



Pathobiology of airway smooth muscle remodeling

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RESUMEN

El mecanismo primario de asma y EBPOC involucra una excesiva contracción de las vías aéreas (VA), cuya severidad se encuentra en relación a inflamación crónica. Evidencia reciente sugiere que las células de músculo liso de las vías aéreas (MLVA) poseen elevada plasticidad celular que puede contribuir en inflamación, resultando en su engrosamiento mediante hiperplasia y/o hipertrofia. La interacción MLVA-microambiente tisular es la base para hiperreactividad y remodelado tisular, con contribuciones importantes de virus y mediadores químicos, especialmente acetilcolina. Esta revisión abarca la fisiopatología del remodelado del MLVA en relación a fenotipos graves de enfermedades inflamatorias bronquiales. Un análisis in silico de hibridación entre secuencias de ARN humano y virales fue realizado, obteniendo datos para apoyar una hipótesis de 'hit and run'. Como una propuesta de integración, se resumen los últimos hallazgos moleculares con una perspectiva que ayude al establecimiento de fundamentos para investigaciones futuras y la comprensión de las vías de señalización que regulan la biología del MLVA.

PALABRAS CLAVE: Asma, EPOC, musculo liso bronquial, receptores muscarínicos, virus ARN

PATOBIOLOGÍA DEL REMODELADO DE LAS VÍAS AÉREAS

SUMMARY

The primary mechanism of morbidity and mortality in asthma and COPD is excessive airway narrowing, which severity is based on chronic inflammation. New evidence suggests airway smooth muscle (ASM) cells show extraordinary cellular plasticity that may contribute to airway inflammation, ensuing ASM thickening by either hyperplasia and/or hypertrophy. Tissue microenvironment-ASM interaction is a complex crosstalk that supports hyperresponsiveness and tissue remodeling, with major contributions of viruses and chemical mediators, especially acetylcholine. This review addresses the ASM pathology in relation with severe phenotypes of airway inflammatory diseases. An in silico analysis of hybridization between human and viral RNA strands was performed, obtaining data to support a 'hit and run' hypothesis. As an integrative proposal, we summarized the last molecular findings in this field with a perspective that helps to set the stage for future research toward understanding the signaling pathways regulating ASM biology.

KEY WORDS: Asthma, COPD, airway smooth muscle, muscarinic receptors, RNA virus

PATHOBIOLOGY OF AIRWAY SMOOTH MUSCLE REMODELING

INTRODUCTION

Asthma and chronic obstructive pulmonary disease (COPD) comprise chronic inflammatory disorders characterized by airway hyperresponsiveness and airflow obstruction that can fluctuate over time. They have an increasing economic burden, not to mention their associated disabilities and fatal outcomes. Despite of outnumbered research, we still have not completely understood the big picture of their natural history. Quite a lot of evidence arising from epidemiological, clinical, pathological, and molecular studies, have only provided a short view of the pathobiological mechanisms generating those diseases. The development of

better functional assessment techniques along with a wider availability of new biomarkers allowed to recognize that inflammatory airway diseases, especially asthma, involve multiple subphenotypes that differ in clinical severity, histopathology, response to therapy, and long-term outcome. In consequence, heterogeneous groups have been identified, which are likely originated from a unique genetic background/ environment combination.

Severe phenotypes of airway diseases that course with airway hyperreactivity, implicate airflow obstruction that is either irreversible or only partially reversible. Their severe nature apparently is due to longstanding inflammation in the airways. In this setting, injury cyclicity, age, genetic factors, and previous tissue history induce structural changes; a phenomenon commonly coined as 'airway remodeling'. Airway remodeling is assumed to result in severe phenotypes. However, several clinical and animal studies indicate that the relationship between inflammation, remodeling, and hyperresponsiveness is complex, and still not completely understood. Considering that airway hyperreactivity results in an abnormal airway tone, smooth muscle thickening is thought as the main substrate of abnormal airway mechanics. This has been deeply explored; hence, considerable data is available. In this review, we gathered the last experimental findings in this field to formulate a model of airway smooth muscle (ASM) remodeling that fits into the natural history of common airway diseases, mainly focusing on molecular mechanisms.

I. Overview of airway smooth muscle remodeling

Growing evidence supports various pathophysiological mechanisms of airway diseases, including structural changes seen on severe asthma, COPD, chronic bronchitis, cystic fibrosis, and bronchiectasis⁽¹⁻⁴⁾. Thus, airway remodeling has been defined by modifications in the composition, amount, and organization of local cells, including epithelium, glands, blood vessels, extracellular matrix (ECM), and smooth muscle (see Fig. 1).

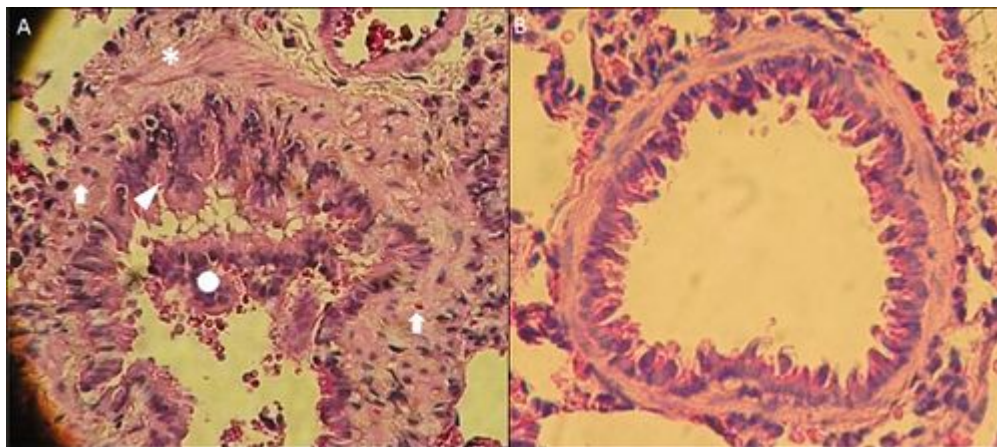


Figure 1. Histopathology of small airways in OVA-sensitized Rats. A bronchiole from OVA-sensitized rat(A) in comparison to a normal bronchiole from saline-nebulized rat(B). Tissue shows remodeling features, such as: epithelial hyperplasia (arrowhead), ASM thickening (asterisk), lymphocytic/eosinophilic inflammation (arrows), and luminal exudate (circle), compare with the normal airway. Lung samples were extracted from rats after a protocol previously described([66](#)). Magnification 200X, Hematoxylin-eosin staining.

Interaction of genetic and environmental factors evolve into assorted outcomes after injury. Many models⁽⁵⁾ and clinical studies have shown that symptoms and functional findings are caused by three interconnected factors: 1) chronic inflammation, 2) airway hyperresponsiveness (AHR), and 3) tissue remodeling. Notwithstanding, a major concern in this field is that there is no clear chronologic and quantitative relationships. A current perspective considers that unbalanced immune responses to external factors, such as allergens in asthma, sets up a harmful microenvironment of cyclic injury and repair, which leads to abnormal structure and function^(6, 7). Furthermore, a recent study suggests that chronic mechanical stress resulting from bronchoconstriction *per se* may also lead to remodeling without inflammation⁽⁸⁾. Despite of airway remodeling could be disorder-specific, the airway structure may play a common role to airway narrowing and airflow limitation carrying out poorly reversible airway obstruction.

Evidence of ASM thickening in Asthma and COPD

Asthma and COPD are well-differentiated clinical entities with some overlapping syndromes in the middle^(3, 9). They share some features, especially at pathological level, including: epithelial hyperplasia and dysfunction, subepithelial fibrosis, increased myofibroblasts, increased vascularization, abnormal neurite branching, and dense ASM layers^(2, 7, 10), highlighting that a greater basement membrane thickness as well as smooth muscle hyperplasia are commonest seen on asthma^(10, 11). Their deepness frequently wedges with clinical expression and severity^(12, 13). A study that evaluated bronchial wall thickness by high resolution computed tomography in mild-to-moderate asthma and COPD revealed the airway diameter and thickness were similar⁽¹⁴⁾, but asthma still has received more attention respect to ASM remodeling. Increased ASM mass could be attributable to hyperplasia, hypertrophy or both. Under physiological conditions, ASM located in the central and peripheral airways are bands that wrap up around the airways in a helical pattern. Its thickness, relative to the diameter of the airway lumen, increases towards the periphery, but in absolute terms, the amount is less in the peripheral airways⁽¹⁵⁾. A morphometric study indicates that the bronchial smooth muscle mass of patients suffering of fatal asthma was twice than non-asthmatics⁽¹⁶⁾. A major concern of this proposal is the ECM volume was not measured. To solve it, a recent study showed ASM hypertrophy in the large airways in both nonfatal and fatal asthma, but hyperplasia was only seen in large and small airways in fatal cases. Both groups were associated with an absolute increase in ECM⁽¹⁷⁾. Some degree of airway wall thickening was regularly detected in asthmatics of all severities with predominance in severe cases⁽¹⁸⁾. The occurrence of remodeling does not seem to depend on the inflammatory response subtype; since, airway structure does not differ between asthmatics with eosinophilia and those without⁽¹⁹⁾. Contrasting results debate the importance of ASM remodeling because it is not always found in asthma, hence, no differences in average of smooth muscle cell cross-sectional area⁽²⁰⁾.

There is less evidence supporting ASM thickening in COPD than asthma. Obliteration and fibrosis of the alveolar wall, mucous gland hypertrophy, and goblet cell hyperplasia are well-

known pathological features of COPD⁽²¹⁾. Increased ASM thickness has been found as compared to control, but lesser than asthmatics⁽¹⁵⁾. Functional implications have been shown, as it correlates with the airway obstruction degree⁽²²⁾. Additionally, ASM mass and adventitia increased together by 50% in severe COPD affecting the small airway physiology⁽²³⁾. Biopsy studies from large airways reported no increase in ASM; moreover, smooth muscle protein isoforms were not increased, but there was a slight increment in myosin light chain kinase (MLCK) without changing the myosin light chain phosphorylation⁽²⁴⁾. Conflicting results showed that remodeling may occur in the central airways by greater ECM protein deposition and increased ASM⁽²⁵⁾.

This data points out that asthma and COPD could progress with variable degree of ASM remodeling, but no direct evidence has been obtained supporting reversibility. A murine model of asthma suggests that after allergen cessation, the goblet hyperplasia and collagen deposition resolved first and then lymphocytic infiltration along with ASM thickening⁽²⁶⁾. This brings up an open question whether in human diseases a complete removal of the tissue hazard can be accompanied by spontaneous resolution of airway remodeling.

Inflammatory Microenvironment Orchestrates ASM Remodeling

Airway remodeling is associated with longstanding inflammation. Interleukin (IL)-1 β , IL-6, and Tumor Necrosis Factor- α (TNF- α) as well as growth factors such as Platelet-Derived Growth Factor (PDGF), Epidermal Growth Factor (EGF), Insulin-like Growth Factor (IGF), and Transforming Growth Factor- β (TGF- β), have pleiotropic effects; however, specific immune responses portray distinctive pathologic features^(7, 27). T cell reactions cover a wide spectrum of divergent cytokine networks. In asthma, for example, clinical phenotypes match inflammatory profiles: I-type hypersensitivity reaction (IgE-dependent), Th2 predominant inflammation, and non-Th2 associated response⁽²⁸⁾. However, a common feature seen in all cases is the ASM thickening (see Fig. 2).

