genomes have thus been computationally reconstructed from these data (Dekker et al., 2013; Lieberman-Aiden et al., 2009). Based on HiC results, the fractal globule model of CT organisation was proposed. According to this model, the chromatin fibre is packed into a 1-Mb domain in a meta-stable conformational state (Dekker et al., 2013; Mirny 2011). In plants, the 3C method has only recently been used (Hovel et al., 2012) and no equivalent or alternative model is yet available for plant CT organisation.

Plant CTs were observed in species both with (Abranches et al., 1998) and without (Lysak et al., 2001; Lysak et al., 2003; Pecinka et al., 2004) Rabl configurations using FISH studies. Using a wheat line containing an extra pair of rye chromosomes, it was shown that the rye CTs were roughly parallel and elongated nuclear domains extending between the centromeric and telomeric nuclear poles, in a Rabl configuration (Abranches et al., 1998). More recently, this organization was shown to be present in meristematic but not in differentiated nuclei (Schubert et al., 2011). In small genome species with non-Rabl configurations, such as *Arabidopsis*, CTs have a different spatial distribution. The association frequencies between *A. thaliana* chromosome pairs were computed based on simultaneous painting of all chromosome pairs (Pecinka et al., 2004). Based on a computer model of CT formation determined by polymer decondensation, it was shown that these frequencies were not significantly different from that expected under randomness, except for NOR-bearing chromosomes that frequently associated with each other, most probably because of their association to the nucleolus (Pecinka et al., 2004). Likewise, no differences were found between random expectations and observed associations of homologous genomic regions of ~100 kb (Pecinka et al., 2004). Similar results were found in related species (Berr et al., 2006) and in differentiated cells (Berr and Schubert 2007). Hence, the current view of CT organisation in *A. thaliana* and related species is a globally random one that contrasts with results from animal studies (Schubert et al., 2012). It has, for example, been suggested that CTs in animals obey a size-dependent radial distribution, with smaller chromosomes being located toward the nuclear centre. Other studies have reported a gene density-dependent spatial distribution, with gene-rich chromosomes being located towards the centre (van Driel and Fransz 2004). The absence of such patterns in *A. thaliana* may be due to its relatively uniform chromosome size and gene density and to low number of chromosomes (Figure 1).

Similarly, few arguments favour any cell type- and tissue-specific organisation of CTs in *Arabidopsis* and other plants. Chromosome painting in *A. thaliana* revealed that CTs were larger in endosperm nuclei than in nuclei of other cell types, corroborating the notion that less chromatin compaction occurs in this tissue (Baroux et al., 2007). The tissue-specific spatial distribution of

CTs has been reported in mouse and CT distribution patterns were found to be maintained throughout mitosis (Parada and Misteli 2002). By contrast, the spatial distribution of CTs is not conserved between mother and daughter cells in Arabidopsis, but only a transient mirror-image distribution has been reported between daughter cells (Berr and Schubert 2007). The absence of maintenance of CT organisation during mitosis and within tissues is probably also related to the small genome and chromosome sizes in Arabidopsis.

No specific role of CT in the organization of genome expression has been reported in plants (Tiang et al., 2012). In animals, preferred localisation of transcription sites at CT boundaries and gene relocalisation outside CT upon activation have been reported (Davidson et al., 2013; Geyer et al., 2011). By contrast, the relative localisation of the flowering gene *FWA* to its CT did not seem to differ with its transcriptional status (Pecinka et al., 2004). In wheat, transcription sites were not preferentially localised to the periphery of CTs (Abranches et al., 1998). Only a few studies have investigated gene-to-CT positioning in relation to transcriptional regulation, and these studies were performed using coarse spatial descriptions. Further large-scale and systematic quantitative analyses are required to better document the role, if any, of chromosome organisation in the regulation of gene expression in plant nuclei.

Chromatin Dynamics at the Locus Scale

Numerous studies in yeast and animals have measured chromatin motion of genomic regions to, mostly, investigate the interplay between gene positioning and gene transcriptional status. In plants, the first evidence of chromatin dynamics and remodelling at the scale of the locus was provided by a 3D FISH experiment that revealed two chromatin conformations, one open and one closed, in the non-hair and hair cell nuclei of the *A. thaliana* root epidermis, respectively, in the genomic region of the *GLABRA2* (*GL2*) transcription factor locus (Costa and Shaw 2006). *GL2* is expressed in non-hair cells; however, mutant analysis revealed that neither *GL2* expression nor the cell lineage is required for the open chromatin conformation in the *GL2* genomic region. The

chromatin conformation in the *GL2* region depends on positional information in root cells and is reset at mitosis.

