Defective autophagy in vascular smooth muscle cells accelerates senescence and promotes neointima formation and atherogenesis

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Abstract

Autophagy is triggered in vascular smooth muscle cells (VSMCs) of diseased arterial vessels. However, the role of VSMC autophagy in cardiovascular disease is poorly understood. Therefore, we investigated the effect of defective autophagy on VSMC survival and phenotype and its significance in the development of postinjury neointima formation and atherosclerosis. Tissue-specific deletion of the essential autophagy gene Atg7 in murine VSMCs (Atg7<sup>−/−</sup> VSMCs) caused accumulation of SQSTM1/p62 and accelerated the development of stress-induced premature senescence as shown by cellular and nuclear hypertrophy, CDKN2A upregulation, RB hypophosphorylation, and GLB1 activity, all features typical of cellular senescence. Interestingly, Atg7<sup>−/−</sup> VSMCs were resistant to oxidative stress-induced cell death as compared to controls. This effect was attributed to nuclear translocation of the transcription factor NFE2L2 resulting in upregulation of several antioxidative enzymes. In vivo, defective VSMC autophagy led to upregulation of MMP9, TGFβ and CXCL12 and promoted postinjury neointima formation and diet-induced atherogenesis.

Introduction

Autophagy is a highly conserved and tightly regulated subcellular process involved in the degradation of long-lived proteins and damaged organelles. During this process, fragments of cytoplasmic material are sequestered in double-membrane vesicles, termed autophagosomes, and delivered to lysosomes for degradation. In this way, essential precursor molecules (e.g., amino acids) are recycled in order to replenish nutrient and energy supply. Basal autophagy is therefore an important housekeeping and life-sustaining process.

Vascular smooth muscle cells (VSMCs) are the major components of the blood vessel wall and play crucial roles in both physiological (e.g., regulation of blood pressure and vascular tone) and pathological (e.g., regulation of blood pressure and vascular tone)
pathological processes (e.g., restenosis and atheroma formation). Accumulating evidence suggests that autophagy is activated in VSMCs in response to various stimuli including lipids, reactive oxygen species, cytokines, and growth factors and may act as an important mechanism for VSMC survival. Moreover, platelet-derived growth factor-induced autophagy promotes the development of a synthetic and proliferative VSMC phenotype, suggesting that autophagy may regulate VSMC phenotype and function. Because our knowledge of the regulation of autophagy in VSMCs is mainly based on cell culture experiments, we focused on the role of VSMC autophagy in arterial disease such as postinjury neointima formation and atherosclerosis. At this moment, the relation between autophagy and neointima formation is debatable because induction of autophagy by platelet-derived growth factor stimulates VSMC proliferation (vide supra) while the autophagy inducer rapamycin or derivatives thereof (e.g., everolimus) are essentially used to prevent restenosis.

Even though autophagy occurs in VSMCs of atherosclerotic plaques, the role of VSMC autophagy in atherosclerosis has not been investigated. To study the role of autophagy in VSMCs in vitro and in vivo, a mouse model was constructed in which ATG7 expression was specifically deleted in VSMCs of the aorta. This model is considered as a backup mechanism of NFE2L2-dependent transcription of detoxifying enzymes such as GSTA and NQO1.

Results

Autophagy is defective in $\text{Ag}^7f^{\text{fl}}\text{Tagl}^{-/-}\text{Cre}^+ (\text{atg}7^{-/-})$ VSMCs

The essential autophagy gene $\text{Ag}^7$ was deleted in VSMCs by crossbreeding mice homozygous for the $\text{Ag}^7f^{\text{fl}}$ allele ($\text{Ag}^7f^{\text{fl}}\text{Tagl}^{-/-}\text{Cre}^+$) with a transgenic mouse strain that expresses Cre recombinase under control of the mouse Tagl/transgelin promoter. According to western blot analyses, the lack of ATG7 expression in isolated $\text{Ag}^7f^{\text{fl}}\text{Tagl}^{-/-}\text{Cre}^+$ VSMCs (further referred to as $\text{atg}7^{-/-}$) was associated with typical features of impaired autophagy such as severe SQSTM1 accumulation, decreased levels of the ATG12–ATG5 complex, an increased amount of unconjugated ATG5 and a marked decrease of MAP1LC3B-II levels with respect to $\text{Ag}^7f^{+/+}$ VSMCs (Fig. 1A). Moreover, unlike $\text{Ag}^7f^{+/+}$ VSMCs, $\text{atg}7^{-/-}$ VSMCs did not show enhanced processing of MAP1LC3B-I into MAP1LC3B-II and autophagosome formation upon starvation, a well-known stimulus of autophagy (Fig. 1B-C). These experiments confirm that $\text{atg}7^{-/-}$ VSMCs were unable to initiate autophagy.

Defective autophagy in VSMCs triggers an antioxidative backup mechanism

ROS production, oxidative damage and cell death are major events in cardiovascular disease and may be regulated by autophagy. To test the role of autophagy in VSMC survival against oxidative stress, $\text{Ag}^7f^{+/+}$ and $\text{atg}7^{-/-}$ VSMCs were treated with 25 $\mu$mol/l tBHP or 50 $\mu$g/ml oxLDL for 24 h. $\text{atg}7^{-/-}$ VSMCs were much more resistant to oxidative stress-induced cell death than $\text{Ag}^7f^{+/+}$ VSMCs (Fig. 2A). Along these lines, treatment with 100 $\mu$mol/l tBHP for 6 h stimulated ROS production in $\text{Ag}^7f^{+/+}$ VSMCs but not in $\text{atg}7^{-/-}$ VSMCs (Fig. 2A). Interestingly, $\text{atg}7^{-/-}$ VSMCs treated with 10 $\mu$mol/l puromycin for 12 h or exposed to UV-irradiation for 10 min did not reveal improved protection against apoptosis (Fig. 2B).

To explain the observed cytoprotection against oxidative stress, RNA of untreated $\text{Ag}^7f^{+/+}$ and $\text{atg}7^{-/-}$ VSMCs was analyzed. Microarray analysis revealed an upregulation of the genes encoding several antioxidative enzymes such as Gsta1/3/4 (glutathione S-transferase, $\alpha 1/3/4$) and Nqo1 (NAD[P]H dehydrogenase, quinone 1) in $\text{atg}7^{-/-}$ VSMCs. The microarray data are available via the National Center for Biotechnology Information Gene Expression Omnibus at: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?token=tyuzumoktdqpipandacc=GSE54019.