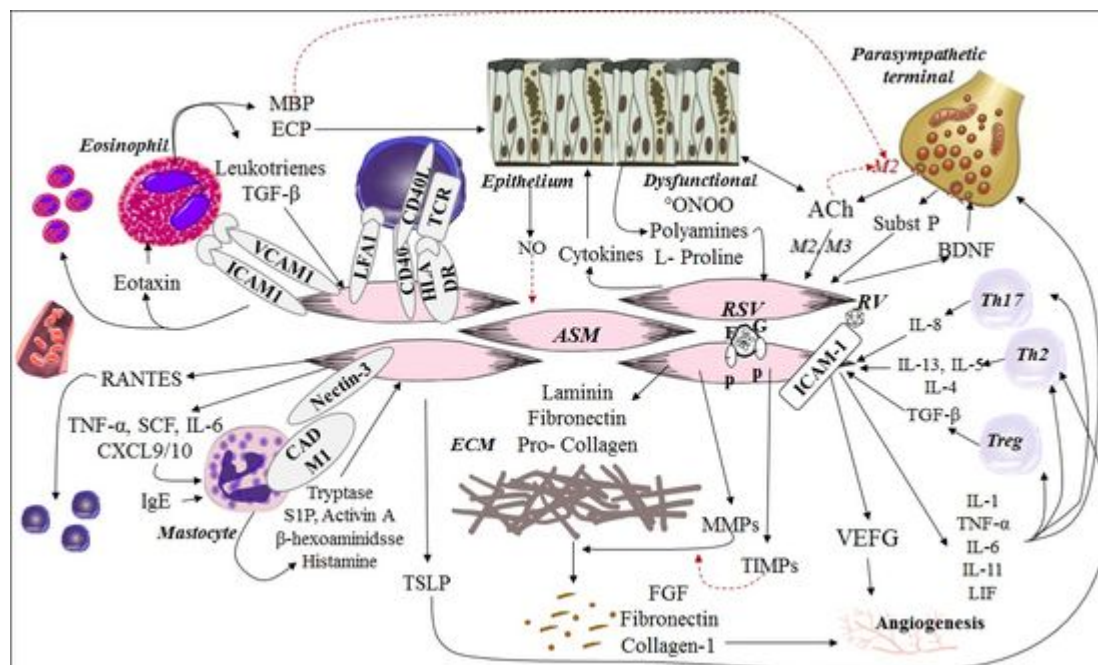


Figure 2. Crosstalk between ASM with cellular and non-cellular components of the airways during inflammation. (See the text for explanation).

Eosinophils are the most prominent inflammatory cells in the airways of asthmatics⁽²¹⁾. In the course of hypersensitivity reactions, eosinophils localize in close relation to ASM. For instance, small airways contain eosinophils in their outer portion (between ASM and alveolar attachment), whereas in the large airways they are present predominantly in their inner portion (between ASM and basement membrane)⁽²⁹⁾. This eosinophil-ASM relationship can enhance cell proliferation by cysteinyl leukotriene secretion⁽³⁰⁾. Eosinophil homing in the airways depends on Th2 cytokines and eotaxin. Adhesion to ASM is mediated by cell adhesion molecules (ICAM-1, VCAM-1) that are constitutively expressed and also upregulated. ASM cells (ASMC)-derived cytokines could promote eosinophil differentiation, perpetuating the burden of eosinophils into ASM bundles⁽³¹⁾.

In a similar way, mastocyte infiltration is prominent in ASM bundles⁽³²⁾. Mastocyte migration and adhesion potentiate tissue remodeling because histamine, tryptase, activin A, sphingosine 1-phosphate (S1P), β -hexosaminidase, and TNF- α , stimulate many ASMC functions⁽³³⁾. Despite these mediators can stimulate cell proliferation, mast cell seems not to be relevant for neither proliferation or survival⁽³⁴⁾. On the other hand, mastocyte can induce the thymic stromal lymphopoietin (TSLP) in ASM that is highly determinant of Th2 polarization⁽³⁵⁾. Mast cell placement, proliferation and survival into the ASM could occur through allergen-independent mechanisms⁽³⁶⁾.

Neutrophilic inflammation also occurs in severe asthma and COPD. Even though, clinical phenotypes that course with predominant eosinophilic inflammation lead to ASM thickening in both large and small airways, the neutrophil infiltration is almost restricted to concurrent small airway remodeling⁽³⁷⁾. A histopathological study of children with fatal untreated respiratory syncytial virus (RSV) infection showed vascular leakage and neutrophil recruitment into the submuscular layer, smooth muscle, and airway epithelium, resembling fatal cases of obstructive diseases⁽³⁸⁾. IL-8 has been implicated, and it seems to be secreted by Th17 cells⁽³⁹⁾. Nowadays, it is known that Th9, Th22, and Th25 cells also modulate countless aspects of airway immunity⁽⁴⁰⁾. Nonetheless, the most significant cytokine expression in asthma includes IL-4, IL-9, IL-13, eotaxin and RANTES. This profile correspond to an upregulated Th2 reaction⁽⁴¹⁾. CD4⁺ T cells transfer from ovalbumin (OVA)-sensitized rats to non-sensitized rats (adoptive lymphocyte transfer), showed that a specific subset of Th2 cells drove airway remodeling in non-sensitized rats after few OVA challenges⁽⁴²⁾. However, evidence from animal models and humans indicate that Th2 hypothesis is an incomplete explanation for asthma pathogenesis, as allergic and nonallergic types are pathologically indistinguishable⁽⁴³⁾. It has also been reported that airway epithelial cells in asthmatics upregulate the EGF receptor (EGFR) expression, a receptor tyrosine kinase (RTK), even in absence of significant eosinophilic inflammation⁽⁴⁴⁾. A recent study demonstrated subepithelial fibrosis in severe asthmatics without evidence of Th2 inflammation⁽⁴⁵⁾. Depletion of CD4⁺ cells, previous to chronic OVA challenge, significantly reduced peribronchial inflammation but did not

completely reverse ASM thickening⁽⁴⁶⁾. Although Th2 cytokines have pro-remodeling actions *in vitro*, controversial results have been found as IL-5 and IL-13 do not increase ASMC proliferation, but they induce phenotypic switching^(47, 48); and IL-4 inhibits ASMC replication⁽⁴⁹⁾. These studies suggest that remodeling can also occur independently of Th2 inflammation and other factors are needed.

COPD is also accompanied by airway inflammation that is different from asthma, but ASM remodeling still occurs⁽²¹⁾. Chronic inflammation induced by chronic cigarette smoking consists of neutrophil, macrophage, B cell, and CD8⁺ T cell recruitment, and it worsens as disease severity increases⁽⁵⁰⁾. T-lymphocytes and macrophages are the predominant cells, being CD8⁺ T-lymphocyte infiltration the most remarkable feature in both large and small airways, and there is also absence of significant eosinophilic inflammation⁽⁵¹⁾. Although, Foxp3⁺ regulatory T cells play a role in fibrogenesis, there is no predominant T CD4⁺ subset. This supports the concept that cyclic events of cytokine and growth factor surges could be the main drivers regardless of the etiology and immune polarization.

An intricate network underlies the ASM and its surroundings, not only immune cells but also neural parasympathetic endings, mesenchymal cells, ECM, and epithelium (see Fig.2). For example, ASM activation by proinflammatory cytokines and substance P can induce the brain-derived neurotrophic factor (BDNF) expression for spatial coordination of neuronal branching⁽⁵²⁾, and vascular endothelial growth factor (VEGF) for control of angiogenesis to assure adequate perfusion, the latter have an important repercussion on vascular leakage and vasogenic edema during fatal asthma⁽⁵³⁾. Neuronal development also would coordinate spatial distribution of ASM, because substance P induces both migration and proliferation⁽⁵⁴⁾. Nevertheless, the airway epithelium could have a greater contribution due to its plasticity and inflammatory properties. Dysfunctional epithelial cells release growth factors, as well as, acetylcholine (ACh) and leukotrienes that could contribute to ASM growth, ECM deposition, and angiogenesis⁽⁵⁵⁾. Moreover, the epithelium is an important source of nitric oxide (NO) in the airways, which has relaxing and other anti-remodeling effects. Physiological NO is produced by constitutively expressed neuronal and endothelial NO synthase (n,e-NOS)⁽⁵⁶⁾. However, cytokines increase inducible NOS (iNOS) and arginase expression. A greater iNOS/arginase activity decreases L-arginine bioavailability, which generates an uncoupled iNOS that not only synthesizes NO, but it also produces superoxide and peroxynitrite. These molecules are capable of causing cellular toxicity and promoting AHR⁽⁵⁷⁾. Functional consequences of increased arginase are reinforced by L-arginine transport blockage with eosinophil-derived polycations. L-Ornithine, a product of urea cycle, is a precursor of polyamines and L-proline, both involved in cell proliferation, collagen synthesis and chromatin remodeling⁽⁵⁸⁾. This exemplifies how noncontractile ASM functions are modulated by many conditions; therefore, the commonest experimental approaches based on univariate analysis can under- or overestimate their contribution on smooth muscle processes.

ASMC are multifunctional

The relevance of ASMCs in pulmonary diseases has been recognized since the last century. The consensus until a few years ago was to consider them just as effectors. However, far from their abilities to contract and relax, ASMCs proliferate, migrate, secrete chemokines/cytokines, and express surface receptors for cell adhesion and leukocyte activation, having a crucial role in airway dysfunction⁽⁵⁹⁾. A concept of plasticity emerged when those functions were associated with specific circumstances and required wide adjustment in gene expression^(60, 61). ASM hypertrophy and/or hyperplasia involve not only outer cell influences, but also ASMC reactions with paracrine/autocrine properties^(7, 62). Quite a lot of molecules could coordinate this loop, such as: growth factors, cytokines, chemokines, ECM molecules, G protein-coupled receptor (GPCR) agonists, natriuretic peptides (NPs), NO, and others⁽⁶³⁻⁶⁶⁾.

Several *in vitro* synthetic functions have been shown. Also, ASM in mild asthmatics has constitutive staining for RANTES⁽⁶⁷⁾. Further cytokines secreted by ASM include IL-1 β and IL-6 family cytokines, such as leukemia inhibitory factor (LIF) and IL-11⁽⁶⁸⁾. These have deeper effects on recruitment, proliferation, and differentiation of eosinophils, mastocytes, T cells, and B cells, establishing a bidirectional regulatory network. Mainly, a CD4⁺ T cell- myocyte crosstalk through direct contact has shown to be determinant of ASM remodeling⁽⁴²⁾. Airway homing of T cells is CCL5 or RANTES-guided, which is released by ASMCs. Likewise, strong adhesion between these two cell types has also been described⁽⁶⁹⁾. Remarkably, even though ASMCs are not usually thought as antigen-presenting cells, evidence supports the expression of major histocompatibility complex class (MHC) II molecules making them capable of antigen presentation. Moreover, ASMCs express the cell adhesion molecules (CAMs)/costimulatory molecules, CD40, CD40L, CD80, CD86, ICAM-1 (CD54), VCAM-1 and LFA-1 (CD11a/CD18)⁽⁷⁰⁾. The CD44-dependent T cell adhesion to ASMCs is not only significant to exchange inflammatory signals, but also to induce ASM hyperplasia through RTK activation⁽⁷¹⁾. This cooperative signaling mediates proasthmatic-like changes in ASM responsiveness, and denotes a potential mechanism of remodeling.