At the present time, our knowledge is still limited due to the complexity of the nuclear system and technical problems in visualizing, recording, and analysing small portions of the genome in their wild-type environments. The chromatin beacon or chromatin-tagging method is a powerful technique developed to analyse the dynamics of tagged genomic regions, in living organisms, and to quantify chromatin structural parameters at these genomic locations (Amini et al., 2011). In this technique, exogenous concatameric arrays (~2 to 10 kb) of a DNA sequence that is specifically recognized by a selected DNA-binding domain are inserted into the genome and the location of the arrays (termed beacon arrays) is molecularly characterized. The expression *in trans* of a chimeric protein resulting from the fusion between the selected DNA-binding domain and a fluorescent reporter protein allows visual tracking of chromatin movement at the tagged loci in the nuclei of live cells. A two-component labelling system based on the recognition of tandem *lac* operator binding sites (*lacO*) by the *lac* repressor (LacI) was successfully used in yeast, *Drosophila*, mammals, and plants (Kato and Lam 2001; Marshall et al., 1997; Robinett et al., 1996; Vazquez et al., 2001). A bacterial tetracycline operator/repressor (*tetO*/TetR-YFP) system (Matzke et al., 2003) and a combination of the *lacO*/LacI-dsRed and *tetO*/TetR-YFP systems (Matzke et al., 2005) were developed to analyse the 3D distribution of chromosomal sites in plants. By introducing a gene into the cassette bearing the *lacO* repeat array, it was possible to study chromatin movement in relation to transcriptional activity of the reporter gene at the location of the insertion (Rosa et al., 2013; Rosin et al., 2008).

The approaches described above were used to study the relationship between the physical and functional properties of chromatin. In animals, it was shown that chromatin undergoes random diffusive motion in interphase nuclei, and that this Brownian motion is constrained such that a given genomic segment moves within a limited nuclear sub-region. Complex motion patterns have been recorded for genomic regions, which exhibit short-range and long-range motion, with different velocities. The long-range diffusive motion

fluctuates over a 36-fold distance range during the cell cycle (Vazquez et al., 2001). These findings support a highly organised nuclear space and the existence of mechanisms that control chromatin motility according to cell type and throughout the cell cycle. Furthermore, these findings suggest that chromatin motion participates in nuclear processes that require chromosome mobility and chromosome reorganisation in the nuclear space. For instance, it was recently shown that the induction of double-strand breaks in the yeast *Saccharomyces cerevisiae* dramatically increases the mobility of the broken loci but also of the homologous unbroken loci, without changing the speed at which chromosomal regions move. The increased mobility allows a wider exploration of the nuclear volume, which facilitates the pairing of homologous regions (Mine-Hattab and Rothstein 2012, 2013).

Using the chromatin beacon technique, a few studies have demonstrated that chromatin in the *A. thaliana* cell nucleus also exhibits constrained diffusive motion, and that the amplitude and kinetics (diffusion coefficient) of the motion depend on the ploidy level and cell type (Rosin et al., 2008) (Kato and Lam 2003). The constrained area increases with the ploidy level: it was 6.6-times larger, on average, in elongated polyploid epidermal pavement cell nuclei compared to smaller disk-shaped diploid guard cell nuclei, whereas the diffusion coefficient was lower (<2.3 times) in polyploid cells than in diploid ones. The confinement radius in the Arabidopsis nucleus ranges from 0.1 to 0.4 μm , depending on the ploidy level and activity of the locus (Kato and Lam 2003; Rosin et al., 2008). In *A. thaliana*, the chromatin compaction ratio, as determined by measuring the *in vivo* distance between two fluorescence-tagged transgene inserts on the same chromosome (Matzke et al., 2005), is approximately 670 fold. For instance, two transgenes located 2.4 Mb apart (which corresponds to a DNA sequence of 0.8 μm) on chromosome 2, had an observed physical separation of 2.1 μm (380 fold), whereas another pair of transgenes situated 25 Mb apart on chromosome 1 exhibited a physical separation of 8.7 μm (960 fold). Furthermore, it was shown that the frequencies of homologous pairing and association with heterochromatin of transgenic repeats differs with the construct, the chromosomal insertion position, the cell type, and the number and repetitiveness of inserts (Pecinka et al., 2005).

