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Chromosome organisation during ageing and senescence

Tamir Chandra[1,2] and Kristina Kirschner[3]

Acute cellular stress caused by oncogene activation or high levels of DNA damage can engage a tumour suppressive response, which can lead to cellular senescence. Chronic cellular stress evoked by low levels of DNA damage or telomere erosion is involved in the ageing process. In oncogene induced senescence in fibroblasts, a dramatic rearrangement of heterochromatin into foci and accumulation of constitutive heterochromatin is well documented. In contrast, a loss of heterochromatin has been described in replicative senescence and premature ageing syndromes. The distinct nuclear phenotypes that accompany the stress response highlight the differences between acute and chronic stress models, and this review will address the differences and similarities between these models with a focus on chromosome organisation and heterochromatin.

Addresses
[1] Epigenetics Programme, The Babraham Institute, Cambridge CB22 3AT, UK
[2] The Wellcome Trust Sanger Institute, Cambridge CB10 1SA, UK
[3] Cambridge Institute for Medical Research, Wellcome Trust/MRC Stem Cell Institute and Department of Haematology, University of Cambridge, Hills Road, Cambridge CB2 0XY, UK

Corresponding authors: Chandra, Tamir (tamir.chandra@babraham.ac.uk) and Kirschner, Kristina (kk429@cam.ac.uk)

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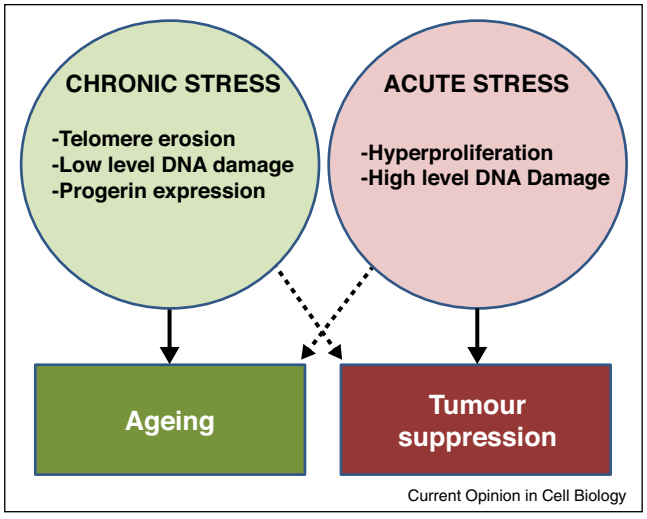
Introduction

Cellular senescence describes the response of a cell to cellular stress, which is mostly linked to genotoxic stress or DNA damage [1–5]. However, the senescence stress response can be very heterogeneous depending on the way the stress is induced. A useful working model of classifying stress responses has been by dividing them into models where damage accumulates slowly over months and years, such as in replicative senescence; and acute stress models that evoke a senescence response within hours, such as oncogene induced senescence (OIS) (Figure 1). The exact event downstream of oncogene activation triggering the senescence response is still debated. However, oncogene activation can lead to complete senescence of a fibroblast population in 48 hours in the presence of ectopic telomerase [6]. This distinction between chronic and acute stress models allows comparisons to stress situations that might not be considered senescence models per se, such as premature ageing (progeroid) syndromes, which can be considered chronic stress situations based on their slow kinetics. In addition there are many lines of evidence linking progeroid syndromes and cellular senescence [7,8,9••]. Werner syndrome is an adult onset premature ageing syndrome caused by mutations in the Wrn DNA helicase gene, leading to increased levels of DNA damage in patients [10••]. Mesenchymal stem cells (MSCs) derived from Wrn null (−/−) embryonic stem cells display a pronounced senescence phenotype upon serial passaging *in vitro* and in stem cell transplantation experiments [10••]. Hutchinson–Gilford progeria syndrome (HGPS or progeria) is caused by a mutation in the lamin A (LMNA) gene and manifests in early childhood [11,12]. Cells from HGPS patients show many hallmarks of senescence such as elevated DNA damage levels and telomere attrition [9••,13,14]. As such, chronic stress situations have mostly been studied in the context of cellular ageing, whereas acute models have served to understand the tumour suppressive role of senescence [15]. While the distinction between stress situations and phenotype seems useful, there have been interesting observations suggesting a crosstalk between the two (indicated by the dashed arrows in Figure 1). One example of such cross-talk is a recently discovered barrier to oncogenic transformation in progeroid cells [16•].