In the airway, a net of collagenous and noncollagenous proteins influences cellular behaviors. ECM components include collagens, fibronectin, members of the matrix metalloproteinase (MMP) family, as well as their inhibitors (TIMP)⁽⁵⁹⁾. After serum stimulation, ASMCs were found to generate elastin, laminin- β 1,-2, and - γ 1, thrombospondin, collagen-I-V, and decorin⁽⁷²⁾. In addition to promoting ECM deposition, ASMCs are capable to affect its degradation. Human ASMCs release progelatinase A (MMP-2 precursor) and, after TNF- α stimulation, gelatinase B (MMP-9)⁽⁷³⁾. MMP production suggests that ASM contributes to ECM turnover, and subsequently the airway remodeling, because inhibition of the autocrine-derived MMP-2 has antiproliferative effects on ASMC culture⁽⁷⁴⁾. Therefore, ECM degradation could be essential for ASM phenotypic modulation, being degradation of the pericellular collagen fibrils a requirement to allow cell division⁽⁷⁵⁾. Serum levels of TIMP-1 and MMP-9 are raised in both asthma and COPD, supporting a straight relationship between clinical expression and tissue remodeling. The MMP-9/TIMP-1 ratio and periostin levels could be consider biomarkers of active disease⁽⁷⁶⁾. Cyclic inflammation/ repair simultaneously occur to cyclic ECM degradation and deposition, which could be a critical phase in ASM thickening.

Crosstalk between ASM Remodeling and Hyperresponsiveness

Airway narrowing and abnormal muscle relaxation are the hallmarks of asthma, COPD, and bronchitis. Multiple mechanisms have been proposed to explain the AHR, like increased vagal tone, cytokine-potentiated increment of free intracellular calcium, increased MLCK activity, and activation of the procontractile Rho kinase pathway⁽⁷⁷⁾. All of them have in common that could hasten the shortening velocity. Therefore, even though remodeling can be triggered by hypersensitivity reactions, infections, environmental pollutants, and developmental abnormalities, AHR could be just generated by unbalanced responses to contractile vs relaxing factors⁽⁷⁸⁾. The role of ASM remodeling as a substrate of AHR was uncertain because functional abnormalities can be seen without changes in the bronchial smooth muscle mass⁽⁷⁹⁾. However, increasingly data supports a role in severe AHR phenotypes, and irreversible or partially reversible airflow obstruction⁽⁴³⁾. The structure determines both passive tone and active responses to agonist stimulation. ASM remodeling involves phenotypic changes that enhance its thickening, and during this process a decline in force induced by repetitive length changes is seen, but then it rapidly adapts and recovers its ability to generate force. In this way, higher passive stiffness could contribute to increased AHR by attenuating the extent of ASM length fluctuations during tidal breathing, i.e., ASMCs adapt by assuming a shorter resting length while retaining its ability to generate force⁽²⁷⁾. For that reason, after induced bronchoconstriction, deep inspiration causes airways of asthmatic individuals to dilate transiently.

Expression of immunomodulatory molecules by ASMCs can delay inflammation resolution and lead to aberrant healing, which is a potential mechanism of AHR⁽⁷⁸⁾. The change in the ASMC population compromises an increase of synthetic properties, which can modulate the contractile mass. Particularly, if it is considered that the whole ASM is coupled by gap junctions, and the calcium dynamic differs between ASMC phenotypes. Propagation of wave-like calcium currents from modulated ASMC to contractile ASM would hypothetically affect not only contractile functions but also noncontractile activities, as discussed in following sections. Other noncontractile elements, including excessive ECM content, may lead to nonreversible airway obstruction by reducing airway distensibility⁽⁸⁰⁾. Whether increased ASM supports abnormal reactions to agonists or makes the airway stiffer, it definitely provides an exceptional substrate for AHR in a framework of progression and severity, at least for asthma. In fatal asthma, airway wall thickness is increased around 50-230%, while in nonfatal asthma it ranges from 25 to 150%, most studies pointing out hyperplasia over hypertrophy as the predominant mechanism^(11-13, 43).

ASMC PLASTICITY: ORIGINS AND PHENOTYPES

The ASM thickening has been studied in many animals and human models, wherein ASMC cultures have provided some ideas about pathways underlying the origin of hyperplasia and hypertrophy. Once ASMC populations were characterized *in vivo* and *in vitro*, heterogeneous

subgroups with distinctive phenotypes were identified. A wide range of functions depend on culture conditions⁽⁶⁰⁾. Manipulating such environments allowed comprehension of the rules for phenotypic transition^(61, 81, 82). Hence, ASMC could be sorted into three categories: 1) contractile (c-ASMC), 2) synthetic/proliferative (s/p-ASMC), and 3) hypercontractile (h-ASMC) (see Table 1). Also, a few switching routes have been described, where *modulation* means a shift from contractile to synthetic/proliferative, and *maturation* is the inverse transition. Turning into hypercontractile is also possible, and some authors have speculated about its irreversibility; however, *in vitro* ASMCs can tolerate cyclic phenotypic adjustments. An important aspect is that modulation and maturation exemplify an adaptation model to tissue microenvironment fluctuations, events that could take place *in vivo* and drive critical phases of airway remodeling. Accordingly, transition from native c-ASMC to s/p-ASMC would be the initial step, then, replication of s/p-ASMC would warrant smooth muscle hyperplasia, and finally aberrant differentiation from either s/p-ASMC or c-ASMC to h-ASMC would cause muscle hypertrophy. How these phenotypical modifications fit in the natural history of airway diseases is a matter of debate.

Phenotypic Markers

Smooth muscle has typical features in primary cultures (see Table 1, Fig. 3). A long cellular body, central nucleus, few granulations, and cytoplasmic inclusions (3A), a confluent monolayer with “hill and valley” aspect (3C), and shrunk reaction to contractile agonists define smooth muscle cells⁽⁸³⁾. However, each ASMC subpopulation has specific characteristics. For example, the synthetic/proliferative phenotype has satellite flattened shape with multiple extensions (3B), a high number of organelles for protein and lipid synthesis, abundant mitochondria, a higher proliferative response, decreased contractile proteins, shutdown of responses to contractile agonists, and secretion of growth factors, collagen, cytokines, bradykinin, and eotaxin^(81,84). Furthermore, modulated ASMCs show increased protein expression of fetal and non-muscle isoforms. Synthetic and proliferative functions do not correspond to different traits. Indeed, the cell distribution with synthetic activities could vary between 20 to 60%, and almost half of replicating ASMCs produce cytokines. Also, secretion can be done by non-replicating cells⁽⁸¹⁾. On the other hand, the contractile phenotype is associated with a decreased number of synthetic organelles, a stronger response to contractile agonists, increased expression of contractile and structural proteins, and an increased M3/M2 muscarinic receptor expression rate⁽⁸⁴⁻⁸⁶⁾. Other markers including Ca²⁺ profiles⁽⁸⁷⁾, miRNA expression⁽⁸⁸⁾, and transcription factors expression⁽⁸⁹⁾ have been useful for phenotype distinction.

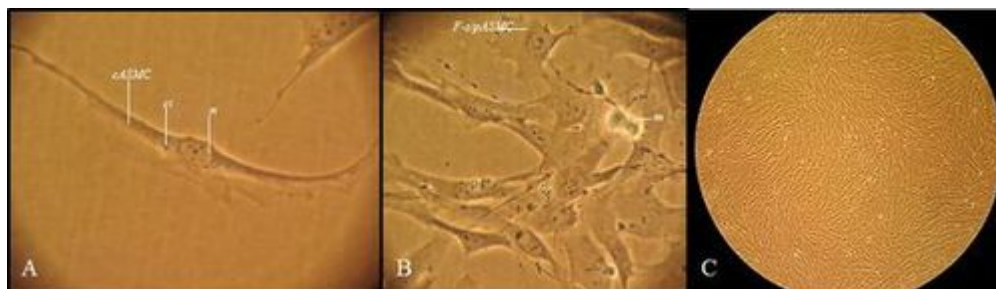


Figure 3. Primary cultured of Rat ASMCs. Cells were obtained by enzymatic digestion of rat trachea and cultured in supplemented medium as previously described(122) . (A) Contractile phenotype, (ci) cytoplasmic inclusions, (n) cell nucleus. (B) When the cell population underwent to growth some cells adopted a myofibroblast-like morphology (F-s/pASMC), (m) mitosis. (C) Cell confluence of 80-90%, cell population readopted contractile morphology with a hill and valley array. Magnification 400X A, B, 100X C.

Table 1. Characterization and Biomarkers of ASMC Phenotypes

Phenotype	Contractile	Synthetic/ Proliferative	Hypercontractile
Function	Regulation of airway resistance	Immunomodulation ECM Turnover Chemotaxis ASM hyperplasia AHR	ASM hypertrophy AHR
<i>Features in primary culture</i>			
Induction	Maturation - High density - Serum starvation	Modulation - Low density - Mitogens	Cyclic exposure to: - Mitogens, TGF- β
Proliferative rate	Slow	Fast	--
<i>Morphology</i>			
Shape	Elongated-spindle	Satellite Flattened	Elongated-spindle
Myofilaments	+	+/-	+++
Contractile	++	↓	++
proteins/cell size ratio			
Mitochondria	+	+++	++
SR/ Golgi apparatus	+	+++	++
Caveolae	+ (> 150.000)	-	+++
Gap junctions	+++	+	+++
<i>Biomechanics</i>			
V₀/V_{max}	Normal	↓	↑↑↑
Contribution to airway resistance	Reversible (normal contraction-relaxation)	-- (affect dynamics of contractile mass)	↑↑↑: ↓ relaxation
Response to agonists	+	+/-	+++ : AHR
<i>Biomarkers</i>			
<i>Contractile Proteins</i>			
sm-α-actin	++	+++	++
sm-MHC	++	+/-	++
<i>Structural Proteins</i>			
non-sm-actin (β/γ)	+/-	+++	++
non-sm-MHC	+/-	+++	?
vimentin	+	+++	?
smoothelin-A	++	+/-	?
SM-22	++	+/-	?
<i>Regulatory Proteins</i>			
MLCK	++	+/-	++++
h-Caldesmon	++	+/-	?
l-Caldesmon	+/-	++	?
Calponin	++	+/-	?
Caveolin	+++	+/-	?
Desmin	++	+/-	?
PKC ($\alpha/\beta I/\beta II$)	+/-	+++	?
CD44	+/-	+++	?
M₃AchR	++	+/-	+++
ET_A receptor	++	+++	?
ET_B receptor	++	+/-	?
Dystrophin	++	+/-	?
Integrin $\alpha_7\beta_1$	++	+/-	?
Cathepsin k	+	++	?
FSP	++	+	?
AKR1C3	-	-	-
<i>Calcium Dynamics</i>	Sparks	Waves	Sparks

