

# Chapter 13

## Stress-Induced (Premature) Senescence

Florence Debacq-Chainiaux, Randa Ben Ameer, Emilie Bauwens, Elise Dumortier, Marie Toutfaire, and Olivier Toussaint

**Abstract** Three main roads lead to senescence: telomere-dependent replicative senescence, oncogene-induced senescence and stress-induced (premature) senescence. This latter type of senescence appears after exposure of normal, immortalized or transformed cells to stress of chemical or physical nature inducing oxidative stress and/or DNA damage. After these exposures, chronic or acute, single or multiple, stressed cells developed a “senescence-like” phenotype. This “senescence-like” phenotype presents several biomarkers of cellular senescence such as irreversible growth arrest, morphological change, senescence-associated  $\beta$ -galactosidase (SA- $\beta$ gal) activity and senescence-associated secretory phenotype (SASP). However, large-scale studies of transcriptome and proteome of cells in replicative senescence or in stress-induced senescence show that although they share similarities, the two phenotypes are not identical. Different signaling pathways involved in the development of stress-induced senescence are presented as those dependent on TGF- $\beta$ 1, p38<sup>MAPK</sup>, IGF-R1 and DNA damage. The possible induction of this type of senescence *in vivo* and in cancer treatment is discussed.

**Keywords** Replicative senescence • Cell cycle • Stress • SIPS • Oxidation • DNA damage • Telomeres

### 13.1 Introduction

Ageing is characterized by a progressive functional decline, leading to increased risk of developing major human pathologies, such as cardiovascular disorders, cancer, diabetes and neurodegenerative diseases. Nine hallmarks of ageing have been established, including cellular senescence (Lopez-Otin et al. 2013). Cellular senescence, first described *in vitro* in normal human diploid fibroblasts (HDFs)

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F. Debacq-Chainiaux (✉) • R. Ben Ameer • E. Bauwens • E. Dumortier • M. Toutfaire  
O. Toussaint  
NARILIS-URBC, University of Namur, Namur, Belgium  
e-mail: [florence.chainiaux@unamur.be](mailto:florence.chainiaux@unamur.be)

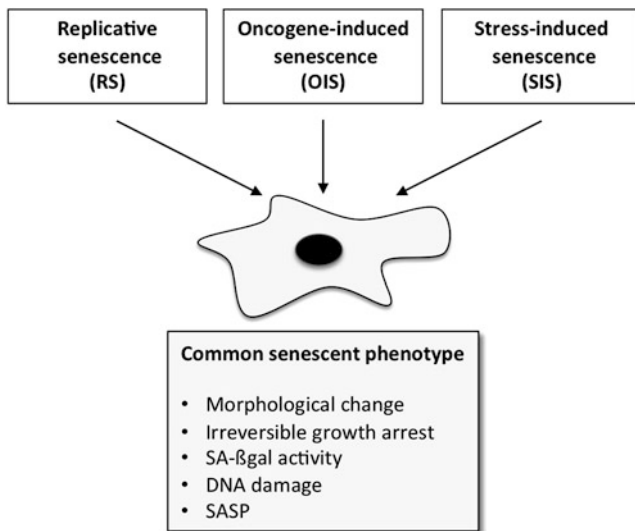
by L. Hayflick in the early 1960s, is defined as an irreversible arrest of the cellular divisions and for this reason also called “replicative senescence” (RS) (Hayflick and Moorhead 1961). Almost 30 years later, it was shown that this type of senescence is associated with a « critical » shortening of the telomeres after extensive proliferation in the absence of endogenous telomerase activity (Harley et al. 1990).

After the discovery of cellular senescence, studies were performed to characterize the senescent phenotype and to identify specific biomarkers that allow to distinguish senescent cells from other non-dividing cells (such as quiescent or terminally differentiated cells). Senescence-associated biomarkers are among others typical morphology (Bayreuther et al. 1988), irreversible growth arrest with overexpression of p21<sup>WAF-1</sup> and p16<sup>INK-4a</sup> (Alcorta et al. 1996; Sherr and Roberts 1999), senescence-associated beta-galactosidase activity (SA-βgal) (Dimri et al. 1995), altered gene expression (Dumont et al. 2000b), senescence-associated heterochromatin foci (SAHFs) and senescence-associated DNA-damage foci (SDFs) (d’Adda di Fagagna et al. 2003) and lamin B1 loss (Freund et al. 2012). Using some of these biomarkers such as SA-βgal and p16<sup>INK-4a</sup> overexpression, it was demonstrated that senescent cells accumulate in tissues with age (Dimri et al. 1995; Ressler et al. 2006).