Defective autophagy in VSMCs elicits cellular hypertrophy, and increases migration capacity and total collagen amount

Microscopic analysis of $\text{atg}7^{-/-}$ VSMCs did not reveal a typical spindle-shaped phenotype as compared to $\text{Ag}^7f^{+/+}$ VSMCs. Instead, $\text{atg}7^{-/-}$ VSMCs were characterized by a more rhomboid shape and an increase in cellular size (Fig. 2B). Importantly, $\text{atg}7^{-/-}$ VSMCs showed enhanced translocation of NFE2L2 into the nucleus (Fig. 2D). Silencing of Nfe2l2 completely suppressed GSTA and NQO1 expression and abolished the protection of $\text{atg}7^{-/-}$ VSMCs against tBHP and oxLDL (Fig. 2E). These experiments indicate that the NFE2L2 signaling pathway is activated in $\text{atg}7^{-/-}$ VSMCs as a backup mechanism to protect against oxidative stress. Overall, $\text{Ag}^7$ deletion in VSMCs did not result in a general prosurvival status but only protected VSMCs against oxidative stress-mediated cell death via upregulation of antioxidative enzymes.
substantial upregulation of different promigratory growth factors such as TGFβ (transforming growth factor β) and CXCL12 (chemokine [C-X-C] motif ligand 12) in \( \text{Atg7}^{-/-}\) VSMCs (Fig. 3C). To test the influence on collagen content, \( \text{Atg7}^{+/+}\) and \( \text{Atg7}^{-/-}\) VSMCs were treated with 10 ng/ml TGFβ for 48 h. \( \text{Atg7}^{-/-}\) VSMCs showed a significant increase in collagen amount in both control and TGFβ-treated conditions as compared to \( \text{Atg7}^{+/+}\) VSMCs (Fig. 3D). Further analysis of COL1A1/2 (collagen, type I, α 1/2) and COL3A1 (collagen, type III, α 1) expression by immunofluorescence showed that \( \text{Atg7}^{-/-}\) VSMCs express less COL1A1/2 but more COL3A1 as compared to \( \text{Atg7}^{+/+}\) VSMCs (Fig. S1C). TGFβ treatment augmented COL1A1/2 and COL3A1 expression in both genotypes.

**Defective autophagy in VSMCs accelerates senescence**

A BrdU incorporation assay was performed to examine the proliferation capacity of \( \text{Atg7}^{+/+}\) and \( \text{Atg7}^{-/-}\) VSMCs. A nearly 2-fold reduction in proliferation of \( \text{Atg7}^{-/-}\) VSMCs was observed as compared to \( \text{Atg7}^{+/+}\) VSMCs (Fig. 4A). Moreover, \( \text{Atg7}^{-/-}\) VSMCs were characterized by a significant increase in nuclear size (Fig. 4A). According to a cell cycle analysis, the percentage of \( \text{Atg7}^{-/-}\) nuclei in G1-phase was increased (36±5% vs. 55±1%) while the percentage of \( \text{Atg7}^{+/+}\) nuclei in G2/M-phase was strongly decreased (38±2% vs. 15±1%), suggestive of a G1-cell cycle arrest and senescence (Fig. 4B). Importantly, cell cycle analysis did not show signs of VSMC polyploidy in both cell types. Staining for senescence-associated GLB1 activity confirmed the presence of senescent cells in \( \text{Atg7}^{-/-}\) VSMC cultures (Fig. 4C). Because cellular senescence can be established by the activation of different tumor suppressor pathways including CDKN2A-RB (stress response) and TP53-CDKN1A (DNA damage response) pathways, these proteins were examined via western blotting. CDKN2A was highly upregulated in \( \text{Atg7}^{-/-}\) VSMCs and accompanied by hypophosphorylation and activation of RB while acetylated TP53 and CDKN1A levels remained unaltered (Fig. 4D), indicating stress-induced premature senescence. Next, we performed a comet assay to determine possible DNA damage. Neither \( \text{Atg7}^{+/+}\) nor \( \text{Atg7}^{-/-}\) VSMCs showed comet tail formation. In contrast, \( \text{Atg7}^{+/+}\) VSMCs treated with 0.5 mmol/l H2O2 for 10 min showed severe comet tail formation representing a large number of DNA strand breaks (Fig. 4E). Given that the DNA damage response pathway was not activated and DNA strand breaks were absent, senescence in \( \text{Atg7}^{-/-}\) VSMCs was not characterized by DNA damage.

Furthermore, we investigated a possible link between senescence and the NFE2L2 pathway. Nfe2l2 silencing in \( \text{Atg7}^{-/-}\) VSMCs did not affect CDKN2A protein expression (Fig. S2A). Overexpression of CDKN2A in \( \text{Atg7}^{+/+}\) VSMCs induced senescence as illustrated by increased GLB1 activity but altered neither NQO1 expression nor NFE2L2 activation (Fig. S2B). These experiments suggest that the senescence and NFE2L2 pathway act independently in autophagy deficient VSMCs.