++: expressed; +++: highly expressed; ++++: very highly expressed; +/-: poorly expressed; V₀: velocity of shortening; V_{max}: maximum shortening capacity. ?: unknown, ↑: increased, ↓: decreased, h: heavy form, l: light form, FSP: fibroblast surface protein, AKR1C3: Aldo-keto reductase 1C3 (specific marker of mesenchymal cells)

Evidence of *in vivo* Plasticity

Several findings support *in vivo* occurrence of ASMC plasticity, especially in asthma. Plasticity is a universal property of primary ASMC cultures derived from both healthy and diseased humans, and healthy and sensitized animals. Immunohistochemistry to identify contractile proteins is highly variable as well, which can reflect a broad heterogeneity of myocytes in the normal airway that is maintained in cell culture, as demonstrated by a divergent proliferative capacity⁽⁹⁰⁾. If functional features are compared, healthy or control vs asthmatic or sensitized groups, significant differences can be found. ASMCs from asthmatics or sensitized animals show more proliferative and synthetic capabilities than their physiologic counterparts, findings that are preserved despite tissue dissolution followed by cell culture^(62, 66, 89, 91-93). Abnormal ASMCs could not only resemble s/p-ASMCs or arise from c-ASMCs, but also have distinctive features such as: abnormal protein synthesis⁽⁹⁴⁾, expression of odd transcription factors isoforms with a lack of response to glucocorticoids⁽⁹¹⁾, increased mitochondrial biogenesis and activity⁽⁹³⁾, abnormal calcium dynamics⁽⁹²⁾, increased CysLTR-1 leukotriene receptor expression⁽⁵⁵⁾, increased activity of promitogenic pathways⁽⁹⁵⁾, and declined of antiproliferative pathways⁽⁶⁶⁾. In consequence, an increased ASM mass may be explained by *intrinsic* alterations in pathological ASMCs that facilitate their proliferative and secretory activities. Asthmatic ASM produces more proinflammatory, proangiogenic, and proremodeling factors, including eotaxin, VEGF, and connective tissue growth factor (CTGF), and fewer antimitogenic factors, such as E2- type prostaglandin (PGE2)⁽⁵⁹⁾. These would reflect deeper differences in cell populations that constitute the ASM under pathological settings, and they would likely originate from comparable modulation and maturation events on native ASMCs.

Many questions arise from the alterations observed on asthmatic or sensitized cultured ASMCs. Based on the plasticity phenomena, any transformation of *in vivo* ASMC phenotype which persistence depends on tissue microenvironment should not be seen *in vitro* because the phenotype will adjust to culture conditions. Although, cited studies do not precise whether those pathologic features are irreversible along culture passages, persistence of functional abnormalities after tissue fragmentation and culturing suggests that these cells underwent through a dysfunctional route of phenotypic modulation, which could be at least partially irreversible. In view of that, epigenetic mechanisms could be a suitable explanation to such phenotypic switch. For example, eotaxin hypersecretion by ASMCs has been related to histone H4 lysine 5 and lysine 12 acetylation at the eotaxin promoter induced by TNF- α ⁽⁹⁶⁾. Other synthetic activities, such as VEGF hypersecretion, were due to a loss of a repression complex, in which a differential histone H3 lysine 9 methylation modulating Sp1 and RNA polymerase II binding to the VEGF promoter was implicated⁽⁹⁷⁾. Binding of serum response factor (SRF), a transcription factor that controls phenotypic stability, to DNA is associated with post-transcriptional histone modifications including di-methylation of lysine residues 4 and 79 on histone H3, acetylation of lysine 9 on histone 3 and acetylation of histone H4. Histone deacetylases (HDACs) have also been implicated in regulating smooth muscle replication because the HDAC inhibitor TSA can prevent cell proliferation⁽⁸⁸⁾. In *in vivo*, the valproic acid (HDAC inhibitor) did not affect inflammation induced by OVA challenges, but notably reduced the airway thickening including the ASM with blunting of AHR⁽⁹⁸⁾. In addition to HDAC modifications, DNA methylation can generate a specific long-term *signature*. For example,

expression of IL-13 in the airways ensued significant changes in methylation of 177 genes, most of which were associated with a Th2 signature over resident cells⁽⁹⁹⁾. Using methylated DNA immunoprecipitation-next generation sequencing (MeDIP-seq), it was determined that airway remodeling and AHR in house- dust- or mite-sensitized rats are related to specific methylation patterns at several TGF- β signaling-related genes⁽¹⁰⁰⁾, explaining the longevity of abnormal pro-fibrotic responses of local cells during inflammation and phenotypic persistence after tissue extraction. Unfortunately, there is currently no direct evidence of epigenetic regulation of ASMC proliferation. Moreover, whether or not DNA methylation or histone acetylation can influence phenotypic switching have to be determined as well. The contribution of miRNAs will be discussed in following sections.

Potential Sources of ASMCs

The *in vivo* source of ASMCs under pathological conditions is unclear. ASM may originate from increased proliferation or prolong survival of preexisting smooth muscle with proliferative and/or contractile phenotype; however they could also arise from other cell lines that could migrate into the bundles and then differentiate into ASMCs (see Fig.4). Remarkably, other airway cells may undergo to phenotypic modulation that is characterized by α -sm-actin expression and development of organelles for synthetic functions. Accordingly, mesenchyme such as fibroblasts may generate myofibroblasts, whose classical phenotypic markers are indistinguishable from s/p-ASMCs⁽¹⁰¹⁾. This fact allowed researchers to postulate a spectrum of mesenchymal plasticity (fibroblasts \leftrightarrow myofibroblasts \leftrightarrow ASMCs)⁽¹⁰²⁾. However, it does not undermine experimental findings obtained with *in vitro* systems, as a high proportion (~60%) of primary airway mesenchymal cultures truly correspond to primary smooth muscle⁽⁶⁰⁾.

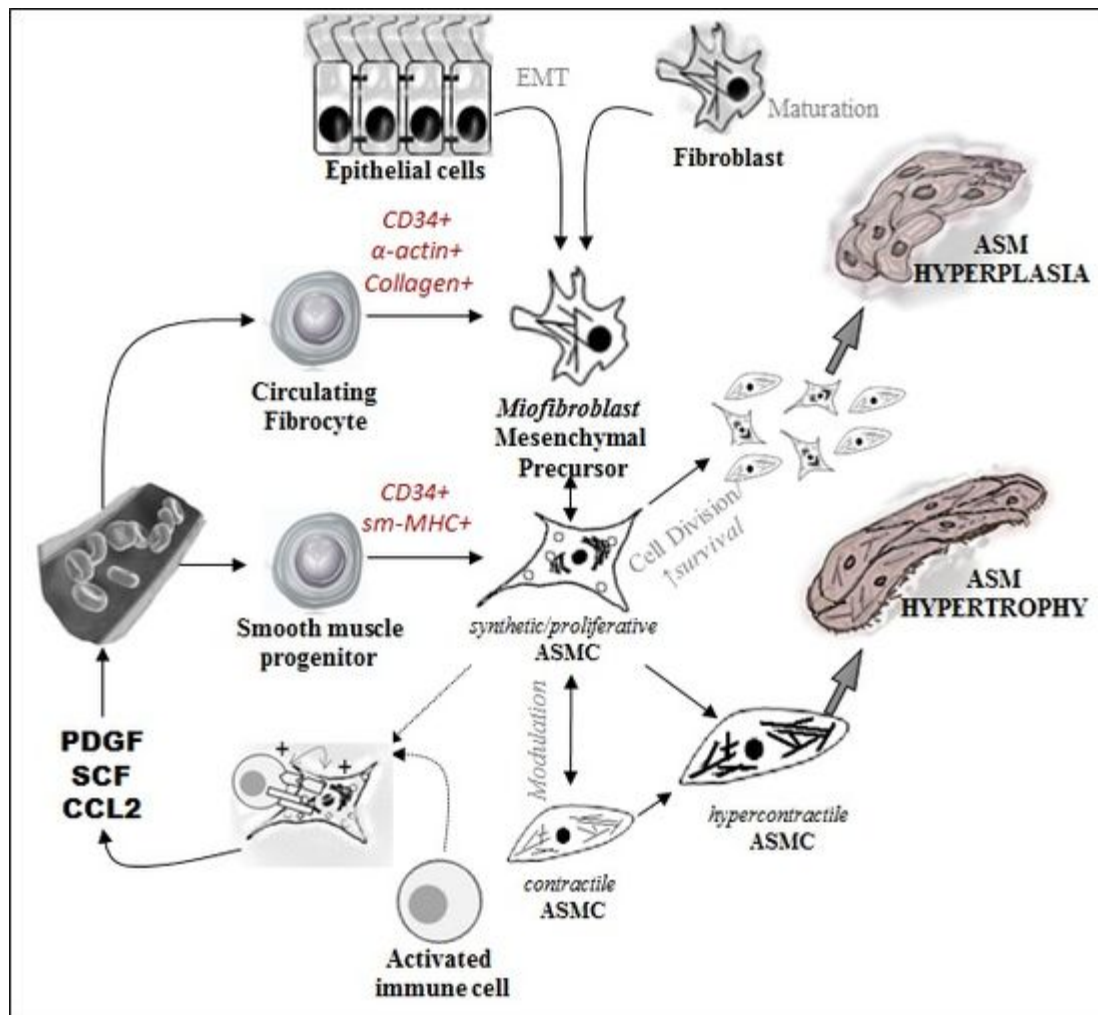


Figure 4. Potential sources of ASMC precursors in the origin of ASM thickening. (See the text for explanation).

Potential progenitors also include true multipotent mesenchymal progenitors and stem cells, either located within the airway or derived from peripheral blood. For example, CD34⁺-CCR7⁺-Collagen 1⁺-sm- α -actin⁺ circulating fibrocytes can migrate towards ASM bundles during inflammatory challenges, and they were unresponsive to the apoptotic effects of glucocorticoids in culture⁽¹⁰³⁾. Fibrocyte migration is directed by the ASM-derived PDGF and CCL2, and at that point its co-locating induces proinflammatory activities in ASMCs^(104, 105). A rare population of CD34⁺-sm-MHC⁺ peripheral mononuclear cells (known as smooth muscle progenitors) has been identified by flow cytometry in OVA-sensitized mice. A similar population seems to generate the smooth muscle in atherosclerosis; however, the study did not precise whether stem cell homing occurred into ASM bundles⁽¹⁰⁶⁾.

The airway epithelium can turn into mesenchymal cells through the epithelial-mesenchymal transition (EMT) route, which has been considered as another source of ASMCs⁽¹⁰⁷⁾, but a lineage-tracing study suggests that it may just be a consequence of culture conditions and could not occur *in vivo*⁽¹⁰⁸⁾. In asthma, epithelial cells show fragileness due to downregulation

of cell adhesion molecules, which makes EMT more likely⁽¹⁰⁹⁾. EMT is initiated by extracellular signals, such as collagen or hyaluronic acids, and by growth factors like TGF- β and EGF⁽¹¹⁰⁾. This process is modulated by bone morphogenesis proteins, and allergen exposure, which amplifies and accelerates it⁽¹¹¹⁾. Hormones have also been associated, since vitamin D attenuates TGF- β -induced expression of EMT markers⁽¹¹²⁾. Epithelial and mesenchymal cells express both type-1 and type-3 muscarinic receptors (M1, M3)⁽¹¹³⁾. TGF- β -induced EMT was abolished by muscarinic receptor (mAChR) antagonists and enhanced by acetylcholinesterase (AChE) inhibitors⁽¹¹⁴⁾. A positive feedback loop of autocrine and paracrine production of non-neuronal acetylcholine (ACh) and TGF- β orchestrates EMT during chronic inflammation, being a likely source of ASM.