The role of senescent cells *in vivo* is still unclear, but from their discovery, it has been speculated that they may be involved in the functional decline associated with ageing. In 2011, Baker et al. (2011) demonstrated that clearance of senescent cells in mice delays ageing-associated disorders as cataract and muscular mass loss, demonstrating the impact of senescent cells on their cellular and matrix environment and on tissue function. This impact is more than probably related to their ability to secrete a variety of factors such as inflammatory cytokines, metalloproteinases and growth factors, identified as the senescence-associated secretory phenotype (SASP) (Coppe et al. 2008).

### 13.2 Different Types of Senescence

Many studies have shown that multiple ways can lead to senescence or at least to a “senescence-like” phenotype. Senescence can be induced by multiple stimuli such as shortened or dysfunctional telomeres, excessive mitogenic signals (including those produced by oncogenes) and stress. Three major types of senescence may thus be highlighted: replicative senescence or telomere-dependent senescence, oncogene-induced senescence and stress-induced (premature) senescence. These three types of senescence share a common senescent phenotype, as highlighted by the appearance of senescence-associated biomarkers (Fig. 13.1).



**Fig. 13.1** Replicative senescence, oncogene-induced senescence and stress-induced senescence share a common senescent phenotype presenting several of the so-called senescence-associated biomarkers

### 13.2.1 *Replicative Senescence or Telomere-Dependent Senescence*

Replicative senescence is intimately linked to telomere shortening. Telomeres are sequences of repetitive DNA (5'-TTAGGG-3' in vertebrates) located at the extremities of linear chromosomes and associated to telomere-specific protein complex, also known as shelterin/telosome, including TRF1, TRF2, TIN2, POT1, TPP1 and hRAP1 (for a review: Palm and de Lange 2008). Length of telomeres are shortened after each cellular division, this is inherently linked to the activity of the DNA polymerase which is not able to completely replicate one strand of DNA, also referred as the « end-replication problem » (Harley et al. 1990). This leads to critically short and dysfunctional telomeres, which are sensed by the cells as double-strand breaks (DSBs). There follows activation of a classical DNA-damage response (DDR) inducing activation of upstream kinases as ataxia telangectasia mutated (ATM) and ATM and Rad-3 related (ATR), DNA-damage adaptator proteins as MDC1 (mediator of DNA-damage checkpoint protein-1), 53BP1 (p53-binding protein-1), BRCA1 (breast cancer type-1 susceptibility protein) and claspin, downstream kinases such as checkpoint-1 and -2 (CHK1 and CHK2) and finally effectors proteins as p53, CDC25 and SMC1 (structural maintenance of chromosomes protein-1). This activated pathway induces cell cycle arrest, mainly by phosphorylating p53, activating the expression of p21<sup>WAF-1</sup> inhibiting CDK-cyclin complexes and triggering DNA repair (Campisi and d'Adda di Fagagna 2007; d'Adda di Fagagna et al. 2003).

### 13.2.2 *Oncogene-Induced Senescence*

Oncogenes are mutant version of normal genes that have the potential to transform cells in combination with additional mutations, notably leading to inactivation of tumor-suppressor genes such as p53 or p16<sup>ink-4a</sup>. Oncogenes activation was shown to induce senescence in normal cells. This response was presented as a way to prevent oncogenic transformation. This was first observed by the expression of oncogenic *ras* (*H-RAS*<sup>G<sup>V12</sup></sup>) form in normal fibroblasts leading to growth arrest and SA-βgal activity (Serrano et al. 1997), independently of the telomere shortening (Wei and Sedivy 1999). Oncogene-induced senescence (OIS) has been displayed by many oncogenes *in vitro* and *in vivo* including members of Ras signalling pathway as *N-Ras*, *Raf*, *BRAF*<sup>E600</sup> (for a review: Gorgoulis and Halazonetis 2010). Senescence can also be induced by the expression of mutated form of tumor suppressor genes like *PTEN*, *VHL*, *RBI*, and *NF-1* leading to their inactivation (Nardella et al. 2011).

### 13.2.3 *Stress-Induced Senescence: Premature or Not?*

Senescence can finally appear after exposure of normal, immortalized or transformed cells to stress from physical or chemical agents inducing oxidative stress and/or DNA damage. This was called « Stress Induced Premature Senescence » or SIPS (Toussaint et al. 2000). “Premature” refers that senescence following stress occurs at earlier population doublings (PDs) than the maximum number of PDs at which appears usually replicative senescence. “Premature” emphasizes the accelerated nature of the process. However, the use of the “premature” term may be questionable.