The way that senescence or chronic cellular stress contributes to organismal ageing is not fully understood. However, there is evidence for at least two independent scenarios in which senescence has been implicated in ageing. The p53 and INK4a/ARF loci have long been associated with senescence and there is emerging evidence that both loci are implicated in organismal ageing via deregulation of the stem cell pool [15]. Chronic hyperactivation of p53 was shown to result in reduced proliferation of haematopoietic stem cells (HSC) upon stress through transplantation experiments [17]. However, there is also evidence that the role of p53 activation in ageing might be more complex [18]. With age, increased DNA damage and p16Ink4a expression leads to a reduction in HSC cell cycle activity [19,20]. Environmental stress or cells reaching their replicative life span stimulate

Figure 1



Chronic (green) and acute stress (red) induced DNA damage leads to different cell fate choice. In the schematic the circles represent the two different types of stress with selected underlying causes. Chronic stress is characterised through slow kinetics and a gradual accumulation of damage, which has mostly been studied in the context of ageing on the cellular and organismal level (left hand side of diagram). In contrast, oncogene activation and subsequent hyperproliferation or high level DNA damage activate an acute stress response, leading to senescence as part of the organismal tumour suppressive response (right hand side of the diagram). However, crosstalk between the two models exist (dashed arrows), for example through progeria mediated resistance to transformation by inhibiting oncogenic dedifferentiation.

stem cells to replenish the pool of somatic cells. As an organism ages, or in chronic stress situations, the stem cell pool is functionally diminished and therefore unable to reconstitute tissue (Figure 1). Slow kinetics characterise this process, with the rate of senescence determining the rate of stem cell exhaustion.

Another way senescence has been implicated in ageing is through its senescence associated secretory phenotype (SASP), which is characterised by secretion of cytokines and matrix-metallo-proteases [21–23]. SASP functions in two ways: it reinforces the senescence response in neighbouring cells through its secretome and it recruits immune cells to clear senescent cells. However, senescent cells that are not cleared can contribute to age-related pathologies over time, most likely through chronic inflammation triggered by their SASP response (Figure 1) [15]. Indeed it seems that some age related pathologies can be alleviated by eliminating p16Ink4a senescent cells from tissue [24].

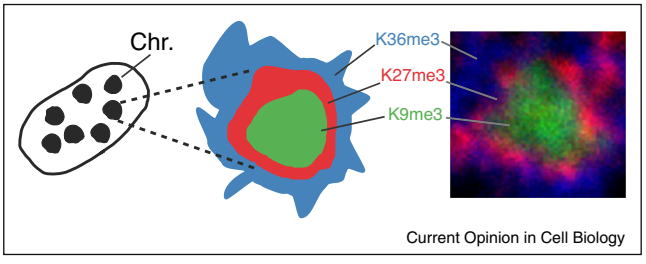
Nuclear organisation and constitutive heterochromatin (cHC)

The distinct nuclear phenotypes that accompany the stress response highlight the differences between acute and chronic stress models, and this review will address the differences and similarities between these models with a focus on chromosome organisation and heterochromatin. Although a role for cHC and the nuclear architecture in cellular ageing was first proposed nearly 20 years ago [25], the concept received spotlight attention in 2003 due to the discovery that HGPS is caused by mutations in the LMNA gene [11,12]. In the same year a new nuclear phenotype was described in cells undergoing oncogene-induced senescence and other forms of acute stress and was named for its spotty pattern of heterochromatic domains: senescence associated heterochromatic foci (SAHF) (Figure 2) [26]. Mapping heterochromatic markers revealed striking differences in the fate of cHC marks: a loss in chronic stress situations [27–29] and an accumulation during stress induced senescence [26].

Acute stress: SAHF positive cells

SAHF formation in senescent cells is a striking nuclear phenotype (see Figure 2), which leads to the formation of 4',6-diamidino-2-phenylindole (DAPI) intense foci. Studies using chromosome painting have revealed that each focus consists of exactly one chromosome [30,31,32•]. The core area of the SAHF is enriched with markers for constitutive heterochromatin such as Histone 3 lysine 9 trimethylation (H3K9me3), heterochromatin protein 1 (HP1) and macro Histone 2A (mH2A) [26,33], whereas the SAHF periphery is enriched with the facultative heterochromatin mark Histone 3 lysine 27 trimethyl (H3K27me3) [32•]. Euchromatic regions can be found outside the DAPI intense focus and the H3K27me3 ring. Figure 2 depicts the overall architecture of SAHF [32•,34]. The geometry of chromatin domains therefore