Additionally, an increased number of fibrocytes was observed in the ASM bundles from asthmatics of all severities⁽¹¹⁵⁾. However, this study failed to show any link with the lung function, and this location could not be considered abnormal as fibrocytes are normal constituents of ASM bundles under physiological conditions⁽¹¹⁶⁾. An increased in mesenchymal cells would be nonspecific and occur in parallel to other cellular changes ongoing in the ASM bundles. Although, many airway cell lines can follow similar modulation pathways as native ASMCs, we focus here on how the behavior and responses of c-ASMC vs s/p-ASMC can explain many abnormal structural and functional features seen on airway diseases.

ACETYLCHOLINE: MORE THAN BRONCHOCONSTRICTION

The parasympathetic network penetrates deeply the airway wall and regulates bronchoconstriction. ACh is the predominant parasympathetic neurotransmitter. Although, ASM express both cholinergic receptors, nicotinic receptors (nAChRs) and mAChRs, the cholinergic effects seem to be mediated by muscarinic activation⁽¹¹⁷⁾. In asthma, cutting the parasympathetic supply of the airways (vagotomy) prevents an increased smooth muscle contraction⁽¹¹⁸⁾, and AHR induced by persistent parasympathetic activation has been shown⁽¹¹⁹⁾. The striking role of ACh in airway remodeling was highly commented in a recent article⁽⁸⁾, where authors proposed methacholine-induced bronchoconstriction as the main driver of epithelial hyperplasia and subepithelial collagen deposition, independently of inflammation, as chronic stretch and mechanotransduction pathways are well-known mechanisms of muscle differentiation. However, the cited study failed to conclusively demonstrate that only mechanical stress was responsible of all histopathological changes, because they did not assess the non-neuronal and non-contractile effects of cholinergic networks, a non-asthmatic group was not included (taking into account that inflammatory signatures on resident cells change their responses), and ASM layers were not assessed. Nonetheless, despite the limitations, the contribution of ACh in airway remodeling was uncovered.

Two ACh sources have been identified: 1. neural, along parasympathetic fibers from vagal

nerve, and 2. non-neural, from airway epithelium and immune cells. Both are implicated in increased ASM thickening in asthma⁽¹²⁰⁾, which was prevented by M3-specific antagonists such as tiotropium bromide⁽¹²¹⁾. Also, M2 is expressed and its downstream signaling has been related to modulation of some ASM functions, either promotion or inhibition⁽¹²²⁾. ACh, either neuronal or non-neuronal, regulates inflammatory cell responses that may explain the anticholinergic benefits in asthma and COPD⁽¹²³⁾. Collectively, these findings are revealing new therapeutic targets, therefore, we chose the cholinergic signaling pathway to be explored deeply in this review as a prototype of GPCR agonism.

Muscarinic Receptor Signaling

The mAChR family consists of five receptor subtypes that belong to GPCRs. Mammalian airways including humans express M1, M2, and M3 subtypes; more precisely, epithelial cells (M1-M4), pulmonary vessel endothelial cells (M1-M5), mesenchymal cells, such as smooth muscle fibers (M2, M3) and fibroblasts (M2 > M1 > M3 > M4), and lung-infiltrating immune cells, such as mononuclear leukocytes (M1-M5)⁽¹²⁴⁾. The M4 mRNA and protein have been reported in rabbit bronchiolar ASM, but not from humans. Although, pharmacological ligand binding studies showed a mixed population M2:M3 in a 4:1 ratio, respectively, a functional dominance of M3 appears to mediate muscarinic effects under physiological circumstances⁽¹²⁵⁾. This predominance could be a consequence of receptor compartmentalization, facilitating or inhibiting signal transduction depending on accessibility to specific transducers or kinetic regulation. M3-induced bronchoconstriction is mainly mediated by a caveolae-dependent system. M2 contribution was mainly uncovered in M3^{-/-} knockout mice with cellular caveolae dissolution. Location of M2 and M3 in caveolae is dependent on Caveolin-1 (Cav-1) and Caveolin-3 (Cav-3) expression, respectively⁽¹²⁶⁾. Many processes involve coupling of mAChRs to their cellular effector systems, via heterotrimeric G proteins. These are composed of one α -, β - and γ -subunit and transduction signals depend on both the α -subunit and $\beta\gamma$ -subunit. In ASMCs, muscarinic activation is classically considered as the main signal for muscle contraction. However, there is increasing evidence indicating that alterations in its downstream signaling pathways might be responsible for ASM remodeling and AHR⁽¹²⁷⁾.

Muscarinic signaling can be divided into pathways for muscle contraction and those with non-contractile effects. In this way, the Gq-coupled M3 activates phospholipase C (PLC), causing hydrolytic conversion of phosphatidylinositol 4,5-bisphosphate (PIP₂) into inositol 1,4,5-trisphosphate (InsP₃) and sn-1,2-diacylglycerol (DAG). InsP₃ is involved in Ca²⁺ mobilization from intracellular stores, which generates a rapid and transient increase for muscle contraction, while generated DAG activates PKC with subsequent triggering of mitogen-activated protein kinase (MAPK) signaling for non-contractile effects. Also, MAPK cascade can be activated through direct phosphorylation of Raf-1, independently of PKC⁽¹¹⁷⁾. β -arrestins mediate homologous receptor desensitization and endocytosis via clathrin-coated pits of agonist-activated GPCRs. The third intracellular loop (i3) of M3 is required for β -arrestin recruitment after homodimerization (M3/M3) and heterodimerization (M2/M3). Those macrocomplexes not only induce downregulation of mAChRs, but also act as scaffolds for components of the MAPK cascade, facilitating its activation⁽¹²⁸⁾. This is a third mechanism of

M3 signal transduction for cell growth and differentiation.

As a counterpart, Gi/o-coupled M2 contributes to muscle contraction either affecting adenylyl cyclase in an inhibitory manner, or directly enhancing potassium and non-selective ion channels opening, and they both depend on the released $\beta\gamma$ dimer. Additionally, M2 modulates the relaxant effects of atrial natriuretic peptide (ANP), as it suppresses the ANP-induced activation of a membrane-spanning guanylyl cyclase via a pertussis toxin (PTX)-sensitive G protein⁽¹²⁹⁾. Since Gi/o is involved in muscarinic-induced actin reorganization, RhoA/Rho-kinase signaling pathway has been related to Ras and phosphoinositide 3-Kinase (PI3-K) activation, contributing to growth factors effects⁽¹²⁰⁾.

The complexity of non-canonical muscarinic signaling is illustrated by the ambiguity of their downstream pathways. The cGMP/PKG pathway is a well-documented mediator of muscle relaxation, and it has also anti-remodeling effects. Molecular evidence suggests it could depend on which compartment is activated and signal pattern. Some cascades activated by mAChRs are linked to second messengers such as cGMP by activation of two distinctive guanylyl cyclases. Muscarinic activation of tracheal ASM fragments is associated with contraction, but it also involves the generation of two cGMP signals, at 20-s and 60-s⁽¹³⁰⁾. These signals seem to be essential in reaching the contractile effects of several muscarinic agonists and might be relevant in ASM remodeling. The proposed model⁽¹³¹⁾ for this novel pathway emphasized that 20-s cGMP signal is linked to Gi/o coupled M2 activation, inducing a massive and transient $\alpha 1\beta 1$ -NO-soluble guanylyl cyclase (sGC) translocation from cytoplasm to plasma membranes, whereas, the 60-s cGMP signal is associated with a natriuretic peptide receptor (NPR)-GC-B, activated by a Gq16-coupled M3 sensitive to mastoparan. Those signals regulate the muscarinic signal transduction efficacy in response to agonists through phosphorylation events. In this way, M3 phosphorylation by PKG-II may correlate to changes in the receptor affinity to agonists and antagonists. It has been proposed that cGMP induces PKG phosphorylation of the i3 loop that confers a potential feedback mechanism to terminate the cGMP-dependent muscarinic signal transduction cascades at the sarcolemma⁽¹³²⁾. Since phosphorylation of the same loop by others serine/threonine kinases downregulates the receptor by endocytosis and G protein uncoupling, indirect observations suggest that PKG-II phosphorylation of M3 induces a mAChR dimer formation. Homodimer formation stabilizes or 'freezes' the M3 population, in a refractory state to agonist activation, and prone to antagonist binding⁽¹³²⁾. We speculate in caveolae systems a higher density M3 receptor population would support positive cooperativity through homodimer/heterodimer formation, which could enhance the signal transduction for MAPK activation and subsequent altered gene expression. Thus, cGMP produced in response to muscarinic agonists could be involved in growth promotion instead of classical cell arrest. Relevantly, we demonstrated that this pathway is still functional in sensitized ASMCs, while cGMP cascade induced by NPs and NO was downregulated⁽¹³¹⁾. A wide-spectrum of outcomes can result from diverse experimental designs. This complicates our understanding of the cholinergic signaling in human airway diseases. A brief scheme that will be discussed herein, includes effects related to remodeling promotion: 1. c-ASMC modulation, 2. s/p-ASMC proliferation synergism, and 3. synergism on h-ASMC induction, and alternatively possible actions for remodeling prevention like decreased s/p-ASMC proliferation. Although, *in vivo* relevance keeps hypothetical, this provide a coherent

and useful picture for planning future research.

MODULATION VS MATURATION

Signaling Pathways Associated with Maturation

Phenotypic switching is regulated by growth factors, GPCR agonists, ECM molecules, and other mediators found in the bronchoalveolar lavage (BAL) of patients with asthma or COPD^(133,134). The contractile phenotype induction is attainable after exposure to either TGF- β , insulin, or laminin⁽¹³⁵⁻¹³⁸⁾. Also, maturation can be supported by lacking of mitogens; in primary ASMC cultures (see Fig.3C), high cell confluence lead to cell cycle arrest by cell contact^(82, 86). sm-specific protein expression is enhanced by RhoA/Rho Kinase and/or PI3-K activation. RhoA/Rho kinase promotes actin polymerization as a downstream effector of either GPCR- or RTK-associated pathways (see Fig.5). Subsequent phosphorylation events, RhoK \rightarrow phospholipase D (PLD) \rightarrow LIMK-1 \rightarrow cofilin could be responsible for G-actin polymerization into F-actin⁽¹³⁹⁾. A decrement in globular actin level releases some proteins into the cytosol, like the transcriptional coactivator megakaryocytic acute leukemia/ megakaryoblastic leukemia-1 (MAL/MKL-1), which can be trafficked into the cell nucleus and make a macrocomplex with both myocardin (other coactivator) and SRF, a transcription factor. As a whole, they bind gene promoters to increase sm-specific gene expression^(140, 141). TGF- β can amplify this pathway for hypercontractile phenotype induction. Type-1 and type-2 TGF- β receptor activation induce phosphorylation and nuclear translocation of Smad proteins that bind to SRF, building up a macrocomplex similar to MAL/MKL-1/myocardin/SRF, with subsequent gene expression modifications⁽¹⁴²⁾.