To investigate the role of SQSTM1 accumulation (typical of defective autophagy, vide supra) in the induction of VSMC senescence, \( \text{Atg7}^{+/+}\) VSMCs were transiently transfected with...
Figure 2. Defective autophagy in VSMCs results in increased protection against oxidative stress-induced cell death. (A) Atg7<sup>+/+</sup>/Tagln-Cre<sup>+</sup> (+/+) and Atg7<sup>−/−</sup>/Tagln-Cre<sup>+</sup> (−/−) VSMCs were treated with 25 μmol/l tBHP or 50 μg/ml oxLDL for 24 h (***, P < 0.001 vs. Atg7<sup>+/+</sup>; ###, P < 0.001 vs. control; n = 3 experiments in triplicate; two-way ANOVA with genotype and treatment as category factors and Dunnett Post Hoc test). To measure ROS production, Atg7<sup>+/+</sup> and atg7<sup>−/−</sup> VSMCs were left untreated or treated with 100 μmol/l tBHP for 6 h, followed by a DCFDA staining (***, P < 0.001 vs. Atg7<sup>+/+</sup>; n = 200 cells/condition in duplicate; two-way ANOVA with genotype and treatment as category factors). (B) Atg7<sup>+/+</sup> and atg7<sup>−/−</sup> VSMCs were treated with 10 μmol/l puromycin (PM) for 12 h or exposed to UV-irradiation for 10 min (NS, not significant vs. Atg7<sup>+/+</sup>; ###, P < 0.001 vs. control; n = 2 experiments in triplicate; two-way ANOVA with genotype and treatment as category factors). (C) Analysis of Gsta and Nqo1 expression in Atg7<sup>+/+</sup> and atg7<sup>−/−</sup> VSMCs by real time RT-PCR (***, P < 0.001; n = 2 experiments in duplicate; Student t test) and western blotting. (D) Western blot analysis of NFE2L2 in cytoplasmic and nuclear fractions of Atg7<sup>+/+</sup> and atg7<sup>−/−</sup> VSMCs. Atg7<sup>−/−</sup> VSMCs were transfected with 100 nmol/l siRNA against Nfe2l2 (siNfe2l2) or non-targeting siRNA (siCtrl). After 72 h, silencing efficiency was confirmed by western blotting by assessment of NFE2L2, GSTA and NQO1 expression and VSMCs were treated with tBHP or oxLDL for 24 h (***, P < 0.001 vs. siCtrl; ###, P < 0.001 vs. control; n = 3 experiments in duplicate; two-way ANOVA with genotype and treatment as category factors and Dunnett Post Hoc test).
Figure 3. Defective autophagy in VSMCs elicits cellular hypertrophy, and increases migration capacity and total collagen amount. (A) VSMCs isolated from Atg7+/+ Tagln-Cre+ (+/+ ) and Atg7+/Tagln-Cre+ (-/- ) aorta were labeled with calcein AM and visualized by confocal fluorescence microscopy. Scale bar: 10 μm. Cell size was measured using z-stack images (*, P < 0.05; n = 2 experiments; Student t test). (B) Thoracic aorta of Atg7+/+ and atg7+/aorta mice were stained with H&E to measure the width of the media (white arrows) (**, P < 0.01; n = 6 regions/aorta; Univariate). Scale bar: 25 μm. Note that the number of VSMC layers between Atg7+/+ and atg7+/aorta was not different. (C) Migratory capacity of Atg7+/+ and atg7+/aorta VSMCs was analyzed using an Oris Migration Assay (***, P < 0.001; n = 2 experiments in triplicate; Student t test). Western blot analysis of TGFB and CXCL12 in Atg7+/+ and atg7+/aorta VSMCs. (D) Atg7+/+ and atg7+/aorta VSMCs were left untreated or treated with 10 ng/ml TGFB for 48 h and stained with Sirius red to examine total collagen amount (***, P < 0.001 vs. Atg7+/+; ###, P < 0.001 vs. control; n = 4 experiments in triplicate; two-way ANOVA with genotype and treatment as category factors).
SQSTM1-encoding plasmid DNA. Overexpression of SQSTM1 in Atg7+/+ VSMCs resulted in increased CDKN2A expression and a slight decrease in RB phosphorylation (Fig. 5A). Moreover, SQSTM1 overexpressing Atg7+/+ VSMCs showed reduced proliferation (Fig. 5B) and increased senescence-associated GLB1 activity (Fig. 5C). These experiments indicate that SQSTM1 mediates the induction of senescence in autophagy defective VSMCs.
Defective VSMC autophagy promotes neointima formation after ligation-induced injury

To evaluate the consequences of defective VSMC autophagy in vivo, neointimal lesion formation was induced by ligation of the left common carotid artery (LCCA) in \( \text{Atg}^{+/+} / \text{Tagln-Cre}^{+} \) and \( \text{Atg}^{-/-} / \text{Tagln-Cre}^{+} \) mice. Five days after ligation, the activity of the gelatinase MMP9 was already strongly elevated in \( \text{Atg}^{-/-} \) LCCA as shown by zymographic analysis (Fig. 6A). Moreover, western blot analysis showed a significant increase in TGFβ and CXCL12 expression in the LCCA of \( \text{Atg}^{-/-} \) mice (Fig. 6B). To investigate the effect on neointimal thickening, LCCA of \( \text{Atg}^{+/+} \) and \( \text{Atg}^{-/-} \) mice were analyzed 5 weeks after ligation. \( \text{Atg}^{-/-} \) mice showed a dramatic increase in stenosis (90 ±3%) as compared to \( \text{Atg}^{+/+} \) mice (54 ± 6%) (Fig. 7A). In addition, the total collagen content was significantly elevated in the neointima of \( \text{Atg}^{-/-} \) mice (Fig. 7B). The level of apoptosis was similar in lesions of \( \text{Atg}^{-/-} \) mice versus \( \text{Atg}^{+/+} \) mice (Fig. S3A). Also the percentage of macrophages within the neointima was not different between both groups (Fig. S3B). SQSTM1 staining confirmed the presence of autophagy deficient VSMCs in media and lesions of \( \text{Atg}^{-/-} \) mice (Fig. S4A).

Figure 5. SQSTM1 accumulation links defective VSMC autophagy to senescence. (A) \( \text{Atg}^{+/+} \) VSMCs were transfected with 5 μg plasmid DNA encoding SQSTM1 (SQSTM1+). Four days after transfection, VSMCs were analyzed for SQSTM1, CDKN2A, phospho RB and total RB expression by western blotting. (B, C) SQSTM1 overexpressing VSMCs were incubated with BrdU (B) to examine proliferation capacity (***, \( P < 0.001 \); n = 2 counting regions of 1000 cells/region/condition in duplicate; Student t test) or (C) stained with X-gal mixture for 24 h to quantify the number of senescence-associated GLB1-positive VSMCs (***, \( P < 0.001 \); n = 3 counting regions of 150 cells/region/condition in duplicate; Student t test). Scale bar: 50 μm.

Figure 6. Defective VSMC autophagy promotes upregulation of MMP9, TGFβ and CXCL12, 5 d after ligation-induced injury. (A) The left common carotid artery (LCCA) of \( \text{Atg}^{+/+} / \text{Tagln-Cre}^{+} \) (+/+ ) and \( \text{Atg}^{-/-} / \text{Tagln-Cre}^{+} \) (−/−) mice (n = 3) was ligated for 5 d. Gelatin zymographic analysis of the LCCA to detect MMP9 and MMP2 activity followed by densitometric analysis (***, \( P < 0.001 \); NS, not significant; Student t test). (B) Western blot analysis of the LCCA for TGFβ, CXCL12 and GAPDH. Relative expression of TGFβ/GAPDH and CXCL12/GAPDH was determined by densitometric analysis (*, \( P < 0.05 \); ***, \( P < 0.001 \); Student t test).
Figure 7. For figure legend, see page 2022.
Furthermore, neointimal $\text{atg}^{-/-}$ VSMCs were characterized by CDKN2A upregulation (Fig. 7C), senescence-associated GLB1 activity (Fig. 7D) and nuclear hypertrophy (Fig. S3C), indicating that neointima formation in $\text{atg}^{-/-}$ mice was associated with VSMC senescence.