First because the *in vitro* cell culture conditions are still not ideal and that the definition of a “classical” number of passages at which cells enter in senescence is dependent of many variables of cell culture conditions. For instance current cell culture conditions consist in maintaining cells at atmospheric oxygen concentration (21 %). However, *in vivo*, cells are exposed to a reduced oxygen concentration ranging between tissues from 3 to 4 % in the brain (Dings et al. 1998), 3–7 % in the muscles (Vedsted et al. 2006), 5–7 % in the dermis and 16–19 % in the epidermis (Stucker et al. 2002). HDFs maintained in culture at a more physiological/reduced oxygen pressure, are able to achieve more passages before undergoing replicative senescence than cells maintained at atmospheric partial oxygen pressure (Packer and Fuehr 1977). From then on, one may wonder what the standard is and if the cells maintained at 21 % oxygen are not themselves subject to some oxidative stress (Toussaint et al. 2011). We understand here the difficulty of setting a classical or a premature onset of senescence. However, the culture conditions are identical between stressed and control cells, “premature” insists on the quickening of the process between the two conditions.

Second, transformed cells are also able to undergo senescence after stress. The mechanisms of growth arrest might be extremely different between cancer cells,

whose cycle is by definition deregulated for many possible reasons, and normal cells exposed to stressful agents. In that case, can we really speak of “premature” senescence, since these cells, by nature, do not enter in senescence?

These examples, beyond the debate on whether the use of the term “premature” is adequate, demonstrate the multiplicity of senescence-like phenotypes. To encompass all forms of senescence induced by stress, it therefore seems more prudent in this review to talk about “stress-induced senescence” or SIS (Dierick et al. 2003; Hornsby 2010).

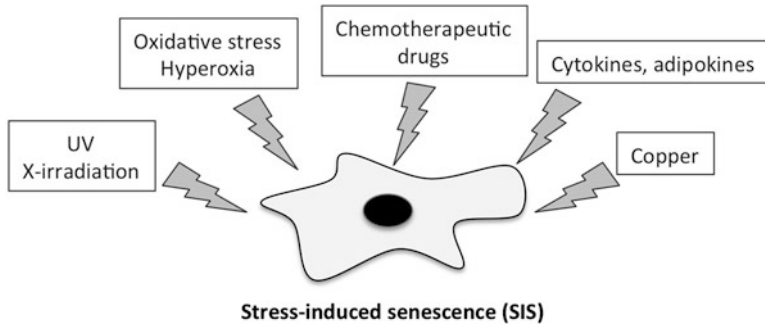
### 13.3 Models of Stress-Induced Senescence

*In vivo*, cells are continuously exposed to different types of stress. Depending on the nature of the stress, its intensity and the cell type, stressed cells can select one of the three main tracks: repair, die or senesce. If the intensity of the stress is low, the cell can repair damage and after a transient cell cycle arrest, resumes its growth. If the stress is intense, apoptosis will be privileged. There is therefore a “moderate” stress zone for which cells exposed to high stress, but still in the subcytotoxic range, will not be able to repair all damage caused by the stress. With reference to the thermodynamic theory of far from equilibrium open systems, cells will drop to a lower steady state of internal entropy (with lower metabolic activity) and if exceeded, its cell cycle will be irreversibly arrested and cells will enter in premature senescence (Toussaint et al. 2002).

Potentially almost any stress from chemical or physical nature can induce cells to undergo senescence by provoking increased oxidative stress and/or DNA damage. Per se, the types of stress that can induce senescence seem infinite and many models of SIS exist which will not be possible to list here. However, we can describe the main classes of stress models that can induce stress-induced senescence: physical stress (UV and X-irradiation), oxidizing agents and hyperoxia, cytokines/adipokines, chemotherapeutic drugs and copper (Fig. 13.2). In the different models, the conditions used reduce the growth rate and the maximum obtainable cumulative population doublings (CPDs) of cells and induce the appearance of senescence-associated biomarkers.

Cellular senescence can be induced by both chronic or acute stress protocols in different cell types such as normal HDFs, endothelial cells, melanocytes and transformed cells. Both protocols use sublethal concentrations of stressors, in accordance with theoretical studies based on the stability of cellular systems (Toussaint et al. 1991).

Chronic stress protocols consist of treating different human cell types with prolonged exposure (several weeks) to a stressor like mild hyperoxia in HDFs (with oxygen partial concentration around 40 %) (von Zglinicki et al. 1995, 2000), chronic exposure of endothelial cells to homocysteine (Xu et al. 2000), prolonged culture of human umbilical vein endothelial cells on glycated collagen (Chen et al. 2002) and chronic exposure of colon fibroblasts to selenite (Rudolf et al. 2014).



**Fig. 13.2** Several types of stress can induce stress-induced senescence (SIS)

In the second type of protocol, cells, such as HDFs, at early CPDs are exposed once or several times to acute sublethal stress such as a unique  $\text{H}_2\text{O}_2$  exposure (Chen and Ames 1994) or a repeated exposure to *tert*-butylhydroperoxide (*t*-BHP) (Dumont et al. 2000b). The use of repeated sublethal stresses allow reducing the concentration of the stressor necessary to trigger stress-induced senescence. The major advantage of this type of protocol is that the induction of senescence can be studied relatively independently from purely adaptive responses, if the cells are allowed to recover for at least 3 days after the stress before analysis of biomarkers of senescence and if the repetition of stresses increases the fraction of cells undergoing stress-induced senescence (Toussaint et al. 2000).