The first evidence that gene position and transcriptional activity are linked in the plant cell nucleus emerged with the study of the nuclear organisation of transgenic *FLC* alleles tagged with the *LacO* repeat array (*FLC-lacO*) in response to vernalization (Rosa et al., 2013). During cold treatment, and after ethanol induction of the LacI-YFP-NLS fusion protein, a cluster of *FLC-lacO* alleles was observed with one to two foci in endoreduplicated root cells and only one in meristematic diploid root cells, whereas in non-vernalized plants, six or more foci were observed. The *FLC-LacO* clustering was quantitatively dependent on the cold treatment and dependent on Polycomb proteins of the PHD-PRC2 complex, which are required for *FLC* silencing before and during the cold treatment. Therefore, physical repositioning of loci associated with transcriptional changes occurs in plants and can be mediated by Polycomb-mediated epigenetic mechanisms in both plants and animals, suggesting that the key mechanisms are conserved.

There are several limitations of the chromatin beacon technique: (i) the beacon array is not targeted precisely, because site-directed mutagenesis can not be performed in most plants; (ii) an artificial transgenic environment that differs from the original one may be created due to the interruption and/or rearrangement of the genomic region where the beacon is inserted, and the 3D organisation of the chromatin fibre resulting from the insertion may be modified; and (iii) the high number of tandem repeats can induce repeat-induced silencing and modifications in the epigenetic chromatin of the beacon array and/or in the adjacent genomic chromatin. Indeed, a high copy number of repeats alters the local chromatin arrangement, resulting in more frequent somatic pairing of the *lacO* harbouring regions and more frequent association with heterochromatic CCs (Pecinka et al., 2005). These changes depend on the size and number of repeat units per locus (Jovtchev et al., 2008). To minimize recombination events, replication instability, and repeat-induced silencing usually associated with tandem repeats, Rosa et al. (2013) used a low number of concatameric *lacO* binding sites of the *lacO* DNA sequence and inserted ~10-bp random sequences in-between *lacO* DNA sequences (Jovtchev et al., 2008; Rosa et al., 2013). There is an urgent need to develop alternative techniques to label specific genomic regions, so that the relationship between the physical and functional properties of chromatin can be analysed more thoroughly. Zinc

finger (ZF) proteins and transcription activator-like effector (TALE) proteins have been customized to introduce targeted genome modifications (i.e., mutations, insertions, and substitutions) (Chen and Gao 2013; Gaj et al., 2013). These proteins have also been adapted to visualize heterochromatic repeat sequences, both in plants (Lindhout et al., 2007) and animals (Miyanari et al., 2013). Novel optimization and adaptation techniques for single-copy gene detection would be tremendously useful. Furthermore, the development of programmable RNA-guided DNA labelling systems derived from RNA-guided nuclease technology (Belhaj et al., 2013; Gaj et al., 2013; Puchta and Fauser 2013) might give rise to alternative useful techniques. A recent study reported an example of gene repositioning associated with transcriptional activation, using rolling-circle amplification of gene-specific padlock probes coupled with FISH (Feng et al., 2014).

Dynamics of Nuclear Protein Compartments

Chromatin occupies only a fraction of the interphase nuclear space (i.e., ~5% for DNA and ~20% for the 10-nm chromatin fibre) (Fussner et al., 2011). Thus, interchromatin and perichromatin nuclear domains correspond to large functional spaces, harbouring numerous and diverse **nuclear bodies** (NBs). NBs are membraneless subdomains that were originally described as being morphologically distinct from their surrounding neighbourhood when observed by transmission electron microscopy (TEM) (Dundr 2012; Shaw and Brown 2004). The definition was extended to subnuclear compartments observed by immunocytochemistry or fluorescence microscopy, but without prior morphological evidence of their ultrastructure (i.e., Polycomb bodies or transcription factories).

NBs are nuclear microenvironments that function in specific biochemical processes, such as splicing (nuclear speckles and Cajal bodies), transcription (transcription factories), or gene silencing (Polycomb bodies). Most are highly conserved in animals and plants, but some, such as **photobodies**, are plant specific. Photobodies are discrete accumulations of photoreceptors with key regulatory functions in plant growth and development in response to light

signals. They contain red and far-red sensing phytochromes (A to E) or cryptochrome blue light receptors (CRY2 and possibly CRY1) and other associated proteins. Light induces rapid conformational changes of the photoreceptors and directly controls the assembly of photobodies. Although photobodies were proposed to have functions in storage, transcriptional regulation, or protein degradation, these possibilities remain to be confirmed (for reviews see (Chen 2008; Chen and Chory 2011; Van Buskirk et al., 2012)). As previously described, light signalling can induce heterochromatin reorganisation. It remains unclear whether photobodies interact with chromatin and participate in such a reorganisation. Based on fluorescence imaging studies, other NBs with specific functions in abscisic acid or auxin signalling pathways (Ng et al., 2004; Tao et al., 2005) or in the control of the circadian clock (Strayer et al., 2000) have been reported. Plant nuclear dicing bodies, which are located close to nucleoli, are sites of plant-specific miRNA processes (Fang and Spector 2007; Liu et al., 2012).