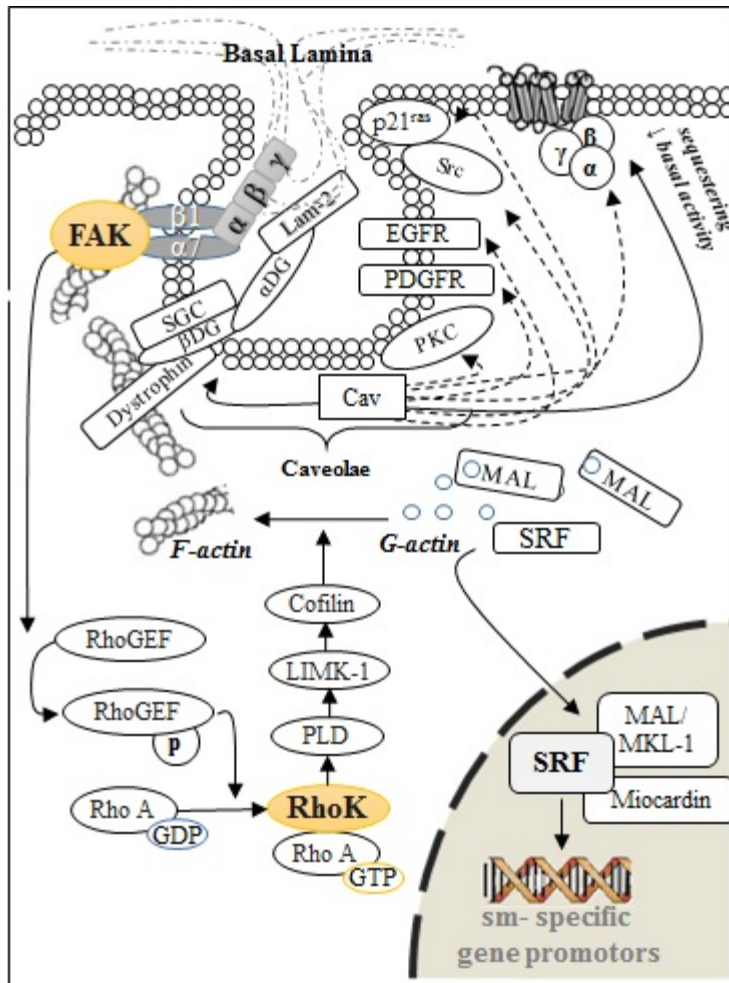


Figure 5. Signaling pathways involve in preserving the ASM in a differentiated state.

The Akt/PI3-K pathway also affect sm-specific gene expression through the transcription factor FOXO-4^(143, 144). Unphosphorylated FOXO-4 binds myocardin and inhibits its association with SRF. Hence, myocardin is released once PI3-K phosphorylates FOXO-4. However, the reach of this pathway goes far beyond transcriptional regulation. Signaling pathways that converge to ribosomal regulation are needed to complete ASMC maturation, which include effectors such as PI3-K, Akt-1, mammalian target of rapamycin (mTOR), and p70 ribosomal S6 kinase (p70^{S6K}). Pharmacologic inhibition of PI3-K and mTOR are enough to prevent p70^{S6K} activation and sm-specific protein accumulation⁽¹⁴³⁾. Moreover, activated mTOR can phosphorylate eIF4 binding protein-1 (4E-BP1), releasing and increasing the eukaryotic initiation factor-4 (eIF4) activity⁽¹⁴⁵⁾, followed by contractile protein accumulation (see **Fig. 6B**).

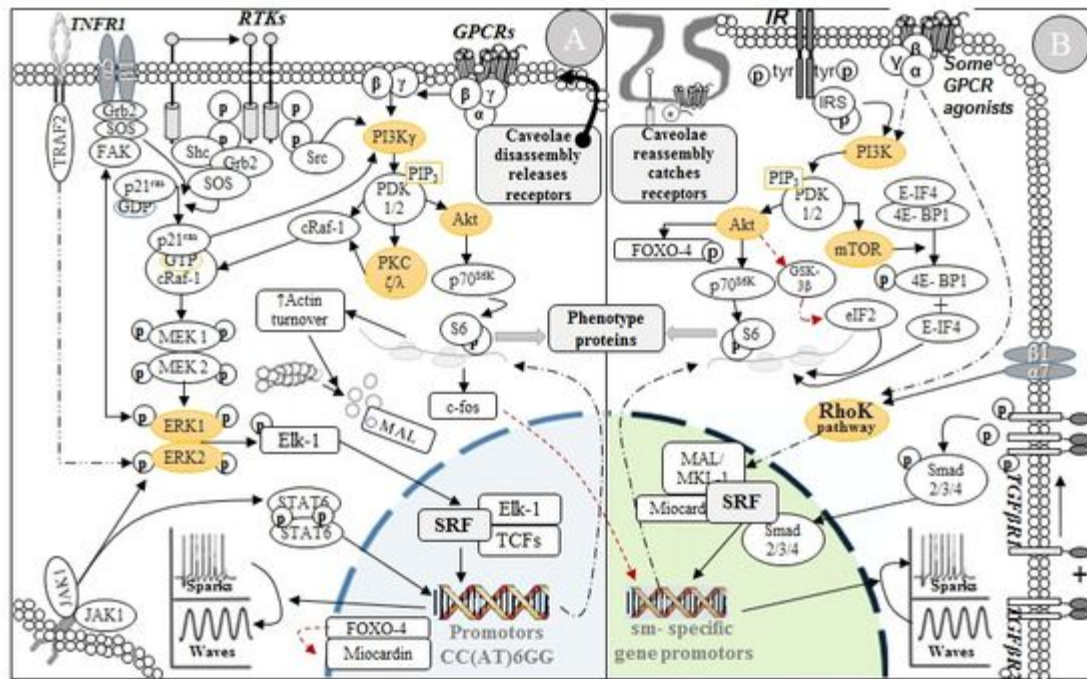


Figure 6. Signaling pathways involve in the control of ASM phenotypes. (A) Modulation, (B) Maturation.

Persistence of the c-ASMC phenotype is highly dependent on caveolae membrane system and cav-1 expression (see Fig. 5)⁽¹⁴⁶⁾. These flask-shaped structures are classically considered as special compartments for signaling regulation. Cav-1 is located inside those microdomains, being responsible for their formation and maintenance. Interestingly, cav-1 leads to reduced basal activity and sequestration of several receptors and signal transducers related to synthetic/proliferative phenotype induction, such as: PKC, PDGFR, EGFR, Src, and p21ras⁽¹⁴⁷⁾. Proteins such as α -subunit of G proteins, Rho family members, adenylate cyclase isoforms, 7TM receptors, and others with binding domains to glycosyl- phosphatidylinositol are regulated as well. Caveolae act on behalf of cell adhesion by linking the actin cytoskeleton with the basal lamina, facilitated by laminin-2/ $\alpha 7\beta 1$ integrin interaction. The triggered downstream pathway activates a guanine nucleotide exchange factor, RhoGEF, leading to Rho Kinase activation⁽¹⁴⁷⁾. For this reason, it is possible that mitogen stimulation is not enough to ignite ASM maturation and cell division, thus caveolae disassembly would be a strict requirement⁽¹⁴⁸⁾.

Laminin is a trimer that bind integrins and non-integrin receptor subtypes, including the dystrophin-glycoprotein complex (DGC). PI3-K inhibition prevents both ASM maturation and accumulation of DGC proteins, β - and α -DG⁽¹⁴⁹⁾. Preferential expression of DGC in c-ASMC is related to a tighter regulation of reactions to contractile agonists by caveolae system. There is also evidence suggesting that DGC, through β -DG, influences signal transduction by scaffolding properties and interactions with cav-1⁽¹⁵⁰⁾. Additionally, basal activity and low grade stimulation of some RTKs, such as the insulin receptor (PI3-K pathway) and GPCRs (Rho Kinase pathway), could have a role in contractile phenotype conservation, especially in confluent cells. These observations acquire more relevance considering that the ASM mass is likely composed of c-ASMC under physiological conditions. In the disease-setting, ECM

component dissolution by MMPs affect the ASMC attachment, shutting down the Rho kinase activity. Unconstrained ASMCs are more susceptible to paracrine influences. Thus, high levels of cytokines and growth factors, and subsequent anomalous repair due to TGF- β , might match with a continuous and dynamic process of phenotypical modulation (contractile \rightarrow synthetic/proliferative \rightarrow hypercontractile/fibrotic), explaining the ASM thickening and dysfunction.

Signaling Pathways Associated with Modulation

Transition to a synthetic/proliferative phenotype is enhanced by mitogens such as PDGF, EGF, IGF, fibronectin, collagen-I and -II, bradykinin, GPCR agonists, cigarette smoke extract, lipopolysaccharide (LPS), and reactive oxide species (ROS)^(151, 152). Modulation is quickly reached when *in vitro* ASMCs are not confluent under mitogenic influences (see Fig. 3B), especially fetal bovine serum (FBS) and fetal calf serum (FCS)^(86, 122). Associated pathways converge to increase c-fos (coactivator) expression, which paradoxically needs a prior SRF activation in order to alter gene expression⁽¹⁴⁴⁾. Nevertheless, this apparent duality could be due to a wide variety of transcriptional coactivators that assertively induce selective gene transcription. Contrasting the SRF-myocardin complex effect, SRF cooperativity with ternary complex factors (TCF) such as Elk-1 affects gene promoters with a CArG (CC(AT)6GG) sequence, inducing cell proliferation instead of maturation. In this way, c-fos upregulation is key to halt contractile gene expression⁽¹⁵³⁾. Furthermore, this coactivator Elk-1 is phosphorylated and activated by the extracellular signal-regulated kinase (ERK)-1 and -2⁽¹⁵⁴⁾. These kinases along with p38, c-Jun N-terminal kinase (JNK), janus kinases (JAKs), and transcriptional factors, like NF κ B and AP-1, could participate in signal delivery to increase synthetic and proliferative activities⁽¹⁵⁴⁾. Protein synthesis associated with modulation is also favored following S6 ribosomal subunit phosphorylation⁽¹³⁸⁾. Increased cytoskeleton metabolism with actin polymerization blockade generates G-actin accumulation that avoids nuclear translocation of MAL/MKL-1. Also, it has been described that *in vitro* both maturation and modulation are reversible.