Among the different models of existing SIS, some are based on physical stress such as ionizing radiation of endothelial cells (ECs) (Igarashi et al. 2007; Pangani-ban et al. 2013), exposure of HDFs or melanocytes to UV light (Rodemann 1989; Debacq-Chainiaux et al. 2005; Medrano et al. 1995), to psoralen pre-treatment and UVA exposure (pUVA) (Ma et al. 2002) and to electromagnetic fields (Rodemann et al. 1989b) and exposure of human mesenchymal stem cells to sublethal heat shock (Aleksenko et al. 2014).

Other models induce oxidative stress as in HDFs exposed to chronic hyperoxia or to acute subcytotoxic exposure to oxidizing agents such as  $\text{H}_2\text{O}_2$  or *t*-BHP (Chen and Ames 1994; Dumont et al. 2000a; von Zglinicki et al. 1995).

Stress-induced senescence can also be provoked by stimulating cells with cytokines or adipokines like repeated stimulation of lung HDFs or endothelial cells with interleukin-1 $\alpha$  (IL-1 $\alpha$ ), tumor-necrosis factor- $\alpha$  (TNF- $\alpha$ ) (Dumont et al. 2000a), transforming growth factor-beta 1 (TGF- $\beta$ 1) (Debacq-Chainiaux et al. 2005, 2008; Fripiat et al. 2001) and visfatin/Nampt (Villalobos et al. 2014).

Senescence can also be induced by subcytotoxic doses of drugs and in particular chemotherapeutic drugs such as mitomycin C (Rodemann 1989), cisplatin (Berndtsson et al. 2007), etoposide (Chiu et al. 2005) and doxorubicin (Maejima et al. 2008; Piegari et al. 2013).

Finally, premature senescence appears by incubating HDFs with copper (Cu), which itself accumulates in cells during replicative senescence. Incubation of HDFs with copper sulphate ( $\text{CuSO}_4$ ) for 16 h induces the appearance of several senescence-associated biomarkers (Boilan et al. 2013; Matos et al. 2012). Conversely, iron-chelation using desferrioxamine mesylate induces growth arrest and the appearance of senescence-associated biomarkers in hepatocyte cell lines (Yoon et al. 2002).

## 13.4 Damage Induced by SIS

### 13.4.1 DNA Damage

DNA is a favourite target of stress, directly or indirectly. Many types of damage can be produced on DNA, but the most critical for the induction of senescence is double strand breaks (DSBs). Shortened and dysfunctional telomeres form similar structures of DSBs, inducing DDR pathway (Takai et al. 2003).

Several models of stress-induced senescence induced in normal or immortal cells by chemotherapeutic drugs (mitomycin C, bleomycin, actinomycin D) (Robles and Adami 1998) or ionizing radiation (X-irradiation) (Kim et al. 2014) generate DNA damage, including DSBs leading to senescence. Once DNA repair machinery detects DSBs, large protein complexes including in particular  $\gamma\text{H2Ax}$  and 53BP1 are recruited at the cleavage site and help to stabilize the damaged strands and to activate the repair process. If the damage is too important for repair, DDR pathway is activated and induces activation of p53 transcription factor and expression of p21<sup>WAF-1</sup>. The overexpression of p21<sup>WAF-1</sup> is transient and followed by a delayed induction of p16<sup>INK-4a</sup>, as it has been demonstrated in RS. The pathway leading to p16<sup>INK-4a</sup> overexpression after DNA damage is still unclear (Robles and Adami 1998) but could be linked to oxidative stress.

### 13.4.2 Oxidative Stress

Oxidative stress is probably the most often used inducer of stress-induced senescence. The link between replicative senescence and oxidative stress was clearly demonstrated by comparing the number of passages in culture performed under conditions of hypoxia or hyperoxia, and by the use of antioxidants and/or free radical scavengers as, for instance *N-tert-butyl-alpha-phenylnitron* (PBN). PBN is a biphasic antioxidant that is soluble in lipid and water, and is stable in cell culture media. Presenescent HDFs incubated with PBN are able to achieve between four and seven additional CPDs than untreated cells (von Zglinicki et al. 2000).

An increase of radical oxygen species (ROS) is highlighted in HDFs exposed to H<sub>2</sub>O<sub>2</sub>, UVB and copper (Boilan et al. 2013; Borlon et al. 2007; Zdanov et al. 2006b). The use of antioxidants as mannitol or trolox significantly reduces the appearance of senescence-associated biomarkers following copper incubation of HDFs (Boilan et al. 2013). Nrf-2 transcription factor is also activated in HDFs incubated with copper (Boilan et al. 2013).