Most NBs are highly dynamic in terms of composition, number, shape, and size, and these dynamics are modulated by the cell differentiation state, metabolic state, and transcriptional activity of the cell cycle. Whereas animal NBs are fairly well characterized, the components, structures, and assembly mechanisms of plant NBs remain elusive, with the exception of the largest NB, the nucleolus. It was proposed that NBs generally result from a local dynamic equilibrium between assembly and disassembly activities of protein complexes. Two distinct assembly models for NBs have been proposed. The first model is based on an orderly manner of assembly that involves central scaffolding factors, whereas the second model hinges on random aggregation (Matera et al., 2009). Due to the spatial and temporal dynamics of NBs in the cell nucleus and their intricate functions in genomic activities (i.e., transcription, replication, and DNA repair), it is difficult to decipher the relationship between NB functions and genome organisation. How the spatial dynamics of NBs relate to chromatin dynamics is largely unknown. Indeed, the spatial distribution of NBs relative to CTs, chromatin domains, and other nuclear compartments is poorly documented.

The largest NB, **the nucleolus**, was first described in 1835 by Rudolf Wagner and is a well-studied multifunctional compartment in both animals and plants. Mainly known for its functions in rDNA transcription, rRNA processing, and pre-ribosome assembly, the nucleolus is also involved in the processing and assembly of RNPs, transcriptional gene silencing, and mRNA surveillance and export (Brown and Shaw 2008; Dundr 2012; Morimoto and Boerkoel 2013). The nucleolus is a complex NB that itself contains different subdomains with their own dynamics (e.g., the fibrillar centre, dense fibrillar and granular components, and peripheral heterochromatic shell) (Nemeth and Langst 2011). Interestingly, it is a chromatin region, the NOR, that plays a crucial role in its assembly (McClintock 1934). In humans, a model was recently proposed for a role of distal- (telomeric side) NOR-flanking regions as anchoring sites for active NORs in the perinucleolar heterochromatic region, whereas inactive NORs are relocated away from the nucleolar periphery (Floutsakou et al., 2013). Recently, the nucleolus has emerged as a genome organisation centre that is involved in nuclear architecture (Nemeth et al., 2010; van Koningsbruggen et al., 2010). Indeed, genomic regions associated with the nucleolus (NADs, nucleolar-associated domains) were identified and found to account for ~4% of the genome. NADs are characterized by a high density of AT-rich sequence elements and satellite repeats, a low gene density, and a significant enrichment in transcriptionally repressed genes belonging to different gene families. It will be interesting to identify the *cis* and *trans* determinants of NAD formation and the mechanism underlying the dynamic maintenance of NADs in different physiological conditions. The plant nucleolus was also intensively studied (Brown and Shaw 2008) and a large set of *A. thaliana* nucleolar proteins (217) was identified within the first extensive proteomic analysis of a plant NB (Pendle et al., 2005). In *A. thaliana*, the nucleolar periphery seems to be an important functional interface with other NBs (D-bodies and Cajal bodies) and also with heterochromatic compartments (NOR, telomeres). It is thus very likely that NADs exist in plants.

In *Drosophila* and mammals, local enrichments in Polycomb group proteins (PcGs) have been described as **Polycomb bodies** (PcG bodies) (for a review see (Pirrotta and Li 2012)). PcG proteins are key chromatin factors that maintain gene repression via several mechanisms, such as histone post-translational