**Defective VSMC autophagy accelerates atherogenesis**

To investigate the role of VSMC autophagy in atherosclerosis, $\text{Atg}^{-/-}/\text{Tagln-Cre}$ and $\text{Atg}^{-/-/F}/\text{Tagln-Cre}$ mice were crossbred with $\text{apoe}^{-/-}$ mice and fed a western-type diet (WD) for 10 or 14 wk. Body weight, total cholesterol and lipoproteins were not different between both groups after 10 and 14 wk on WD (Table S1, Fig. S5), indicating that $\text{Atg}7$ deletion in VSMCs does not influence normal growth and lipid metabolism. Plaques of $\text{Atg}^{-/-/F}/\text{Tagln-Cre},\text{apoe}^{-/-} (\text{atg}^{-/-/F},\text{apoe}^{-/-})$ mice were characterized by increased accumulation of SQSTM1 as compared to $\text{Atg}^{-/-/F}/\text{Tagln-Cre},\text{apoe}^{-/-} (\text{Atg}^{-/-/F},\text{apoe}^{-/-})$ mice, confirming autophagy deficiency (Fig. S4B). Plaques in the brachiocephalic artery of 10-wk WD-fed $\text{atg}^{-/-},\text{apoe}^{-/-}$ mice showed a 3-fold increase in size as compared to $\text{atg}^{-/-/F},\text{apoe}^{-/-}$ mice (58 ± 9 μm² vs. 156 ± 19 μm²; $P < 0.001$). Furthermore, plaques of $\text{atg}^{-/-},\text{apoe}^{-/-}$ mice were characterized by elevated plaque necrosis, plaque apoptosis, macrophage content, total collagen and fibrous cap thickness (Fig. 8A). After 14 wk on WD, plaque size (171 ± 11 μm² vs. 166 ± 9 μm²; $P > 0.05$), macrophage content as well as the degree of necrosis and apoptosis was similar in $\text{Atg}^{-/-/F},\text{apoe}^{-/-}$ and $\text{atg}^{-/-/F},\text{apoe}^{-/-}$ mice (Fig. 9A-C). However, total collagen content and fibrous cap thickness were still elevated in plaques of $\text{atg}^{-/-/F},\text{apoe}^{-/-}$ mice (Fig. 9D-E). Interestingly, the amount of COL1A1/2 was significantly decreased in $\text{atg}^{-/-/F},\text{apoe}^{-/-}$ plaques while the amount of COL3A1 was increased (Fig. S6A and S6B). Plaques located in the aortic root showed a similar plaque composition as compared to plaques in the brachiocephalic artery (data not shown). Next, we investigated whether VSMCs in $\text{atg}^{-/-/F},\text{apoe}^{-/-}$ plaques revealed characteristics of senescence. VSMCs within the fibrous cap of $\text{atg}^{-/-/F},\text{apoe}^{-/-}$ plaques were characterized by enhanced senescence-associated GLB1 activity (Fig. 10A), hypophosphorylation and activation of RB (Fig. 10B), and nuclear hypertrophy (Fig. S6C), indicative of senescence. Importantly, plaque formation in $\text{atg}^{-/-/F},\text{apoe}^{-/-}$ mice was not attributed to increased proliferation of medial VSMCs as shown by severe hypophosphorylation of RB in the media (Fig. 10C).

**Activation of the NFE2L2 and senescence pathway occurs in autophagy defective VSMCs but not in macrophages**

Because it was previously demonstrated that defective autophagy in macrophages led to increased plaque destabilization after 12 and 16 wk of WD, antioxidative mechanisms and cellular senescence were further examined in autophagy deficient macrophages (Fig. 11A). Unlike $\text{atg}^{-/-}$ VSMCs, $\text{atg}^{-/-}$ macrophages did not overexpress GSTA and NQO1 and were much more sensitive to tBHP-induced cell death as compared to $\text{Atg}^{+/+}$ macrophages (Fig. 11B-C). This effect was attributed to the lack of NFE2L2 activation in $\text{atg}^{-/-}$ macrophages (Fig. 11D). Furthermore, besides the unaltered proliferation (Fig. 11E), $\text{atg}^{-/-}$ macrophages showed neither cell cycle arrest nor upregulation of CDKN2A (Fig. 11F-G), indicating that defective autophagy in macrophages does not result in cellular senescence.

**Discussion**

In this study, we provide novel evidence for a prominent role of autophagy in the regulation of VSMC survival and phenotype. Defective autophagy has major effects on the mechanistic, functional and morphological properties of VSMCs, with significant implications for the development of cardiovascular diseases such as postinjury neointima formation and diet-induced atherosclerosis (Fig. 12).

The relationship between autophagy and cell survival has been thoroughly investigated by several research groups. Because autophagy is considered as an important mechanism for the survival of VSMCs, it is plausible to assume that defects in the autophagic machinery could aggravate VSMC death. Surprisingly, our data indicate that $\text{atg}^{-/-}$ VSMCs were highly resistant to oxidative stress as compared to $\text{Atg}^{+/+}$ VSMCs. The protection against oxidative stress-mediated cell death was attributed to increased expression of different antioxidative enzymes such as GSTA and NQO1. These phase II enzymes serve as a detoxification mechanism to protect cells against electrophilic insults and oxidative stress. Accumulation of the protein SQSTM1, one of the hallmarks of defective autophagy, plays a central role in the upregulation of these antioxidative enzymes. SQSTM1 accumulation triggers nuclear translocation of the transcription factor NFE2L2, a well-known key regulator of the intracellular redox balance. Under basal conditions, NFE2L2 is immobilized in the cytoplasm by binding to its inhibitor KEAP1 (kelch-like ECH-associated protein 1). However, when SQSTM1 accumulates, it will interfere with the NFE2L2-KEAP1 binding complex by sequestering KEAP1 into aggregates. As a result, NFE2L2 is released from its inhibitor and translocated to the nucleus where it promotes transcription of multiple antioxidative genes by binding to the antioxidant response element (ARE) in their promoter region. Therefore,
SQSTM1 is considered to be a crucial activator of NFE2L2. In the present study, \( \text{atg}^{+/+} \) VSMCs showed increased nuclear translocation of NFE2L2. Silencing of Nfe2l2 suppressed the expression of GSTA and NQO1 and abolished the protection of \( \text{atg}^{+/+} \) VSMCs against oxidative stress. Importantly, \( \text{atg}^{+/+} \) VSMCs did not reveal improved protection against ROS-independent apoptosis. Hence, Atg7 deletion in VSMCs did not result in a general prosurvival status but only protected VSMCs against oxidative stress-mediated cell death. Interestingly, this antioxidative backup mechanism seems to be cell-type specific. \( \text{atg}^{+/+} \) macrophages revealed neither NFE2L2 activation nor elevated phase II enzyme expression, which is in line with previous reports showing that various cell types including hepatic cells, neurons, pancreatic \( \beta \) cells, and macrophages are more susceptible to (oxidative stress-mediated) cell death under defective autophagy conditions.