An hypothesis to explain the expression of p16<sup>INK-4a</sup> after DNA damage is the induction of a second phase of stress after direct DNA damage via oxidative stress inducing accumulation of ROS, activation of p38<sup>MAPK</sup> and p16<sup>INK-4a</sup> overexpression (Hornsby 2010).

## 13.5 Cellular and Molecular Characteristics of SIS

### 13.5.1 Biomarkers of Senescence

Cells in stress-induced senescence share common features with replicative senescence as it was highlighted by the study of biomarkers of senescence.

Senescent cells are characterized by morphological change, they generally enlarge, often doubling in volume, and, if adherent, adopt a flattened morphology. Using the morphotypes classification of HDFs (Rodemann et al. 1989a), it was shown that after sublethal stress under H<sub>2</sub>O<sub>2</sub>, *t*-BHP, UV light, mitomycin C, etc., the treated HDFs acquired the morphological features of senescent HDFs (Chen and Ames 1994; Debacq-Chainiaux et al. 2005; Dumont et al. 2000b; Rodemann et al. 1989a).

Their growth is irreversibly arrested at the G1/S phase of the cell cycle due to the overexpression of several cyclin-dependant kinase inhibitors as p21<sup>waf-1</sup> and p16<sup>ink-4a</sup> and hypophosphorylation of the retinoblastoma protein (pRb) (Chen et al. 1998).

Senescence-associated β-galactosidase (SA-βgal) is a commonly used marker of senescent cells allowing to identify easily senescent cells both *in vitro* and *in vivo* (Dimri et al. 1995). This activity derives from the lysosomal β-galactosidase, overexpressed in senescent cells, and then detectable at a suboptimal pH (Kurz et al. 2000). After exposure to stress inducing senescence, proportion of cells positive for SA-βgal activity increases.

Mitochondrial DNA undergoes many changes during replicative senescence among which a 4977 bp « common » mitochondrial DNA deletion. This deletion is clearly detected in HDFs exposed to sublethal stresses with *t*-BHP or UVB (Debacq-Chainiaux et al. 2005; Dumont et al. 2000b).

HDFs in RS and in SIS induced by X-irradiation or by bleomycin display a highly correlated SASP including increased expression of IL-1β, IL-8, GROα and MMP-1 (Coppe et al. 2008; Bavik et al. 2006).



### 13.5.2 *Gene and Protein Expression: Are RS and SIS Identical Phenotypes?*

Senescent cells show striking changes in gene expression, including gene expression changes of cell-cycle effectors. Two cyclin-dependent kinase inhibitors (CDKIs) are often overexpressed in senescent cells:  $p21^{waf-1}$  (*CDKN1a*) and  $p16^{ink-4a}$  (*CDKN2a*). On the contrary, senescent cells can also repress genes that encode for cell-cycle activators as *c-fos*, *cyclin B* and *PCNA* (*proliferating cell nuclear antigen*).

But many changes in gene expression are unrelated to growth arrest. Senescent cells overexpress genes encoding secreted proteins that can alter the tissue microenvironment, for instance to remodel extracellular matrix or to mediate local inflammation (Campisi et al. 1996).

If similar gene expression change is observed in stress-induced senescence as overexpression of  $p21^{waf-1}$ ,  $p16^{ink-4a}$ , *apolipoprotein J*, *osteonectin* and *fibronectin* (Debacq-Chainiaux et al. 2005; Dumont et al. 2000b; Pascal et al. 2005), large-scale studies also show specific gene expression change associated either to replicative senescence or to stress-induced senescence (Pascal et al. 2005).

The study of the different biomarkers tends to show the similarities between the two phenotypes of RS and SIS. But are they identical phenotypes? To answer this question, the simple study of the presence of replicative senescence biomarkers after SIS was not enough. It was therefore necessary to achieve a more global comparison between these two phenotypes, through larger studies of gene and protein expression in both phenotypes.

Studies on global gene expression using differential display or cDNA microarray firstly confirmed the presence of genes whose expression is identically modified between RS and SIS, but also demonstrated that specific changes were associated either to RS or to SIS induced by *t*-BHP, ethanol,  $H_2O_2$  or bleomycin in HDFs (Pascal et al. 2005; Debacq-Chainiaux et al. 2008; Bavik et al. 2006). In parallel, a proteomic identification by mass spectrometry after two-dimensional gel electrophoresis (2DGE) came to the same conclusion on the comparison of the same models (Dierick et al. 2002). This observation was confirmed by a proteomic analysis of HDFs in RS and in  $H_2O_2$ -induced senescence (Aan et al. 2013). These results reinforced that despite displaying the so-called common biomarkers of senescence, RS and SIS are not alike.

These studies demonstrated that gene and protein expression changes of HDFs in SIS can be classified in three groups: firstly, the changes common with RS, secondly, the changes specific to each kind of stressor and thirdly, changes common to SIS induced by different stressors.