Figure 2



Senescent chromosomes form senescence associated heterochromatic foci (SAHF), which show a segregation and clustering of different chromatin types. On the left a schematic of a SAHF positive nucleus is drawn as it would appear after being stained by DAPI (black). Each of the foci represents a SAHF, which represents an individual chromosome (Chr). One of the foci is schematically enlarged to visualise the multilayer chromatin structure found in SAHF (center). To the right, an immuno-fluorescently stained SAHF is shown for comparison. The chromatin types are represented here through histone modifications. The core of the SAHF is enriched in H3K9me3 (green, constitutive heterochromatin). A ring at the periphery of the SAHF is enriched in H3K27me3 (red, facultative heterochromatin/polycomb silencing). Active euchromatin can be found outside the SAHF and is shown by H3K36me3 (blue).

seems inversed when compared to proliferating cells, where the heterochromatin is found in the periphery of chromosomal territories [35]. Initial theories surrounding the function of SAHF speculated that SAHF might be the result of *de novo* heterochromatin formation in euchromatic areas, for example for the silencing of cell cycle genes. However, through ChIP-seq and DNA labelling studies it has been shown that the heterochromatic regions forming the core of the SAHF are not *de novo* heterochromatic regions, but are the same regions that form the heterochromatin in proliferating cells, at least on a global level [32•]. In agreement with this finding, SAHF positive cells show a loss of heterochromatin at the nuclear periphery under the electron microscope and SAHF are found away from the nuclear lamina [32•,36••]. The nuclear lamina forms a mesh that supports the structural integrity and shape of the nucleus. In addition it serves as scaffold for coordinating other key events within the nucleus such as transcription and DNA replication [37,38]. The key structural components of the lamina are Lamins A/C and B and the loss of Lamin B1 (LMNB1) in senescence might be responsible for the detachment from the nuclear periphery [36••,39,40]. It has also been shown that LMNB1 reduction is a requirement, although not sufficient, for SAHF formation [36••]. While mapping of LMNB1 through ChIP-seq studies confirmed a global loss of LMNB1 on heterochromatic areas in senescence, it also identified a small region of the genome (2%) with increased levels of LMNB1 [36••]. Interestingly, fluorescence *in situ* hybridisation (FISH) studies suggested that these regions with increasing LMNB1 levels show a tendency to reposition towards the nuclear lamina and might be involved in gene silencing in senescence [36••,41••]. In OIS, SAHF formation and destabilisation of the lamina are completed within hours/days and how this dynamic change occurs is not well understood, however a recent study has shown an active and specific involvement of the autophagy machinery in turning over the nuclear lamina [42••].

Chronic stress: replicative senescence and progeroid syndromes

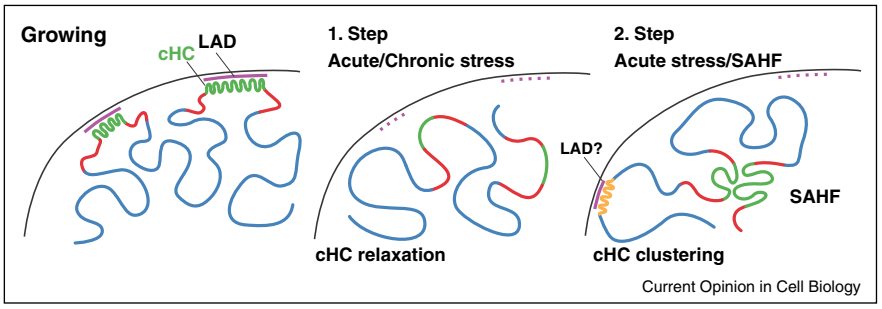
Dramatic changes to the nuclear lamina and nuclear morphology are also the hallmark of HGPS. The expression of mutant LMNA, called progerin, prevents an important step in the processing of LMNA from occurring and leads to a permanently farnesylated form of LMNA, which seems to be immobilised at the nuclear periphery [43]. How progerin causes changes in the lamina and how these changes relate to nuclear defects is not entirely understood and is discussed in more depth in other review articles [44,45]. However, the repositioning of heterochromatin from the nuclear periphery is also seen in HGPS and seems to be achieved through independent mechanisms: by LMNA mutation in HGPS and LMNB1 downregulation in SAHF positive cells. In addition, the progeroid nucleus shows a global loss of heterochromatic marks, such as H3K9me3 and H3K27me3, and similar reductions have been observed in replicative senescence and in cells from older individuals [27,28,46]. A loss of heterochromatic marks has also been noted in a Werner syndrome model, WRN−/− MSCs [10••]. The loss of heterochromatic marks in HGPS, Wrn knockout cells and replicative senescence is in stark contrast to the perceived increase in heterochromatin based on the DAPI intensity in SAHF positive cells and the increase in heterochromatin proteins (HP1) on senescent chromatin [26].