Besides an improved antioxidant defense, \( \text{atg}^{+/+} \) VSMCs were characterized by cellular hypertrophy, nuclear hypertrophy, a decline in proliferative...
Moreover, atg7−/− VSMCs show an increase in TGFβ and CXCL12 expression, which is most likely related to the increase in migration potential and the development of a senescence-associated secretory phenotype.29,30 Cellular senescence can be established by the activation of 2 different tumor suppressor pathways: TP53-CDKN1A and CDKN2A-RB.20,21 TP53 pathway is triggered by DNA damage and generally associated with CDKN1A upregulation to initiate growth arrest. The CDKN2A-RB (retinoblastoma) pathway is engaged when cells are exposed to cellular stress, leading to the development of stress-induced premature senescence (SIPS).31 During SIPS, the increased expression of CDKN2A leads to hypophosphorylation and activation of RB, resulting in prevention of transcription of proliferation-promoting genes.20 In the present study, senescence in atg7−/− VSMCs was associated with the activation of the CDKN2A-RB pathway but not with DNA damage-mediated activation of the TP53-CDKN1A pathway. Importantly, the senescence pathway acts independently of the NFE2L2-ARE pathway as shown by CDKN2A overexpression and Nfe2l2 silencing experiments.

Several research groups have shown that senescence contributes to the aging process and to the development of age-related pathologies.29,32 Given that CDKN2A expression is elevated in aged VSMCs33 and CDKN2A is considered as a biomarker of aging,29,34 we define here a possible link between autophagy deficiency and VSMC aging. The relationship between autophagy and aging has been strongly investigated over the last 10 y. Induction of autophagy by caloric restriction, spermidine, resveratrol or rapamycin extends life span in different organisms.35 For example, the autophagy-inducers rapamycin and resveratrol suppress cellular senescence by partially preventing loss of proliferative potential36,37 whereas inhibition of autophagy by knockdown of ATG7 or ATG12 induces premature senescence.38 In the present study, we dissected out the molecular link between defective autophagy and VSMC senescence. Overexpression of SQSTM1 induced senescence in Atg7+/+ VSMCs as shown by CDKN2A accumulation, RB hypophosphorylation, reduced proliferation capacity and increased senescence-associated GLB1 activity. This experiment indicates that severe accumulation of SQSTM1, which occurs during defective VSMC autophagy, mediates the induction of senescence in VSMCs. Although some researchers have suggested that SQSTM1 could play a role in the induction of senescence in other pathologies,39,40 this is the first study that addresses SQSTM1 accumulation as the direct link between defective autophagy and VSMC senescence. The inverse relationship between autophagy and senescence seems logical if they are both considered as 2 cytoprotective pathways.41 Indeed, autophagy is an important homeostatic regulator by eliminating damaged intracellular components and may play a critical role in the prevention of cellular senescence.42 When autophagy is impaired, however, senescence can be engaged as a backup mechanism to protect the cell.41

Because changes in VSMC survival, phenotype, proliferation and migration are critical factors in the development of arterial vascular disease, we investigated their functional significance in 2 mouse models for postinjury neointima formation and atherosclerosis. Postinjury neointimal lesions are formed by the accumulation of VSMCs and extracellular matrix.43 Five wk after carotid ligation, atg7−/− mice developed larger and more collagen-rich neointimal lesions as compared to Atg7+/+ mice. The mechanism behind this excessive neointimal formation includes high MMP9 activity in the ligated LCCA of atg7−/− mice already 5 d after ligation. Matrix metalloproteinases facilitate migration of VSMCs by remodeling the extracellular matrix.44 In particular MMP9 and MMP2 are upregulated in response to vascular injury and to trigger intimal thickening.45 Because MMP2 levels rise at a later time and remain lower than MMP9 levels,46 we failed to detect MMP2 activity 5 d after ligation. Moreover, the expression of TGFβ and CXCL12 was significantly increased in the LCCA of atg7−/− mice. TGFβ plays a crucial role in intimal thickening and may stimulate MMP9 and MMP2 expression after arterial injury which in turn may augment the bioavailability of TGFβ, thereby creating a positive feedback loop promoting intimal thickening.47 Given that TGFβ is also involved in collagen synthesis, RB-dependent G1-growth arrest and induction of several senescence markers (e.g. GLB1 activity),48-50 this growth factor most likely plays a central role in both the development of senescence and the formation of postinjury neointima in atg7−/− mice. CXCL12 is an important chemoattractant that is released by VSMCs after mechanical injury and triggers the recruitment of SMC progenitor cells to the lesion.51,52 All together, the excessive neointimal thickening in atg7−/− mice could be attributed to a combination of factors: cellular hypertrophy of neointimal VSMCs, increased deposition of collagen, improved VSMC migration, and recruitment of smooth muscle progenitor cells due to increased MMP9 activity and elevated levels of TGFβ and CXCL12. These findings support our in vitro data that autophagy defective VSMCs exhibit improved migration potential and develop a senescence-associated secretory phenotype which is characterized by the increased secretion of growth factors (TGFβ), cytokines (CXCL12) and proteases (MMPs).29,30 Furthermore, neointimal atg7−/− VSMCs were characterized by CDKN2A upregulation, senescence-associated GLB1 activity and nuclear hypertrophy, indicating that neointima formation in atg7−/− mice was associated with VSMC senescence.

Atherosclerotic lesions are characterized by the accumulation of VSMCs, immune cells, lipids and extracellular matrix within the arterial wall. Ten-wk-old WD-fed atg7−/−,apoe−/− mice developed larger and more advanced plaques as compared to Atg7+/+,apoe−/− mice, due to an increase in necrotic core size, fibrous cap thickness, macrophage and total collagen content. After 14 wk on WD, the differences in plaque size, macrophage content, necrosis and apoptosis between both groups were no longer significant. Still, the fibrous cap thickness and total collagen content were significantly elevated in plaques of 14-wk WD-fed atg7−/−,apoe−/− mice. To assess the contribution of collagen to plaque stability, the amount of COL1A1/2 (more rigid) and COL3A1 (less rigid) was measured. In accordance with our in vitro findings, plaques of atg7−/−,apoe−/− mice showed a
significant decrease in COL1A1/2 while COL3A1 was increased. Taken together, we cannot define that plaque stability was improved in atg7<sup>−/−</sup>, apoe<sup>−/−</sup> mice because several important criteria such as a sufficient decrease in plaque necrosis and plaque apoptosis and high amounts of COL1A1/2 were not evident. Moreover, VSMCs within the fibrous cap of atherosclerotic plaques of atg7<sup>−/−</sup>, apoe<sup>−/−</sup> mice were characterized by several senescence markers including RB hypophosphorylation, senescence-associated GLB1 activity and nuclear hypertrophy. Different research groups have shown that VSMC senescence is present in atherosclerotic plaques and contributes to the pathogenesis of atherosclerosis.21,32,53,54 Our observations confirm once more the dual role of VSMCs in atherosclerosis. Although VSMCs are considered beneficial in terms of plaque stability due to the formation of a thick fibrous cap that safeguards plaques from rupturing, VSMCs also play a fundamental role in promoting plaque development.55
Because defective autophagy in VSMCs accelerates atherogenesis, we do not recommend inhibition of VSMC autophagy but rather suggest controlled stimulation of autophagy as a therapeutic strategy to treat atherosclerosis as recently suggested. Caloric restriction for example, is a powerful tool to induce autophagy and has both life-span-prolonging and antiatherogenic properties in mice. Also SIRT1 (sirtuin 1) deacetylase, an inducer of autophagy and a negative regulator of cellular aging, plays a protective role in atherosclerosis. VSMC-specific deletion of SIRT1 deacetylase in apoE−/− mice promotes atherosclerosis associated with increased DNA damage and senescence. Finally, it is worthwhile to mention that MTOR (mechanistic target of rapamycin [serine/threonine kinase])-inhibitors such as rapamycin (or rapalogs) are able to stimulate autophagy and have significant promise to treat patients with unstable plaques, particularly in combination with statins or metformin.