The specific changes related to one of several SIS models were presented as long-term effects of the stress and named “molecular scars”. These “molecular scars” might occur from a few days after the stress and be maintained at long term, after many types of stress (oxidative stress and/or DNA damage, inflammation) *in vitro* and *in vivo* (Dierick et al. 2003).

## 13.6 SIS, Telomeres and Telomerase

Telomere shortening, intimately linked to replicative senescence, is not always related to the induction of senescence after stress.

After chronic exposure to hyperoxia, telomeres are shortened five to ten times faster than normal (von Zglinicki et al. 1995). This increased shortening is due to accumulation of single-strand breaks in telomeres with hyperoxia, leading to faster telomere loss during DNA replication (von Zglinicki et al. 2000). Surprisingly, the presence of telomerase does not prevent telomere shortening due to oxidative stress, as shown in human endothelial cells with ectopically overexpressed telomerase (Kurz et al. 2004). This is linked to the export of *TERT*, the catalytic subunit of human telomerase, from the nucleus to mitochondria. *TERT*, once localized in mitochondria, protects mtDNA integrity (Ahmed et al. 2008).

In other models of SIS induced by H<sub>2</sub>O<sub>2</sub>, *t*-BHP or ionizing radiation, no increased telomere loss was brought out after stress whereas senescence biomarkers were well detected (Chen et al. 2001; Dumont et al. 2001; Suzuki et al. 2001).

Moreover, several HDFs strains expressing telomerase and exposed to subcytotoxic doses of H<sub>2</sub>O<sub>2</sub>, UV, UVB or  $\gamma$ -irradiation in conditions inducing senescence, displayed biomarkers of senescence (de Magalhaes et al. 2002; Gorbunova et al. 2002). This shows that telomere shortening is not detected systematically in all models of SIS and that SIS could be induced independently of telomere erosion.

## 13.7 Molecular Pathways

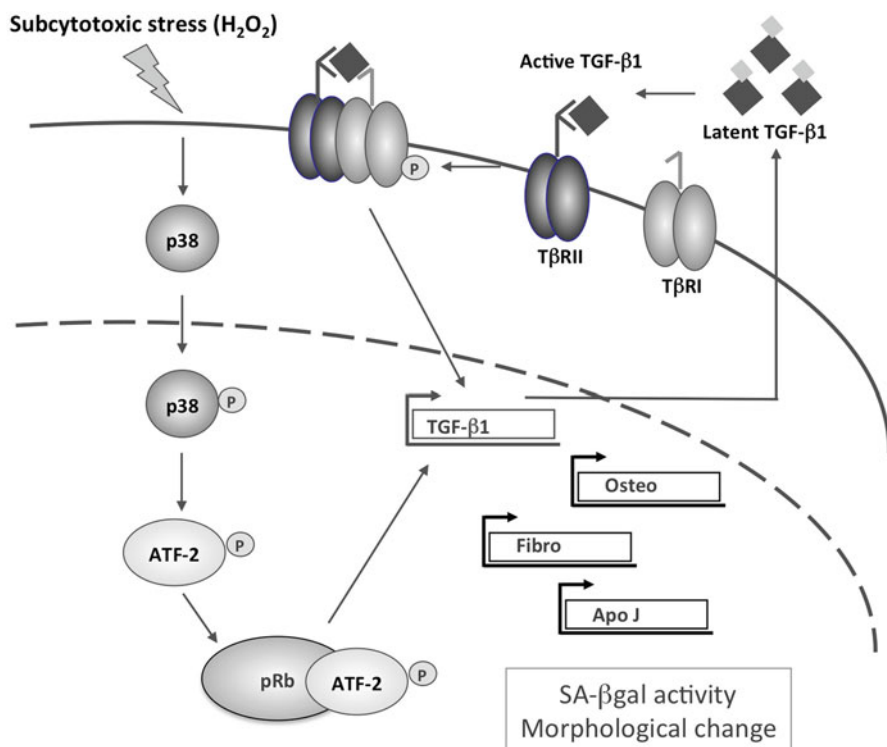
### 13.7.1 TGF- $\beta$ 1 Pathway

TGF- $\beta$ 1 (Transforming Growth Factor- $\beta$ 1) is overexpressed in skin and lung foetal HDFs after a single exposure to H<sub>2</sub>O<sub>2</sub> (Fripiat et al. 2001) and after a series of exposures to UVB (Debacq-Chainiaux et al. 2005), *t*-BHP or ethanol (Pascal et al. 2005). TGF- $\beta$ 1 overexpression is necessary for the overexpression of *apolipoprotein J*, *osteonectin*, *fibronectin* and *TGF- $\beta$ 1* itself, namely via a positive feedback on the activation of p38<sup>MAPK</sup> (Fripiat et al. 2002). Incubation of lung or skin HDFs with TGF- $\beta$ 1 for 3 days induces the same phenotype. If neutralizing antibodies directed against TGF- $\beta$ 1 or its receptor II (TBR<sub>II</sub>) are incubated with cells after the last stress inducing senescence, this blocks the appearance of the biomarkers of senescence (Fripiat et al. 2001). This has been confirmed in lung or skin HDFs in various models of SIS (*t*-BHP, ethanol (Debacq-Chainiaux et al. 2008) and UVB (Debacq-Chainiaux et al. 2005)), reinforcing the major role played by TGF- $\beta$ 1 activation in the SIS phenotype.