modifications, chromatin compaction, or formation of higher-order chromatin structures (Bantignies and Cavalli 2011; Schuettengruber and Cavalli 2009; Simon and Kingston 2013). PcG proteins participate to the formation of multiprotein complexes, such as Polycomb Repressive Complex1 (PRC1) and PRC2, which are the main studied complexes in eukaryotes (Schuettengruber and Cavalli 2009). Animal PcG bodies can be visualised in the cell nucleus by labelling subunits of PRC1, such as Polycomb and Polyhomeotic (see references in (Pirrotta and Li 2012)). They participate in gene silencing by creating a specific microenvironment in which remote PcG-silent targets colocalise as a result of long-distance interactions between silent targets and chromatin-fibre folding (Bantignies et al., 2011; Cheutin and Cavalli 2012; Delest et al., 2012). Some RNAi components, such as Dicer-2, PIWI, and Argonaute1, which also form nuclear bodies, can colocalise with PcG bodies, and participate in PcG repression (Grimaud et al., 2006). Furthermore, PcG bodies are dynamics with rapid protein exchange between nucleoplasm and PcG bodies and vary both in number and size with cell type, their number increasing as cells differentiate. Time-lapse experiments also revealed a fast regime of PcG motion within volumes smaller than CTs, as well as a slow regime of long-range motion dependent on coordinated large-scale chromatin movements, which might be associated with displacements of whole or large parts of chromosomes and lead to the few observed association and dissociation events of PcG bodies (Cheutin and Cavalli 2012). However, whether PcG bodies are true nuclear entities or 3D chromosomal domains enriched in PcG proteins is still a matter of debate (Pirrotta and Li 2012; Smigova et al., 2011). Thus, the mechanism by which PcG bodies form, which may involve PRC1 components with polymerisation properties (Isono et al., 2013), as well as the role of PcG bodies in transcriptional regulation remain to be clarified. In *A. thaliana*, LHP1, the plant functional homolog of Polycomb, represses gene expression (Turck et al., 2007; Zhang et al., 2007). LHP1 is located in discrete nuclear foci and its distribution changes during cell differentiation (Gaudin et al., 2001; Libault et al., 2005). In young proliferating cells, a uniform LHP1 distribution pattern was reported. As root hair cells mature progressively from the root apex to the crown area, the number of foci in the root hair nuclei increases. The distribution of LHP1 in the nucleus was dynamic throughout the cell cycle (Libault et al., 2005). Therefore, LHP1 foci are reminiscent of

Polycomb bodies in animals. LHP1 was shown to repress *FLC* expression. However, LHP1 does not seem to be required for the vernalization-induced clustering of *FLC-LacO* alleles, whereas PRC2 subunits participate in such processes (Rosa et al., 2013). The colocalisation of the ectopic *FLC-LacO* cluster with a plant PcG body remains to be established (Rosa et al., 2013). EMBRYONIC FLOWER1 (EMF1), a putative PRC1 subunit, has been shown to participate in chromatin compaction (Beh et al., 2012). Whether EMF1 or others PcG proteins participate in the formation of plant PcG bodies and function in the spatial organisation of the genome as in animals will require further investigation.

First described in 1903 by Ramon y Cajal, **Cajal bodies** (CBs) are subnuclear structures that appear to contain many coiled threads (previously named coiled bodies) in TEM images. They are present in most animal species and in several plant species (Dundr 2012; Machyna et al., 2013; Shaw and Brown 2004). CBs are mainly involved in the maturation of RNA species and the assembly and trafficking of transcription-related ribonucleoprotein particles involved in splicing, ribosome biogenesis, or telomere maintenance. In *A. thaliana*, CBs have specific functions in siRNA and miRNA biogenesis (Pontes and Pikaard 2008). CBs are composed of a wide range of proteins (some of which also occur in the nucleolus and histone locus bodies) and various types of small RNAs that are related to their specific and various functions (Fong et al., 2013; Machyna et al., 2013). The coilin protein, which is considered as a signature of CBs, has structural scaffolding function and is a key regulator of CB formation and activity (Collier et al., 2006; Machyna et al., 2013). The CBs are either free in the nucleoplasm and/or physically associated with specific regions of chromatin, such as the nucleolus, in line with the original description of CBs as nucleolar accessory bodies (Shaw and Brown 2004). The *A. thaliana* nucleus usually contains a single spherical CB of ~1 μm in diameter, which is often closely associated with the nucleolus of different cell types. *A. thaliana* CBs can be visualized by TEM or by using marker proteins, such as AtCoilin (Collier et al., 2006) or the spliceosomal protein U2B'' (Beven et al., 1995; Boudonck et al., 1999). Mutants with multiple CBs have been described (Collier et al., 2006), suggesting the existence of plant factors involved in the maintenance of CB cohesion. As in animals (Platani et al., 2000), plant CBs are

highly motile and travel within the nucleoplasm and nucleolus (Boudonck et al., 1999). Their numbers fluctuate with the cell cycle, with coalescence occurring mainly at the nucleolar periphery (Boudonck et al., 1999).

Nuclear speckles (NSs), which are enriched in splicing regulators, such as Ser/Arg-rich RNA-binding proteins and 3'end processing factors, correspond to another type of NB that is also related to RNA splicing. These NBs are considered to act as storage and assembly environments for splicing regulators, which are translocated to transcription sites for RNA maturation (for reviews (Reddy et al., 2012; Spector and Lamond 2011)). The nuclear speckle components shuttle rapidly from the nucleoplasm and nucleolus to the nuclear speckles. These NSs are motile within a constrained region, and vary in size, shape, and number, as do other NBs.