In conclusion, defective autophagy in VSMCs accelerates senescence and promotes ligature-induced neointima formation and diet-induced atherogenesis. Although neointimal and atherosclerotic lesions of VSMC-specific autophagy deficient mice show several features of senescence, we cannot exclude that other pathways, besides senescence, are engaged in response to defective VSMC autophagy and involved in the accelerated plaque formation. Overall, our study uncovers for the first time the role of VSMC autophagy in postinjury neointima formation and diet-induced atherogenesis and reveals SQSTM1 as a key player in the induction of VSMC senescence, supporting the growing body of evidence that autophagic dysfunction plays a major role in cardiovascular disease.

Materials and Methods

Mouse studies

Mice homozygous for a vector that disrupts Atg7 in exon 14 by Cre-loxP technology (Atg7F/F mice) were crossed for >10 generations with Tagln-Cre mice (C57BL/6, Jackson Laboratory, 004781) which express Cre recombinase under the control of the mouse lysozyme M promoter. To obtain VSMC-specific atg7 knockout mice (referred to as Atg7−/−Tagln-Cre+ mice or simply atg7−/− mice). To induce neointimal lesions, blood flow was disrupted in the left common carotid artery of Atg7+/+ and atg7−/− mice for 5 d (n = 4/group) or 5 wk (n = 14/group) by ligating the vessel near the bifurcation. During the surgical procedure, 0.1 mg/g BW ketamine i.p. (Anesketin, 100mg/ml, Eurovet) and 0.01 mg/g BW xylazine i.p. (Rompun, 20 mg/ml, Bayer Health Care) were used as anesthetics and 0.1 mg/kg BW brupenofine s.c. (Temgesic, 0.3 mg/ml, Schering-Plough) as analgesic agent. For atherosclerosis studies, Atg7+/+ and atg7−/− mice were crossedbed with apoE−/− mice (C57BL/6, Jackson Laboratory, 002052) and fed a western-type diet (Harlan Teklad, TD88137) for 10 (n = 16/group) or 14 wk (n = 16/group). At the end of the experiment, mice were fasted overnight and blood was collected by puncture of the retro-orbital plexus. Plasma lipoprotein profiles were determined by fast performance liquid chromatography gel filtration on a Superose 6 column. Cholesterol levels were assessed by a commercially available kit (Randox, CH200). Tissues were fixed in formalin 4% for 24 h before paraffin embedding. In some experiments, tissues were imbedded in OCT (Thermo Scientific, Neg-50) and stored at −80°C. Macrophage-specific atg7 knockouts were obtained by crossingbreeding Atg7−/− mice for >10 generations with Lysm-Cre mice (C57BL/6, Jackson Laboratory, 004781) which express Cre recombinase under the control of the mouse lysozyme M promoter. All experiments were approved by the Ethics Committee of the University of Antwerp.

Cell culture

VSMCs were isolated from mouse aorta as previously described. Briefly, aortas were preincubated in HBSS (Gibco Life Technologies, 14025-050) containing 1 mg/ml collagenase (Worthington, type II CLS, 4176), 1 mg/ml soybean trypsin inhibitor (Worthington, 3571) and 0.74 units/ml elastase (Worthington, 2279) for 15 min at 37°C, in 95% air/5% CO2. Next, the adventitia was stripped off and the aorta was opened longitudinally to remove blood clots and endothelial cells. Subsequently, aortas were placed in fresh enzyme solution and incubated for 1 h (37°C, in 95% air/5% CO2). Isolated cells were centrifuged, washed and resuspended in DMEM/F-12 medium (Gibco Life Technologies, 11320-074) supplemented with 20% fetal bovine serum (FBS; Sigma Aldrich, F6178). Cells were used from passage 4 till 10 and cultured in DMEM/F-12 medium supplemented with 10% FBS. Cells were isolated from 2 or 3 mice. In each individual experiment, cells from the same passage number were used. Bone marrow-derived macrophages (BMDM) were harvested by flushing bone marrow from the hind limbs of mice. Cells were cultured for 7 d in RPMI medium (Gibco Life Technologies, 61870-010) supplemented with 15% L-cell conditioned medium (LCCM). LCCM is produced by L929 cells cultured in RPMI medium. Once cells are confluent, medium is changed and cells are left alone for 7 d to secrete M-CSF (monocyte colony-stimulating factor). Then, the medium (=LCCM) is collected and stored at −80°C. To induce oxidative stress, cells were treated with 25 μmol/l tert-butyl hydroperoxide (tBHP; Sigma-Aldrich, 458139) or 50 μg/ml oxidized LDL (oxLDL) for 24 h. oxLDL was prepared as previously described. In some experiments, cells were treated with 10 μmol/l puromycin (Sigma Aldrich, P8833) for 12 h or exposed to UV-irradiation for 10 min. Cell viability was evaluated by a neutral red assay. ROS production was determined using the fluorescent marker carboxy-H2DCFDA (Image-iT™ LIVE Green Reactive Oxygen Species Detection Kit, Molecular Probes, I36007). The DCFDA-positive cells were immediately visualized by fluorescence microscopy and then quantified using ImageJ software. To measure cellular size, VSMCs were labeled with 1 μmol/l calcein AM (Molecular probes, C3099) and visualized with an inverted microscope attached to a microtens-enhanced dual spinning disk confocal system (UltraVIEW VoX, PerkinElmer, Seer Green, UK). Images were analyzed with Volocity software (PerkinElmer). Cellular protein quantity was determined using the BCA
method (Pierce BCA Protein Assay Kit, Thermo Scientific, 23225). To induce starvation, cells were incubated in Earle’s balanced salt solution (EB SS; Gibco Life Technologies, 14155-048) for 48 h.