Heterochromatin relaxation in chronic and acute stress responses

Heterochromatin can be defined either by its enrichment by marker proteins or by its structural properties. One approach that maps the structural properties of the genome is the Hi-C technology [47], which has been used on SAHF positive (~86%) senescent cells to shed light on the seemingly contradictory roles of heterochromatin in chronic stress models and SAHF formation [41••]. In proliferating cells, constitutive heterochromatic regions display the highest amount of internal contacts, measured by Hi-C, when compared to other regions in the genome. Hi-C data in SAHF positive cells show a loss of local interactions within constitutive heterochromatic domains. These domains can be further identified by their low GC content and their lamin association in proliferating cells [41••,48]. FISH experiments measuring the compaction of changing heterochromatin suggest that the loss of local interactions leads to a relaxation of these domains. This observation is contrary to the previously held view of enhanced heterochromatin in SAHF formation. Despite the increase in heterochromatic marks in SAHF positive cells, the heterochromatin seems to relax on a structural level. Notably, in Hi-C data from HGPS, heterochromatic domains show a similar tendency as observed for the SAHF positive cells [41••,49•]. In addition late passage HGPS cells show a global loss of genome structure, such as the partitioning into active and inactive domains [49•]. SAHF cells also show long-range clustering of large cHC domains along the chromosome, which may reflect the clustering of constitutive heterochromatin in the core of the SAHF. Indeed, HGPS cells, devoid of SAHF formation do not show clustering of HC domains (see Figure 3) [41••].

While the observation that heterochromatin relaxes in OIS was unexpected it aligned well with the observation that high mobility group A (HMGA) proteins, which stabilise a more open chromatin conformation, are among the most dramatically enriched proteins in oncogene-induced senescent chromatin reaching an abundance similar to core histones [50,51]. HMGA1/2 knockdown almost completely blocks SAHF formation. Knockdown in an OIS population reduces the number of SAHF positive cells suggesting that this plays a role in SAHF maintenance [32•,50]. Their described function as architectural proteins and abundance

Figure 3



A two-step model for heterochromatin dynamics in chronic and acute cellular stress. Depicted on the left is the nuclear periphery of a proliferating cell. Lamin associated domains (LADs), consist of compacted constitutive heterochromatin (cHC, green) and are attached to the nuclear lamina (purple). H3K27me3 (red) often flanks the cHC in LADs. Euchromatic regions are shown in blue. As an initial stress response in acute (for example oncogene activation) and chronic stress (for example progeria and replicative senescence) LADs detach from the lamina (purple) and it comes to a relaxation of the heterochromatin (green). In this model, Step 1 presents the endpoint for chronic stress response, whereas it might be an intermediate step for SAHF forming cells. Step 2 shows the spatial clustering of cHC (green domains coming together) as suggested for SAHF positive cells. A set of unexplored regions in the genome (2%) gain LMNB1 and move towards the periphery in SAHF positive cells (yellow, LAD?).

of HMGA1/2 proteins suggest that they might be structural components of SAHF. Ectopic HMGA1/2 expression works synergistically with LMNB1 knockdown to induce some *de novo* SAHF formation [36••]. HMGA1/2 might compete with the linker histone 1 (H1) for the same niche in the genome, as both proteins preferentially bind to the minor groove of AT-rich DNA [51]. Notably, H1 is absent on senescent chromatin [30]. To our knowledge HMGA has not been studied in chronic stress situations, such as replicative senescence or progeria. Other factors involved in SAHF formation including histone chaperones and histone variants have been reviewed recently and go beyond the scope of this review [52,53].