Transcription factories (TFAs) are discrete local subnuclear regions enriched in RNA polymerase and ribonucleoproteins (RNPs) and in close contact with chromatin (Davidson et al., 2013). Nascent transcripts are synthesized at the surface of most TFAs, but some are not active and nascent transcripts were not detected for some TFAs. Genomic loci were found to relocate to TFAs in animals in a manner that was dependent on the transcriptional status of the loci and it was proposed that TFAs co-regulate gene sets, with several transcription units being associated with a single TFA and some being remotely located. As for most NBs, TFAs differ in number, size, and distribution, depending on the cell type, the metabolic and transcriptional activity of the cell, and the phase in the cell cycle. Recent imaging of RNA production at the single cell level demonstrated that transcription is a discontinuous process, with bursts of transcriptional activity (Chubb and Liverpool 2010). Furthermore, there is recent evidence that Polymerase II clusters form transiently, and due to the resulting molecular crowding occurring at these sites, they might participate to the assembly of the transcription machinery during the rate-limiting transcription steps (Cisse et al., 2013). In plants, parameters describing the dynamics of TFAs in the nucleus remain to be determined.

Modelling approaches to uncover plant nuclear architecture

An increasing number of studies use multidisciplinary approaches based on quantitative image analysis and biophysical modelling to identify the organisational principles of the nucleus and underlying mechanisms. However, these new research tools need to be refined before they can adequately address these objectives.

Since nuclear patterns are dynamic and do not fully obey deterministic rules, statistical analysis over large samples of nuclei is required to better describe and analyse these patterns. However, the high variability in nuclear size and shape makes integration and comparison of data from different nuclei difficult. In some species, such as *Saccharomyces cerevisiae* (budding yeast), nuclear landmarks can be used to superimpose different nuclei and to generate statistical representations of intra-nuclear distributions (Berger et al., 2008). Since nuclear landmarks are absent in plant nuclei or have not yet been identified, alternative quantitative strategies for integrating data are required. The need for quantitative approaches also results from the remarkable properties of the spatial distributions in 3D volumes. For example, the outer shell of a half radius width represents 90% of a sphere volume, and this proportion remains as high as 50% when reducing the shell width to a fifth of the sphere radius (Figure 3A).

Since nuclei frequently have a spherical topology, peripheral positioning of nuclear compartments is thus very likely to occur under random distribution. Therefore, demonstrating a specific peripheral positioning requires a quantitative analysis.

Before nuclear images can be subjected to quantitative analysis, objects of interest (e.g., nucleus, CTs, genes) must be localised in 3D. This process, called image segmentation, is generally achieved by setting an intensity threshold that separates object voxels from the others. For example, nuclear contours are frequently identified using DAPI counterstaining. The difficulty in achieving this task automatically is generally underestimated. For example, the popular

Otsu's thresholding method (Otsu 1979) is sensitive to intensity distribution features (Xu et al., 2011; Xue and Zhang 2102). Setting an accurate threshold is all the more critical because errors are magnified in three dimensions. This point can be illustrated by segmenting a 3D image at two slightly different thresholds: the 2D section areas displayed in Figure 3B appear almost identical, differing by less than 2%; by contrast, in 3D, the difference between nuclear volumes is 8%. When there is uncertainty about the intensity threshold, it is recommended to evaluate the potential impact on quantitative measurements using, for example, sensitivity analysis, or to rely on threshold-insensitive measures, or to integrate measurements over a range of threshold values (Eils et al., 1996).

Alternative methods for intensity thresholding can also use *a priori* information about the number or size of the expected objects. Additional image processing steps may be important to include, before or after the segmentation steps, such as deconvolution, noise reduction, or shape regularization using mathematical morphological operators (Ronneberger et al., 2008). Some of these steps may be simplified when better images become available due to technological advances in microscopy. However, the need for accurate segmentations will remain.

Two broad approaches are used to analyse nuclear positioning data, which typically consist of sets of points and sometimes also of the associated object sizes. In the first approach, object positions are analysed individually, thus focusing on the absolute positioning in the nucleus. The prominent paradigm is radial distance analysis, in which object location is defined based on its distance from the nuclear envelope or nuclear centroid, or on its relative position along the radius passing through it. The radial distance measurement is generally binned into a finite number of classes corresponding to concentric shells. To test for any preferential location towards/away from the envelope, the resulting histogram is compared to the expected distribution under random repartition. Continuous variants have been proposed (Ballester et al., 2008) that avoid the loss of statistical power inherent in class binning. In plants, distance analysis was used to demonstrate the preferential localisation of *A. thaliana* centromeres at the nuclear periphery of diploid cells (Fang and Spector 2005).