ASMC modulation is improved by Th2 cytokines. A mix with TGF- β and leukotriene D4, triggers the expression of 29 transcription factors⁽¹⁵⁵⁾. IL-13 is relevant to control the expression of around 300 locus. Its receptor, the IL-13R α 1/IL-4R α complex, mediates the phosphorylation of STAT-6, triggering MAPKs for phenotypic modulation⁽¹⁵⁶⁾. IL-13 can also affect calcium dynamics by upregulation of sarcolipin, which is a transmembrane protein placed at the sarcoplasmic reticulum (SR) that inhibits the sarco/endoplasmic reticulum Ca²⁺-ATPase (SERCA) activity⁽¹⁵⁷⁾. Expression of calcium regulatory proteins changes with modulation, therefore, a decrease in voltage-dependent calcium channels, ryanodine receptors, and SERCA2 levels translate into a calcium dynamics dominated by wave-like propagations. This kind of flow contributes to MAPK pathway activation. Ca²⁺ waves also affect the conformational stability of cis elements in 5'untranslated regions (UTRs) of mRNAs and interactions between translational components, regulating protein synthesis⁽¹⁵⁸⁾. IL-13 signaling is under control of the type-1 suppressor of cytokine signaling (SOCS-1), a protein with chaperone properties. SOCS1 expression is decreased in asthmatic ASMCs and its

inactivation raises synthetic activities when exposure to Th2 cytokines⁽¹⁵⁹⁾. In summary, diverse signaling pathways are responsible for driving phenotypic modulation of ASMCs (see Fig. 6A).

Muscarinic Activation leads to ASMC modulation

ASM thickening is attainable by persistent muscarinic stimulation⁽¹²⁷⁾. Both pathways, Gi/o coupled M2 and Gq coupled M3, could generate the activation of MAPK, Rho-kinase, and PI3-K signaling⁽¹¹⁷⁾. Moreover, shifting from a synthetic-proliferative to a contractile phenotype is accompanied by a decrease in M2 and a parallel increase in M3 expression⁽¹⁶⁰⁾. Those observations inquire whether or not cholinergic stimulation may affect phenotypic switching. Accordingly, long-term incubation of rabbit ASMCs with ACh or carbachol (CCh) induced a switch towards s/p-ASMC⁽¹⁶¹⁾. Prolonged treatment of bovine ASM strips with the methacholine also diminished contractile protein expression⁽¹⁶²⁾. Transition to a synthetic-proliferative phenotype is characterized by M3 downregulation and blunted contractile responsiveness to cholinergic stimulation⁽¹⁶¹⁾. In cited studies, signaling pathways were not evaluated, but considering that cholinergic-induced mitogenesis is related to MAPK activation, it is possible that muscarinic activation allows the nuclear translocation of Elk-1, affecting gene expression linked to the phenotype transition.

Role of non-coding RNAs on Phenotypic Stability

The miRNAs are small noncoding RNAs that have an outstanding participation in gene expression regulation. It makes them excellent candidates to control cell plasticity. Multiple mechanisms are involved in miRNA synthesis and gene regulation, as it was previously described⁽¹⁶³⁾. Shortly, mature miRNA is part of the active RNA- induced silencing complex (RISC) that mediates miRNA/mRNA interaction in a specific fashion. This interaction mostly occurs in the 3'UTR by partial complementarity, thus, miRNAs inhibit elongation during translation, or destabilize mRNA promoting its degradation. In smooth muscle biology, multiple miRNAs regulate cell differentiation and proliferation, under physiological and pathological conditions, especially in vascular smooth muscle, although little is known about ASM (see **Table 2**)⁽¹⁶⁴⁾.

Table 2. Functions of non-coding RNAs in ASM

	RNA (Contribution/ Effect)
<i>Phenotypic Stability</i>	miR-25 (↑modulation) miR-10a (↑maturation, keeps steady state, stem cell differentiation to smooth muscle) miR-26a (↓proliferation, hypercontractile induction) miR-143, miR-145 (↑ accumulation contractile proteins)
<i>Inflammatory Response</i>	let7, miR133a (↑RhoA, AHR induction), miR-143 (modulates cell migration), miR-145 (cytoskeletal remodeling, affects podosome formation), miR146a (see table 4), miR 155 (see table 4), miR-708 (negative feedback to TNF- α)
<i>Cell Division</i>	miR-25 (↑proliferation), miR221 (↑proliferation), miR-371-5p, miR-718, miR-1181, miR-1207-5p, miR-1915, miR-3663-3p, LINC00882-002, LINC00883-005, BCYRN1, RP11-46A10.4
<i>Airway Remodeling</i>	miR-16, miR-25 (↓matrix protein synthesis), miR26a (airway remodeling by chronic stretch, ↓GSK-3 β), miR-133a (↓SRF), miR-146a
<i>Innervation</i>	miR-206 (neuronal branching)

Around 11 miRNAs are upregulated in cytokine-exposed ASMCs. Particularly, miR-25 is significantly modulated after prolonged OVA-challenge⁽¹⁶⁵⁾. Some cytokines through the \uparrow miR-25/ \downarrow KLF-4 system promote ASMC modulation⁽¹⁶⁶⁾. The transcription factor kruppel-like factor-4 (KLF-4) represses sm-specific gene expression by recruiting histone H4 deacetylase activity to smooth muscle cell genes, thereby blocking SRF association with methylated histones and CARG box chromatin. Next-generation sequencing identified miR-10a as the most abundant miRNA expressed in primary human ASMCs, accounting for more than 20% of all small RNAs. miR-10a directly suppresses PI3KCA expression and its overexpression reduces ASMC proliferation⁽¹⁶⁷⁾. TNF- α -induced expression of miR-708 in asthmatic ASMCs is greater than in non-asthmatic. miR-708 decreased JNK, MAPK and Akt phosphorylation and increased MAPK phosphatase-1 (MKP-1) and phosphatase and tension homolog (PTEN) expression. It constitutes a negative feedback for TNF- α signaling downregulation⁽¹⁶⁸⁾. miR-133a levels were decreased in human ASMCs, along with upregulated RhoA expression during AHR. Those findings were replicated after treatment with IL-13⁽¹⁶⁹⁾. Sonic hedgehog signaling blocks miR-206 expression to increase the release of BDNF by ASMCs, coordinating branch innervation⁽⁵²⁾.

A recent study explored the RNA expression profile in cultured ASM⁽¹⁷⁰⁾. Remarkably, over 200 miRNAs were detected including: miR-371-5p, miR-718, miR-1181, miR-1207-5p, miR-1915, and miR-3663-3p. These miRNAs had been previously related to aberrant proliferation in other cells. Paradoxically, predicted targets cut down gene expression of proteins that are known for remodeling promotion. They also detected a specific long non-coding RNA (lncRNA) profile. lncRNAs have recently emerged as epigenetic tools for gene expression regulation. They can regulate miRNAs as target site decoys, can also directly bind to transcription factors and

participate in assembly of chromatin-modifying complexes as structural components and recruiters of genomic targets⁽¹⁷¹⁾. Stimulated human ASMCs expressed 29 lncRNAs, and some of them were previously identified as cell proliferation regulators. Relevantly, an increase in LINC00882-002 and LINC00883-005, and a decrease in BCYRN1 and RP11-46A10.4, could explain why despite of specific miRNAs, a target mRNA transcript is still translated. These lncRNAs could act as 'sponges' for the miRNAs-1207, -150, -940, and -371, blocking the RISC association with the translational machinery. The analysis is more complex if it is considered that a variable expression is seen in each cell cycle phase. In summary, phenotypic switching encompasses responses exquisitely coordinated by multiple signaling pathways, orchestrating gene expression not only at a promoter level, but also involving specific changes in the RNA metabolism.

ASM REMODELING AS A THERAPEUTIC TARGET: EXPERIMENTAL EVIDENCES

Our current failure to treat some phenotypes of severe asthma is a reflection from our poor understanding of its underlying etiology. Classic interventions are directed to exacerbation management and prevention, including mainly bronchodilators and steroids to keep most patients away from flares, but in many cases they are ineffective as shown by clinical trials. Prospective placebo-controlled studies have not shown long-term beneficial effect of steroid treatment for RSV bronchiolitis and subsequent wheezing or asthma⁽²⁴³⁾. Doubling the dose of inhaled steroids in moderate to severe asthmatics was ineffective in two unrelated studies^(280, 281). Moreover, in adults with persistent asthma even optimal therapy is only able to reduce the frequency of exacerbations by around 40%⁽²⁸²⁾. In school-age children, moderate doses of inhaled steroids are completely ineffective at reducing exacerbation frequency, duration and severity of wheezing episodes associated with viral infection⁽²⁸³⁾. Furthermore, 5-day course of oral steroids at the onset of exacerbations in preschool children was ineffective at reducing the duration or exacerbation severity, even in children with systemic eosinophilia⁽²⁸⁴⁾. Not to mention the detrimental effects of glucocorticoids, seen on patients who had fatal asthma, in addition to the side effects by a prolonged therapy⁽²⁸⁵⁾. The reasons of failure could be secondary to an acquired insensitivity to glucocorticoid actions, which could prevent these drugs from blocking many events that conduce to airway remodeling. A review of the potential mechanisms has been recently published⁽²⁸⁶⁾. It is beyond the objectives of this review to analyze all the current recommended asthma and COPD therapies, for which there are available guidelines^(287, 288), or to underestimate the corroborated benefits of steroid treatment in the vast majority of asthmatic patients. However, recognizing that common interventions could not affect final outcomes is crucial to find better therapeutic targets. If novel therapies for airway remodeling are developed, it is possible that steroids might be sent apart from the primary treatment of asthma, and COPD progression could be effectively delayed. In this section, we explore some experimental evidence that supports such potential interventions.

Long-Acting Muscarinic Receptor Antagonists

The long-acting muscarinic antagonists (LAMAs), acclidinium, glycopyrronium and tiotropium, bind to human M1-M5 receptors in a concentration-dependent manner, but the highest selectivity is for M3, followed by M2⁽²⁸⁹⁾. Blockage of mAChRs has anti-inflammatory and anti-remodeling properties, although, most studies include only tiotropium in their protocols. For example, the anti-inflammatory activity associated with tiotropium on cigarette smoke-induced pulmonary inflammation in mice was related to a dose-dependent reduction of leukotriene-B₄, IL-6, chemokines and TNF- α , and also a decreased cell numbers in BAL⁽²⁹⁰⁾. In the same way, eosinophil recruitment and AHR in a guinea-pig model of asthma were inhibited by vagal blockade-independent mechanisms⁽²⁹¹⁾. The mechanism of tiotropium was linked to inhibition of TGF- β -induced MAPK signaling and a decreased MMP expression⁽²⁹²⁾. LAMAs would further affect cell plasticity, as it was demonstrated that acclidinium can inhibit the CCh-, TGF- β -, and cigarette-induced transition from human fibroblast to myofibroblast⁽²⁹³⁾. Tiotropium also significantly inhibited ASM thickening and Th2 cytokine production by human peripheral blood mononuclear cells in a murine model⁽²⁹⁴⁾. The anti-remodeling effect also include decreased α -MHC expression and decreased isometric relaxation of tracheal strips that were previously exposed to repeated allergen challenge⁽¹²¹⁾. From the clinical standpoint, in COPD, all three drugs produced significant FEV1 improvement, but only glycopyrronium reduced dyspnea. In severe asthma, only tiotropium has been tested, and it has demonstrated to raise FEV1 and decline the risk of exacerbations⁽²⁸⁹⁾.