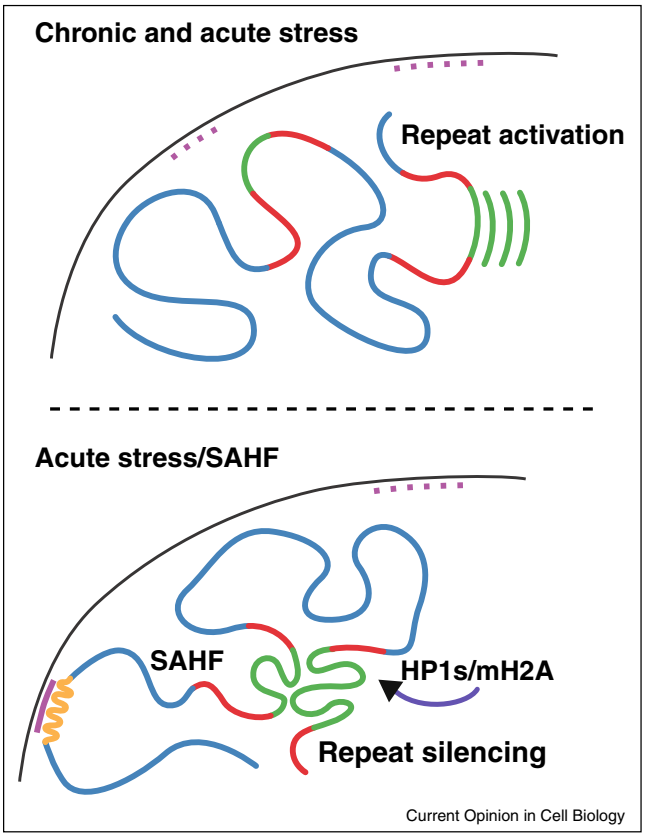
The observation that heterochromatin might be relaxing in senescence aligns well with the finding that heterochromatic alpha-satellite and satellite II repeats relax in senescence. This process is termed senescence associated distension of satellites (SADS) and has been described as an early event in a variety of senescence models and HGPS cells [54,55]. In addition, extensive transcription and retro-transposition of Long Interspersed Nuclear Elements (LINEs) has been described in replicative senescence, partially mediated through downregulation of Sirtuin 6 (SIRT6) [56–59]. However no upregulation of repeats has been reported for acute senescence systems with a high number of SAHF positive cells. In addition our preliminary data do not show LINE activation in OIS cells.

Discussion

In this review we compare the different nuclear phenotypes that accompany chronic and acute cellular stress responses, such as replicative senescence and progeria (chronic), and oncogene induced senescence (acute). While these models agree on a number of key insights, the role of constitutive heterochromatin (cHC) had been controversial, with chronic stress models showing a reduction and acute stress models showing an increase in cHC based on analysis of marker proteins [27–29]. Recent work has examined changes in nuclear architecture by genome-wide sequencing (using Hi-C), which has led to the finding that architectural changes are conserved between Hutchinson–Gilford progeria and OIS, resulting in a relaxation of the cHC compartment in both [41••]. Another recent study found a loss of cHC in Werner Syndrome, an adult onset progeria so far associated with genome instability [10••]. The common architectural changes in the cHC compartment, achieved through independent mechanisms (for example dysfunctional LMNA in progeria and LMNB1 degradation in OIS) point towards a functional role for the relaxation of the cHC compartment in cellular stress and ageing. However, we currently do not know what that function might be. One possible scenario was proposed in a recent study showing the activation and transposition of LINE elements in replicative senescence. These retrotransposition events may be a mechanism to induce or amplify a DNA damage signalling cascade, thereby inducing or reinforcing senescence [56,57].

In contrast to cHC relaxation being found in chronic and acute stress, spatial clustering of heterochromatic regions and an upregulation of heterochromatin proteins seems SAHF specific, suggesting a second step unique to acute stress induced senescence (see Figure 3). A possible scenario that would also explain the difference in the upregulation of heterochromatic markers, such as HP1 and macroH2A, could be that SAHF formation acts as a compensatory mechanism to maintain or re-silence repetitive elements (Figure 4). More precisely the relaxation of cHC domains could trigger the rise of chromatin bound HP1 and macroH2A, which might lead to the spatial clustering of cHC domains to maintain heterochromatic silencing, which might result in the SAHF phenotype.

Figure 4



Tentative model for the involvement of SAHF formation in compensating heterochromatin relaxation and repeat activation. Decompaction of heterochromatic regions involved in the silencing of satellite repeats has been suggested as an early event for all types of senescence. In addition transcriptional activation of LINE elements has been shown for replicative senescence, but has not been found in acute stress, such as oncogene induced senescence. The upper nucleus in the figure depicts the detached and decompacted heterochromatin, including the activation of repeats during the initial stress response (green, see also Figure 3). The lower nucleus shows a speculative role for SAHF formation in compensating the repeat activation. SAHF formation is represented here through the influx of heterochromatin associated markers (heterochromatin proteins and the macroH2A histone shown here in purple) and the spatial clustering of heterochromatic regions (green).

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- •• of outstanding interest

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