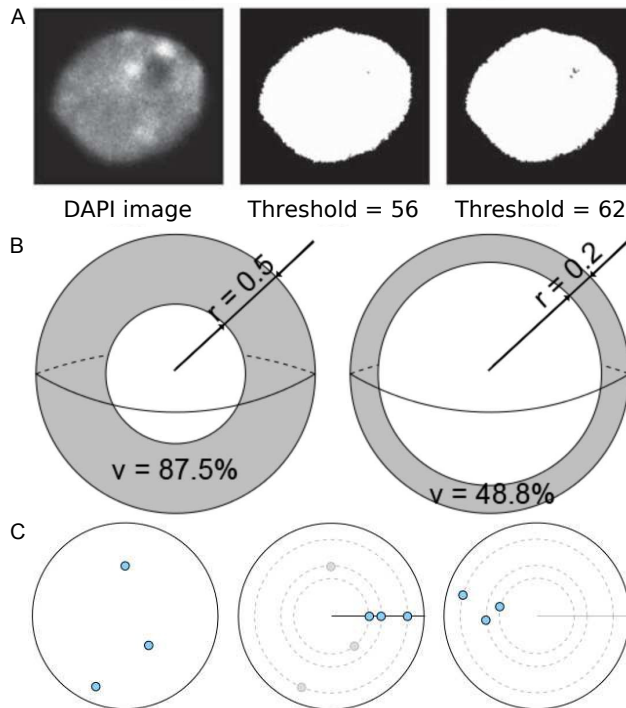


Figure 3: Some important issues in quantitative image analysis of nuclear patterns.

A. In a 3D sphere, the probability of a point being located by pure chance closer to the periphery than to the centre is large. **B.** Image segmentation errors may have a large impact on the delineated nuclear volumes. The left image shows a 2D section from a 3D image stack that has been segmented at two thresholds (middle and right images). On 2D sections, the differences of the surfaces after thresholding are small (less than 2%). However, the volume differences are much larger (8%). **C.** In radial analysis, based on distances from the object to the periphery or the centre, any pattern (e.g. left pattern) is virtually considered as a 1D pattern (middle). This results in a loss of spatial information and possible misinterpretation. Although different, patterns (for instance the left and right patterns) may yield the same 1D projection (middle) and thus become indistinguishable after analysis.

The popularity of radial distance analysis in nuclear organisation studies (Shiels et al., 2007) is probably due to the simple spherical shape of cultured animal cell nuclei. The diversity of plant nuclear shapes (Chytilova et al., 1999), however, challenges the general relevance of this approach in plant studies. Further, radial distance analysis entails a projection of 3D data onto a single dimension, thus resulting in a significant loss of spatial information (Figure 3C).

The second approach considers all object positions from a single nucleus together, thus evaluating their mutual positioning. In its simplest form, such an analysis relies on object association frequencies, with an association being defined by the inter-object distance below some fixed threshold. Comparing measured frequencies with expected frequencies under random object repartitions allows to reveal associations or exclusions. This approach revealed a random association between homologous genomic regions of ~100 kb in *A. thaliana*, thus demonstrating the absence of somatic homologous pairing in this species (Pecinka et al., 2004). Similar results were obtained later in other species (Berr et al., 2006; Schubert et al., 2007). Spatial statistics, offer more elaborate tools for analysing point patterns based on summary statistics such as cumulated distance functions (Diggle 2003). Standard spatial descriptors are the distance from any object to its nearest neighbour or the distance between any position and the nearest object. As above, measured distribution functions are compared to expected functions under the hypotheses of reference models, which are generally based on complete spatial randomness. Spatial statistics have historically been developed for ecology, forestry, and epidemiology studies, where data are positions recorded within a single sampling window. This contrasts with nuclear data, which result from exhaustive position recordings over finite domains, with replication over samples of nuclei. Initial attempts to apply spatial statistical tools to nuclear studies ignored these difficulties by considering nuclear data as classical spatial data sampled from virtually infinite point processes (Beil et al., 2005; Buser et al., 2007; Noordmans et al., 1998). Adapting methods rather than data was recently proposed as an alternative, with the introduction of spatial statistical tools specifically designed to analyse nuclear organisation data (Andrey et al., 2010).

Because of the lack of statistical power in *per* individual analyses, uncovering spatial effects of small amplitude requires integrating data extracted from large populations of nuclei. Early studies incorporated no size or shape normalization and relied, for example, on average cumulated distance functions (Beil et al., 2005; Noordmans et al., 1998). In other studies, inter-nucleus size normalization was achieved by dividing measured distances by nuclear size (Fang and Spector 2005) or maximal observed distance (McManus et al., 2006). Shape normalization was recently proposed for testing spatial models of object

repartitions, based on the comparison of nuclear patterns to model outcomes conditioned by nuclear morphology. Comparisons were either performed on an individual basis (Russell et al., 2009) or at the group level (Andrey et al., 2010). The latter was made possible by introducing a normalized measure of model/data discrepancy for each nucleus. Results reported on simulated data later demonstrated the superior statistical power of this method as compared to other strategies for data integration over samples of nuclei (Weston et al., 2012). This methodology is particularly relevant for nuclear organisation studies in plants, as plant nuclei have diverse shapes that deviate significantly from simple spherical ones (Chytilova et al., 1999). Since this methodology is generic, it is also likely that it will be generalized in the future to evaluate more elaborate spatial models and to support inter-group comparisons.