Transmission electron microscopy
Samples were prepared for transmission electron microscopy (TEM) as previously described. Sections were examined with a Tecnai microscope (FEI, Eindhoven, The Netherlands) at 120 kV.

Analysis of proliferation, collagen amount and migration
Cellular proliferation was assessed using a BrdU incorporation test. Once 80% confluent, BMDM and VSMCs were treated with 10 μmol/l BrdU (Sigma-Aldrich, B5002) for 2 h or 6 h respectively, followed by an anti-BrdU staining (rabbit anti-BrdU antibody; Abcam, ab6326). The BrdU-positive nuclei were quantified using ImageJ software. Collagen synthesis in VSMCs was stimulated by 10 ng/ml TGFB (Peprotech, 100-21) for 48 h in serum-free medium. Total collagen amount was assayed using Sirius red staining as previously described. COL1A1/2 and COL3A1 expression was analyzed by immunofluorescence with rabbit anti-COL1A1/2 antibody (Abcam, ab21286) and anti-rabbit Alexa Fluor 555 secondary antibody (Molecular Probes, A21428), and goat anti-COL3A1 antibody (Bioss, bs-4938); and goat collagen type III antibody (Abcam, ab3836) and rabbit anti-COL3A1 antibody (Bioss, bs-4938). The migratory capacity was evaluated, independently of cell size and chemotactic effects, using an Oris™ Cell Migration Assay (Platypus Technologies, CMA1.101). Briefly, 2.5×10⁶ cells/well were added to a 96-well plate with Cell Seeding Inserts and incubated overnight to permit cell attachment. Subsequently, the stoppers were removed to allow cell migration into the empty zone; 24 h later, cells were fixed and stained with 0.1% crystal violet (Sigma Aldrich, C3886) in 20% methanol for 3 min to visualize and quantify the migrated cells using an inverted microscope. The migratory capacity of the cells was evaluated by measuring the percentage closure area: 100 × ((premigration)area – (migration)area) / (premigration)area.

Western blotting
Cells were lysed in Laemmli sample buffer (Bio-Rad, 161-0737) containing β-mercaptoethanol (Sigma Aldrich, M3148) and boiled for 4 min. Protein samples were loaded on NuPAGE 4-12% Bis-Tris gels (Life Technologies, BG04120) and after electrophoresis transferred to Immobilon-P membranes (Millipore, IPVH304F0). Membranes were probed with the following primary antibodies: goat anti-GSTA (ab53940), rabbit anti-NFE2L2 (ab137550), mouse anti-COL1A1/2 antibody (Abcam, ab137550), mouse anti-CDKN2A/p16 (ab54210) and rabbit anti-CDKN1A/p21 (ab7960) from Abcam; rabbit anti-CXCL12 (Bios, bs-4938); rabbit anti-GAPDH (sc-7150), rabbit anti-TGFB (3711) and rabbit anti-phospho RB (8516) from Cell Signaling Technology; mouse anti-MAP1LC3B (Nanotools, clone 5F10, 0231-100); rabbit anti-NQO1 (Novus Biologicals, NBP1-40663); rabbit anti-PARP1 (sc-7150), rabbit anti-PARP1 (sc-7150), rabbit anti-PARP1 (sc-7150), rabbit anti-PARP1 (sc-7150), rabbit anti-PARP1 (sc-7150).
anti-CDKN2A/p16 (sc-1207) and rabbit anti-total RB (sc-50) from Santa Cruz Biotechnology; mouse anti-ACTB (clone AC-15, A5441), rabbit anti-ATG7 (A2856), rabbit anti-ATG5 (A0856), rabbit anti-SQSTM1/p62 (P0067) and rabbit anti-acetyl-TP53 (SAB4503014) from Sigma-Aldrich. Thereafter, membranes were incubated with HRP-conjugated secondary

Figure 11. Defective autophagy in macrophages triggers neither an antioxidative backup mechanism nor senescence. Bone marrow-derived macrophages were isolated from Atg7<sup>+/-</sup>Ly5m-Cre<sup>+</sup> (+/+) and Atg7<sup>+/−</sup>Ly5m-Cre<sup>-</sup> (−/−) mice. (A) Western blot analysis of ATG7 and SQSTM1 in untreated Atg7<sup>+/-</sup> and atg7<sup>+/−</sup> macrophages. (B) Real-time RT-PCR and western blot analysis of GSTA and NQO1 in Atg7<sup>+/-</sup> and atg7<sup>+/−</sup> macrophages (NS, not significant; n = 2 experiments in duplicate; Student t test). (C) Atg7<sup>+/-</sup> and atg7<sup>+/−</sup> macrophages were treated with 50 μmol/l tBHP for 24 h (***, P < 0.001 vs. Atg7<sup>+/-</sup>; ###, P < 0.001 vs. control; n = 2 experiments in duplicate; Two-way ANOVA with genotype and treatment as category factors). (D) Western blot analysis of NFE2L2 in cytoplasmic and nuclear fractions of Atg7<sup>+/-</sup> and atg7<sup>+/−</sup> macrophages. (E) Proliferation of Atg7<sup>+/-</sup> and atg7<sup>+/−</sup> macrophages were examined by BrdU incorporation assay (NS, not significant; n = 6 counting regions of 500 cells/region/condition; Student t test) (F) DNA cell cycle analysis of Atg7<sup>+/-</sup> (blue) and atg7<sup>+/−</sup> (red) macrophages. The bar graph shows the percentage of Atg7<sup>+/-</sup> and atg7<sup>+/−</sup> nuclei in G<sub>1</sub> and G<sub>2</sub>/M phase of the cell cycle (NS, not significant; Student t test). (G) Western blot analysis of CDKN2A in Atg7<sup>+/−</sup> and atg7<sup>+/−</sup> macrophages.
antibodies (Dako, anti-rabbit P0399, anti-mouse P0260, anti-goat P0160) to allow chemiluminescent detection. In some experiments, cytoplasmic and nuclear fractions were isolated from cultured VSMCs and BMDM using the NE-PER Nuclear and Cytoplasmic Extraction kit (Thermo Scientific, 78833) prior to western blot analysis. Tissue samples were homogenized in RIPA buffer (Sigma Aldrich, R0278) and protein content was determined using the BCA method (Pierce BCA Protein Assay Kit, Thermo Scientific, 23225). Samples were mixed with Laemmli sample buffer without β-mercaptoethanol before loading on a 10% Zymogram Gelatin gel (Life Technologies, EC6175). After electrophoresis in Tris-Glycine SDS Running Buffer (Life Technologies, LC2675), proteins were renaturated in Zymogram Renaturing Buffer (Life Technologies, LC2670) and incubated with Zymogram Developing Buffer (Life Technologies, LC2671) overnight. Gels were stained with Coomassie brilliant blue (Merck, 115444) for 3 h and subsequently destained twice for 1 h. Finally, gels were scanned to visualize the gelatinolytic activity of MMP9 and MMP2 in the left common carotid artery.