P38 Mitogen-activated protein kinase (MAPK) is activated in RS, in OIS induced by oncogenic Ras and in SIS induced by H<sub>2</sub>O<sub>2</sub>, UVB and X-irradiation (Debacq-Chainiaux et al. 2010; Wang et al. 2002; Freund et al. 2011). Activation of p38<sup>MAPK</sup> by phosphorylation is rapidly detected after the stress. Inhibition of p38<sup>MAPK</sup>

activity attenuates the increase of SA- $\beta$ gal positive cells and modifies the profiles of senescence-associated gene expression in  $H_2O_2$ -induced senescence (Zdanov et al. 2006a) and reduces the secretion of SASP factors in X-irradiation-induced senescence (Freund et al. 2011).

Once activated,  $p38^{MAPK}$  phosphorylates and activates ATF-2 transcription factor. ATF-2 is then responsible of *TGF- $\beta$ 1* overexpression and interacts with pRb (Frippiat et al. 2002). TGF- $\beta$ 1 protein is overexpressed both in latent and active forms and induces several biomarkers of senescence such as senescent morphology, SA- $\beta$ gal and senescence-associated gene expression (Debacq-Chainiaux et al. 2005; Frippiat et al. 2001), probably via downstream proteins as IGFBP-3 (Debacq-Chainiaux et al. 2008) (Fig. 13.3).



**Fig. 13.3** Activation of  $p38^{MAPK}$ , ATF-2 and TGF- $\beta$ 1 following  $H_2O_2$ -induced senescence.  $H_2O_2$  stress immediately activates  $p38^{MAPK}$  which is responsible of ATF-2 activation. Phosphorylated ATF-2 binds to hypophosphorylated pRb, which activates its transcription factor function, and is responsible for the overexpression of TGF- $\beta$ 1, increasing the secretion of its latent and active protein forms. Active TGF- $\beta$ 1 is able to bind to its receptors  $T\beta RI$  and  $T\beta RII$  (TGF- $\beta$  receptor I and II), leading to their interaction and phosphorylation. Activated TGF- $\beta$ 1 pathway is responsible for the overexpression of senescence-associated genes as *osteonectin* (*osteo*), *fibronectin* (*fibro*) and *apolipoprotein J* (*apo J*), of morphological change and SA- $\beta$ gal activity as demonstrated by using neutralizing antibodies against TGF- $\beta$ 1 or  $T\beta RII$

### 13.7.2 IGF-1R

Several studies have highlighted the role of insulin like growth factor-1 receptor (IGF-1R) in the induction of stress-induced senescence. IGF-1R is a transmembrane tyrosine kinase receptor activated by binding with its ligands IGF-1 and IGF-2, leading to the autophosphorylation of its cytoplasmic domain. This pathway is responsible for the activation of PI3K/Akt, MAPK and mTOR (for a review: Riedemann and Macaulay 2006). Ionizing radiation of human pulmonary artery endothelial cells (HPAEC) induces senescence-associated biomarkers, IGF-1 and IGF-2 overexpression and IGF-1R activation. Treatment of HPAEC cells with an IGF-1R inhibitor (AG1024) protects from ionizing radiation-induced senescence (Panganiban and Day 2013). It was also demonstrated that the presence of a functional IGF-1R receptor was required for the activation of the UVB-induced senescence in normal human keratinocytes (Lewis et al. 2008).

## 13.8 Stress-Induced Senescence *In Vivo*

It is well established that senescent cells accumulate in tissues with age, as shown by studying SA- $\beta$ gal activity and DNA damage (Dimri et al. 1995). These senescent cells could be involved in the functional decline associated with ageing as postulated by Hayflick at the time of the discovery of replicative senescence. Indeed, a link between senescent cells accumulating in tissues and ageing-associated disorders such as cataract and muscular mass loss has been shown in mice by Baker et al. (2011).

How do these senescent cells appear *in vivo* and accumulate with age? Do they appear by telomere-dependent senescence or by another mechanism? By performing a simple calculation of the number of cells that could generate the two first telomerase-negative cells, appearing during the *in vivo* differentiation, based on the number of generations that HDFs can achieve before reaching replicative senescence under physiological low O<sub>2</sub> partial pressure (80 PDs), 2<sup>80</sup> cells (>10<sup>24</sup> cells) must be produced before the first telomere-dependent replicatively senescent HDFs appear. Of course, to be correct, this extrapolation should also take account of the cellular turnover and of asymmetric divisions, but should also consider that more than two telomerase-negative cells will be generated by *in vivo* differentiation (Dierick et al. 2003).