Emerging Therapies: Statins, Macrolides, Endothelin Antagonists, Calcium Channel Antagonists and PPAR γ Agonists

Statins, through inhibition of 3-hydroxy-methylglutaryl-coenzyme A reductase (HMG-CoA reductase), reduce the synthesis of groups needed for protein isoprenylation, farnesylation and geranylgeranylation, influencing cell signaling. The inhibitory effect of simvastatin on FBS-induced RhoA activation is antagonized by geranylgeranyl pyrophosphate, but not by farnesyl pyrophosphate. These isoprenoids are required for prenylation of the small G proteins RhoA and Ras, and it was shown that inhibition of ASMC proliferation by simvastatin was due to prevention of geranylgeranylation of RhoA, but not by farnesylation of Ras⁽²⁹⁵⁾. Moreover, lovastatin, isoprenylation inhibitors, or other pharmacological approaches for preventing localization of RhoA in the membrane localization should be considered as a preventive antiviral therapy for selected groups with high risk for severe RSV disease⁽²⁹⁶⁾. However, statins are known to decrease cell survival, impacting on signaling that also contributes to bring cells under molecular stress. Autophagy, especially macroautophagy, was discussed as a potential mechanism of phenotypic modulation. Considering that some RNA viruses take advantage of the double-membrane vacuoles, potential improvement of RV replication could be an undesirable effect due to autophagic induction in response to statins⁽²⁷⁴⁾. Affecting some pathways associated with maturation can also reinforce ASMC modulation. This may explain why despite the well-established anti-inflammatory and pleiotropic effects of statins, clinical trials still failed to show any improvement of inflammatory and functional outcomes in patients with severe asthma⁽²⁹⁷⁾.

Macrolides are antibiotics that have been widely used in the treatment of infectious diseases.

Additionally, immunomodulatory and anti-inflammatory effects have been shown in relation to a suppression of goblet cell hyperplasia and cytokine secretion by regulating the activation of a MAPK/NF- κ B pathway⁽²⁹⁸⁾. Experimental evidence supports anti-remodeling actions of macrolides, e.g., roxithromycin inhibited ASMC proliferation in a dose-manner dependent. This effect was dependent on the loss of the mitochondrial membrane potential, cytoplasmic accumulation of Cyt c, caspase activation and increasing of p27^{Kip1} expression⁽²⁹⁹⁾. The same researcher group showed that roxithromycin decreased bronchial wall thickness and ASM layer in OVA-sensitized rats, and also downregulated ERK1/2 and upregulated caveolin-1 expression⁽³⁰⁰⁾. Long-term therapy may improve some functional parameters without affecting clinical outcomes, as showed by a recent metanalysis⁽³⁰¹⁾.

Endothelin-1 induces bronchoconstriction, mediates eosinophil recruitment during allergic inflammation, and contributes to airway remodeling by inducing fibroblast and ASMC differentiation and proliferation⁽³⁰²⁾. Despite of *in vitro* results obtained with endothelin receptor antagonists, such as sitaxsentan or bosentan, a recent small clinical trial did not demonstrate any improvement of functional tests or symptoms in poorly controlled asthma when compared to placebo⁽³⁰³⁾. On the other hand, calcium channel blockers were classically tested as bronchodilators, but after recent findings of pro-remodeling effects of altered calcium signals, long-term blockade has been proposed. Therefore, gallopamil administration reduces the mitochondrial mass and subsequent ASMC proliferation⁽³⁰⁴⁾. A recent doubled-blind randomized clinical trial showed that this calcium channel blocker decreased ASM thickness after 1 year of treatment. Although, there was no immediate clinical improvement during the treatment phase, a significant reduction in asthma exacerbations related to ASM mass reduction was seen during the follow-up⁽³⁰⁵⁾. In the same way, the PPAR- γ ligands, rosiglitazone and pioglitazone, have shown to regulate noncontractile and contractile functions of *in vitro* ASMCs, including decreased proliferation and synthetic activities by increasing heme oxygenase-1 activity, and β 2-AR expression that could reduce AHR⁽³⁰⁶⁾. However, its benefits in obstructive airway diseases remains to be tested in humans.

Biologic Therapy

Current management of autoimmune diseases and cancer, is based on blocking specific molecular targets through inhibitors and monoclonal antibodies. Unquestionable evidence has been obtained with anti-IgE (omalizumab) for treatment of severe asthma associated with high IgE levels, being included in GINA guidelines. Similar medications have been considered on behalf of their efficacy in chronic inflammatory diseases. A large list, including anti-IL-5 (mepolizumab, reslizumab, enralizaumab), anti-TNF- α (etanercept), anti-IL-4 (pascolizumab, nuvance), anti-IL-4/13 (pitrakinra), anti-IL-9, anti-CD25 (daclizumab), anti-VCAM-1 and anti-TSLP, are now under clinical trials, and some recent publications have shown controversial results^(307, 308). Based on animal models, blocking those pathways results in a reduced airway remodeling via decreased eosinophil, monocyte and T cell recruitment. However, decreasing inflammation was not always correlated with anti-remodeling effects. Clinical studies have not shown consistent results regarding improvement of FEV1, symptom control, and decreased use of short-acting β 2-agonists. A common finding is that the number of exacerbations tends

to decrease in the higher-steroid dose groups, without significant clinical efficacy. Whether or not these results were related to prevention of remodeling is unknown, because histopathological assessment were not included in their protocols.

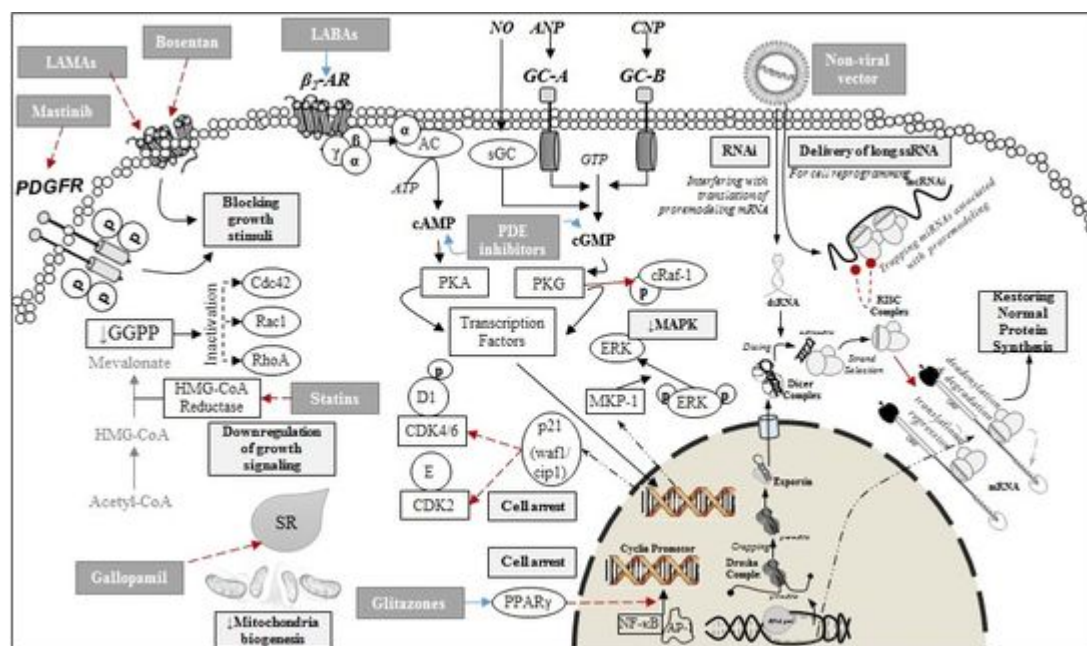
A specific approach is attained with the c-kit/PDGF receptor tyrosine kinase inhibitor mastinib. RTK inhibition by imatinib mesylate decreases collagen deposition, eosinophil infiltration, and ASM thickening in a murine model⁽³⁰⁹⁾. Mastinib improved the asthma control score and number of exacerbations⁽³¹⁰⁾. However, no significant improvement in lung function was observed. More randomized clinical trials are needed to precise what biologic therapy is suitable for specific subgroups. New drugs that target specific pathways, such as: antiproteases for modulation of ECM deposition, NFκB inhibitors, PI3K inhibitors, chemokine receptor antagonists, and even old drugs with anti-inflammatory properties, like thalidomide, increase the spectrum of therapeutic interventions⁽³¹¹⁾, but no experimental and clinical research focusing on ASM remodeling have been addressed.

Bronchial Thermoplasty

Reduction of dense ASM using physical forces, like radiofrequency energy, has shown promising results. Bronchial thermoplasty is a FDA-approved bronchoscopy procedure for patients with severe asthma, which delivers high thermal energy to the airway wall to heat and reduce the amount of its cellular components. Although, airways swell on immediate heat administration, this blanching and erythema usually resolved within 1 week, and no long-term adverse effects were noted. In essence, epithelial, blood vessel and nerve injury are followed by tissue regeneration, however for unknown reasons, ASM has demonstrated almost no capacity of regeneration after this procedure, being replaced by connective tissue, instead. Increased airway distensibility, decreased bronchomotor tone both at baseline and in response to increasing doses of methacholine suggest that the AHR reduction correlated well with the degree of ASM reduction, supporting a role of ASM remodeling in humans⁽³¹²⁾.

Conclusion ASM thickening is a consistent finding in airway remodeling that most likely contribute to the AHR and irreversible or partially reversible airflow obstruction seen on airway diseases, especially those with severe symptoms. Chronic inflammation is a major mechanism of structural transformation occurring at all airway layers. Nevertheless, ASM can also be generated by means of non-inflammatory pathways that would explain the lack of clinical correlation between inflammation and AHR. It remains unclear if ASM thickness depends on resident smooth muscle plasticity, mesenchymal expansion, myofibroblast migration, or stem cell differentiation, all with considerable evidence suggesting a role in this process. A complex molecular network between heterogeneous ASM bundles, containing the contractile, synthetic/proliferative, and hypercontractile phenotypes, and its tissue microenvironment determine the ASM function and outcome after injury, which real contribution can only be estimated by a system biology approach. Cytokines, growth factors, ACh, and viruses seem to have major influences in the genesis of ASM hyperplasia and hypertrophy, particularly, muscarinic signaling has potent effects on the ASMC metabolism regardless of its phenotypic status. Therefore, muscarinic receptors activation catalyzes processes for remodeling modulation, besides its well-known contractile effects, hence, it is an attractive target for long-term pharmacologic blockage by LAMAs. Further understanding of these mediators and the

interaction immune cell-smooth muscle at a epigenetic level could help to identify accurately the pathobiologic mechanisms of abnormal ASM functions and thickening, providing so, specific targets to develop future treatments (see Fig. 7) in the advent of gene therapy and nanotechnology⁽³¹³⁾.



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The authors are not aware of any affiliations, memberships, funding, or financial holdings that might be perceived as affecting the objectivity of this review.

Authors' contributions

C.A.F.A., M.J.A., I.L.B and R.F.R. participated in selection and reviewing of cited literature. C.A.F.A. aimed and wrote the preliminary version of this manuscript, designed tables, performed art-work of figures, and performed the *in silico* analysis for miRNA target and RNA hybridization prediction. F.A.P.U. did the staining technique for figure 1. C.A.F.A., R.F.R., and F.A.P.U. implemented cell culture techniques for figure 3. C.A.F.A, R.F.R, F.A.P.U, R.G.A, M.J.A, I.L.B read, drafted, discussed and approved the final version of this manuscript.

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