Several studies in both animals and plants have used polymer modelling to analyse the mechanisms underlying the spatial organisation of the genome. The chromatin fibre is generally modelled as a linear chain of monomers and an energy function is defined to incorporate physical forces and constraints, such as attraction, repulsion, and volume exclusion between adjacent or distant monomers. Starting from initial configurations, computer simulations iteratively update monomer positions to progressively reach lower energy configurations. In the Spherical Chromatin Domain (SCD) model, which has been used both in animal and plant studies, chromosomes are modelled as strings of 1-Mb spherical domains connected by elastic springs and obeying short-range exclusion/long-range attraction potentials. Chromosome territories are obtained by relaxing initially condensed linear configurations representing metaphase chromosomes (Kreth et al., 2004). By comparing observed association frequencies between homologous chromosomes with those predicted by the SCD model, it was shown that homologue associations, in *A. thaliana* and the closely related species *A. lyrata*, are globally not significantly different from random, except for chromosome pairs 2 and 4, which bear NORs (Berr et al., 2006; Pecinka et al., 2004). Using a coarse-grain molecular dynamics model closely related to the SCD model, the contribution of non-specific physical interactions in the positioning of CCs and nucleoli in *Arabidopsis* leaf nuclei was examined (de Nooijer et al., 2009). In that study, chromosomes were represented by heteropolymers that could form loops and large monomers were

used to model CCs. Based on a comparison of the different models of polymer structure, the authors concluded that non-specific interactions between polymers with CC-anchored loops were sufficient to explain the experimentally observed positioning of CCs and nucleoli, as well as the segregation of chromosomes into territories, thus supporting the previously proposed rosette model (Fransz et al., 2002). One difficulty in interpreting the results of this model is that equilibrium configurations were obtained through chromosome condensation and reduction of nuclear volume. It is also unclear how a completely non-specific determinism of heterochromatin positioning in *A. thaliana* nuclei can be reconciled with the heterochromatin reorganisations described previously. An important future challenge will be to shift from simulations in theoretical, simple nuclear shapes (spheres or ellipsoids) to actual shapes determined from 3D images. In parallel, the ability to associate heterogeneous properties with monomers along chromosomes will be essential for further expanding the potential of these models in investigations of the principles underlying nuclear organisation and genetic determinants.

Conclusion

In the past decade, tremendous progress has been made in deciphering chromatin properties at the genomic scale in Eukaryotes, and the molecular and biochemical diversity of chromatin has been highlighted. Despite its repetitiveness, which for a long time largely excluded it from molecular studies, heterochromatin has started to reveal its secrets, and is no longer considered as a monotonous and silent compartment. Furthermore, besides key functions in chromosome segregation and genome stability and maintenance, a new function in genome organisation has emerged for heterochromatin, highlighting the interdependence of euchromatin and heterochromatin. The development of 3C and related methods, which have been used to unravel the three-dimensional conformation of the genome and, in turn, have raised questions about the relationship between 3D genome organisation and its main functions in the interphase nucleus (i.e., transcription, replication, and DNA repair), has revolutionized chromatin biology. Combining these molecular approaches and classical cytological studies with modelling approaches promises to answer

these questions, while taking nucleus-to-nucleus variability and the stochasticity of nuclear processes into account.

In *A. thaliana*, most cytological studies have been performed on 2D nuclei. However, the number of 3D approaches is rapidly increasing, and this increase calls for a change in perspective and tools. The principles that govern plant heterochromatin organisation are slowly emerging. It will be interesting to determine whether these principles, which were established in a diploid model plant, extend to plants with complex and large genomes containing large heterochromatin fractions. The repertoire of known plant nuclear compartments has expanded tremendously with the description of their components. However, the mechanisms underlying their assembly and functions are still poorly understood, as is their functional interplay particularly with the 3D conformation of the plant genome.

The complex and intricate interplay between nuclear components, nuclear architecture, and genome functions remains to be further investigated. We predict that much will be learnt about the interphase plant nucleus and its dynamics in the coming years, and that this knowledge will hinge on intense interdisciplinary dialogues on subjects ranging from biophysics and modelling to imaging and cytology.

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