**MicroArray**

Total RNA was prepared using the Absolutely RNA Miniprep Kit (Agilent, 400800) and treated with RNase-free DNase I. RNA quality was verified on an Agilent 2100 Bioanalyzer System (Agilent Technologies, Waldbronn, Germany) using the RNA 6000 Nano LabChip kit (Agilent Technologies, 5067-1511). Samples were then analyzed by the Microarray Facility of the Flanders Interuniversity Institute for Biotechnology using a Whole Mouse Genome Oligo Microarray Kit (Agilent Technologies, G4122F) representing over 41,000 mouse genes and transcripts.

**Real time RT-PCR**

TaqMan gene expression assays (Applied Biosystems) for Nfe2l2, Gsta and Nqo1 were performed in duplicate on an ABI Prism 7300 sequence detector system (Applied Biosystems, Foster City, CA, USA) in 25-μl reaction volumes containing Universal PCR Master Mix (Applied Biosystems, 4324018). The parameters for PCR amplification were 95°C for 10 min followed by 40 cycles of 95°C for 15 sec and 60°C for 1 min. Relative expression of mRNA was calculated using the comparative threshold cycle method. All data were normalized for quantity of cDNA input by performing measurements on the endogenous reference gene Actb.
Nfe2l2 silencing and CDKN2A and SQSTM1 overexpression

VSMCs were transfected with 100 nmol/l Nfe2l2-specific siRNA (ON-TARGETplus™ SMART Pool, Mouse Nfe2l2, Dharmaco, L-040766-00-0005) or siRNA control (ON-TARGETplus™ Control Pool, nontargeting pool, Dharmaco, D-001810-10-05) via nucleofection using the Human AoSMC Nucleofector™ Kit (Amaxa, VPC-1001). Silencing efficiency was assessed by real time RT-PCR and western blotting.

To overexpress CDKN2A or SQSTM1 in VSMCs, full-length cDNA encoding mouse CDKN2A or SQSTM1 protein was amplified by PCR from VSMCs using Platinum Pfx DNA polymerase (Invitrogen, 11708-013). The following primers were used: 5’-CCAGCTTACGACATGGAGTCCGCTG CAGACAG-3’ (Cdkn2a FW), 5’-CCCTCTAGATTAGCTCTGCT TCTTTGGGATTGGCC-3’ (Cdkn2a RV), 5’-CAGAATTCT TATGCGGCTGTTCACGGTGAAAGCC-3’ (Sqstm1 FW) and 5’-CAGCGGCCGCCTATCACAATGGTGGAGGGTGCTTG-3’ (Sqstm1 RV) from Sigma Aldrich. The resultant PCR products were HindIII/XbaI (Cdkn2a) or EcoRI/NorI (Sqstm1) digested and cloned in the similarly opened plasmid pEGFP-N3 (Clontech, 6080-1), thereby replacing the eGFP coding sequence. After sequencing, VSMCs were transfected with 5 μg plasmid DNA via nucleofection using the Human AoSMC Nucleofector™ kit (Amaxa, VPC-1001).

Analysis of cellular senescence

Senescence was determined using the Senesence Cells Histochemical Staining Kit (Sigma-Aldrich, CS0030). Briefly, cells were incubated with 1x Fixation Buffer for 7 min at RT. Next, cells were washed and incubated with staining mixture (containing X-gal) at 37°C for 24 h. Subsequently, cells were counterstained with Nuclear Fast Red (BDH, 34209), thereby replacing the eGFP coding sequence. After sequencing, VSMCs were transfected with 5 μg plasmid DNA via nucleofection using the Human AoSMC Nucleofector™ kit (Amaxa, VPC-1001).

Histological analysis

The percentage neointima formation after ligation [(neointima area/lumen area) × 100] as well as the plaque area and necrotic core in the brachiocephalic artery and aortic root were measured on H&E sections. Atherosclerotic plaques located in the aortic root were analyzed in 5 different sections sliced at equally spaced intervals (every 50 μm). A 3000 μm² minimum threshold was implemented in order to avoid counting of regions that likely do not represent substantial areas of necrosis. Lesions were further analyzed by immunohistochemistry with the following primary antibodies: rabbit anti-LAMP2 (BD Pharmingen, 553322), rabbit anti-cleaved CASP3 (Cell Signaling Technology, 9661), rabbit anti-phospho RB (Cell Signaling Technology, 8516), rabbit anti-CDKN2A/p16 (Santa Cruz Biotechnology, sc-1207), goat anti-TAGLN (Abcam, ab10135), mouse anti-ACTA2 (FITC labeled; Sigma-Aldrich, A2547) and rabbit anti-SQSTM1/p62 (Sigma Aldrich, P0067). Thereafter, tissue sections were incubated with species-appropriate HRP-conjugated secondary antibodies followed by 60 min of reactive ABC (Vector Laboratories, pk4001). 3,3'-diaminobenzidine (Sigma Aldrich, D5637) or 3-amino-9-ethyl-carbazole (Sigma Aldrich, A5754) were used as a chromogen. A Sirius red (Sigma Aldrich, 36548) staining was used for detection of total collagen and COL1A1/2 under polarized light. COL3A1 was detected using goat anti-COL3A1 antibody (Biodsign, T33330G). The Senesence Cells Histochemical Staining Kit (Sigma Aldrich, CS0030) was applied on the left common carotid artery (LCCA) and aortic root. Frozen sections of the LCCA were counterstained with periodic acid-Schiff (PAS) to visualize the basal lamina. Sections of the aortic root were counterstained with Nuclear Fast Red (BDH, 34209). Consecutive sections of the aortic root were double stained with rabbit anti-phospho-RB antibody (Cell Signaling Technology, 8516) and rabbit-anti Alexa Fluor 550 secondary antibody (Molecular Probes, A21428), and mouse anti-ACTA2-FITC (Sigma Aldrich, F3777) antibody and visualized by fluorescence microscopy. All other images were acquired with Universal Grab 6.1 software using an Olympus BX40 microscope (Tokyo, Japan) and quantified with ImageJ software.

Statistical analysis

All data were analyzed with SPSS 22.0 software (SPSS Inc.) and presented as mean ± SEM. All in vitro experiments were analyzed by the Student t test or two-way ANOVA with genotype and treatment as category factors, followed by a Dunnett Post hoc test if applicable. The n-value represents the number of independently performed experiments unless mentioned otherwise. The in vivo data were analyzed by a Student t test or a Mann Whitney test in case of nonparametric analysis, and the n-value represents the number of mice. In some cases, a repeated measure or univariate analysis was applied whereas the n-value represents the number of measurements per mouse. Differences were considered significant at P < 0.05.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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