*In vivo*, cells are exposed to a multitude of stresses whose nature depends on their location (pneumocytes facing air pollution and tobacco smoke; melanocytes, keratinocytes and skin HDFs facing UV; enterocytes facing food oxidants), particular conditions (endothelial cells facing inflammation, ischaemia/reperfusion, hypertension, shear stresses or diseases, etc.) and pathologies such as atherosclerosis, diabetes and age-related neurodegenerative diseases (for a review: Toussaint et al. 2002).

Chronic inflammation is associated to ageing and age-related diseases (Chung et al. 2009). This chronic inflammation could increase ROS accumulation and could induce appearance of senescent cells as detected by many studies in which premature appearance of cells presenting certain senescence-associated biomarkers in disease sites, including diseases subjected to chronic inflammation such as venous ulcers (Mendez et al. 1998), arteries subjected from balloon angioplasty (Fenton et al. 2001), emphysema (Muller et al. 2006), chronic hepatitis C and hepatocellular carcinoma (Paradis et al. 2001), prostatic hyperplasia (Choi et al. 2000) and intestinal metaplasia from the stomach (Going et al. 2002).

The premature appearance of these senescent cells could reinforce the inflammation by their SASP phenotype. This could lead to amplification of the phenomenon, worsen the inflammation and accelerate ageing. This hypothesis was confirmed recently *in vivo* in mice, in which chronic inflammation provoked by knockout of the *nfkb1* subunit of the transcription factor NF- $\kappa$ B induces telomere dysfunction and accelerates ageing (Jurk et al. 2014).

Many studies showed the implication of metals (Cu and Fe) in the development of age-related diseases and more precisely in age-related neurodegenerative diseases. These metals are able to generate ROS through the Fenton and Haber-Weiss reactions (Brewer 2007) and to induce accumulation of DNA damage, by their ability to inhibit a family of DNA glycosylases by oxidation, changing their structure and preventing their binding to downstream repair proteins (Hegde et al. 2011). Interestingly, these metals accumulate in HDFs with RS (Boilan et al. 2013; Killilea et al. 2004). The accumulation of Cu during RS of HDFs was detected by specific fluorescence-probes (CS1) or cytochemistry (rubeanic acid), but the mechanisms and the kinetics of this accumulation is still unknown. Incubation of HDFs at young CPDs with CuSO<sub>4</sub> induces senescence, this suggests that a transient increase of copper concentration is sufficient to launch the senescence process.

### 13.9 SIS in Cancer Treatment

Several studies have shown that in addition to induce apoptosis of cancer cells, some anti-cancer treatments such as chemotherapy and ionizing radiation were also able to induce senescence, generally using lower concentrations than those necessary to provoke apoptosis.

Chemotherapeutic agents able to induce senescence *in vitro* include among others cisplatin (Berndtsson et al. 2007), etoposide (Chiu et al. 2005), doxorubicin (Sliwinska et al. 2009), bleomycin (Aoshiba et al. 2003), vinblastine (Duan et al. 2007), etc (for a review: Bilsland and Keith 2010). An analysis of tumor tissues from patients treated with chemotherapeutic agents show a greater proportion of senescent cells (SA- $\beta$ gal positive, p16<sup>ink-4a</sup> overexpression) compared to healthy tissues in patients suffering from breast cancer, non-small-cell lung carcinoma or prostate cancer (Coppe et al. 2008; Roberson et al. 2005; te Poele et al. 2002). *In vivo*, first clinical data show that senescence markers (p16<sup>ink-4a</sup> overexpression,

VEGFA and MCP1 secretion) are more expressed in T lymphocytes from patients suffering for breast cancer treated with adjuvant chemotherapy (anthracyclin-based) than controls (Sanoff et al. 2014). This therefore accelerates senescence of hematopoietic tissues.

Furthermore ionizing radiation induces senescence in normal and tumor cells *in vitro* (Suzuki and Boothman 2008). So we should be careful about the possible induction of senescence by radiotherapy on the tumor being treated and its (micro)environment.

Induction of senescence-like phenotype in transformed cells and particularly of irreversible cell cycle arrest is seen as an interesting concept in the treatment of cancer. Indeed cancer cells manage to escape cellular senescence. A promising strategy is to successfully redirect cancer cells to cellular senescence by developing senescence-targeted drug. This pro-senescence therapy is presented as a new promising approach in cancer treatment (Nardella et al. 2011). The main pro-senescence strategies are to inhibit the activity of telomerase, to reactivate or stabilize p53, to induce Pten loss induced senescence (PICS) and to inhibit CDKs and MYC (Acosta and Gil 2012).

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