

MicroRNAs and Smooth Muscle Cells Phenotypic Switching in PAH

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Abstract

Smooth muscle cells undergo a switching from contractile phenotype to synthetic phenotype in pulmonary hypertension characterized by excessive proliferation and migration of smooth muscle cells. MicroRNAs are small non-coding RNAs that can negatively regulate gene expression by directly binding with the 3'-UTR of mRNA. Numerous microRNAs have been reported to modulate the smooth muscle cells phenotypic switching and been urged to become possible therapeutic targets for pulmonary hypertension. This review will focus on the roles of microRNAs in regulating smooth muscle cellular phenotypic switching in PAH.

Keywords: microRNAs; Smooth muscle cells; Phenotypic switching; PAH

Pulmonary Arterial Hypertension (PAH) is a progressive fatal disorder with a poor prognosis characterized by elevated pulmonary arterial pressures leading to right ventricular failure and death [1,2]. Abnormal switching from a contractile phenotype to a synthetic phenotype [3], are pivotal events in the development structural remodeling of vasculatures associated with PAH [4]. In response to a variety of environmental cues including growth factors, cell-cell contacts and altered mechanical load, circulating hormones, smooth muscle cells experience a phenotypic switching [5].

MicroRNAs (miRNAs) are a novel class of endogenous, small and non-coding RNAs that function in transcriptional and post-transcriptional regulation of gene expression by directly binding with the 3'-UTR of mRNA [6-8]. miRNAs can directly regulate about 30% of the genes in a cell [9], therefore it is not surprising that miRNAs are involved in the regulation of almost all major cellular function, including developmental timing, cell death, cell proliferation [10,11], fat storage [12], haematopoiesis [13-18] and patterning of the nervous system [19-22]. Recent studies have revealed that many non-coding miRNAs can be as novel phenotypic markers and modulators of Vascular Smooth Muscle Cells (VSMCs). These findings display extensive implications for the diagnosis and therapy of a variety of proliferative vascular diseases [23], including PAH. The review will focus on the roles of microRNAs in regulating smooth muscle cellular phenotypic switching in pulmonary hypertension.

There are two classic pulmonary hypertension animal models apart induced by monocrotaline (MCT) and hypoxia [24]. In pulmonary hypertension induced by MCT, it usually occurs that endothelial cells damage accompanied with the increasing release of growth factors. PDGF is one of the most common growth factors in PAH and released primarily by vascular endothelial cells and platelets at the sites of vascular injury [25]. Indeed, an increased expression of signaling proteins in the PDGF pathway has been demonstrated in several cardiovascular disorders [26]. Activation of PDGF inhibits smooth muscle cell (SMC)-specific gene expression (SM22 α , SM α -actin and calponin) and increases the rate of proliferation and migration, leading to dedifferentiation of VSMCs. Many miRNAs have been demonstrated to play important roles in the stimulation of PDGF with indistinct mechanisms.

MiR-15b is shown to be induced by PDGF in pulmonary artery smooth muscle cells and it is critical for the repression of SMC-specific contractile genes [27]. MiR-638 is abundantly expressed in SMCs and markedly down-regulated in the PDGF stimulation. In differentiation medium, miR-638 expression is significantly up-regulated to inhibit SMC proliferation by targeting the orphan nuclear receptor NOR1

[25]. MiR-24 also functions in the process and directly down-regulates Tribbles like protein-3 (Trb3) expression which results in decreased Smad protein levels and VSMC contractile genes expression [28]. Non-coding small miR-221/222 are novel regulators of vascular neointimal lesion formation during PDGF pathway via their target genes p27 (Kip1) and p57 (Kip2) [29]. PDGF stimulation could inhibit the expression of miR-221, leading to down-regulation of the targets p27 (Kip1) and c-Kit. Down-regulation of p27 (Kip1) is critical for PDGF-mediated induction of cell proliferation. Decreased c-Kit causes inhibition of SMC-specific contractile gene transcription by reducing the expression of myocardin (myocd), a potent SMC-specific nuclear coactivator [30]. Additionally, Davis BN et al. also found myocardin reduced SMC migration by increasing expression of miR-24/29a, resulting in down-regulation of platelet-derived growth factor receptor β (PDGFRB) expression [31]. Meanwhile, another report shows that overexpression of myocardin leads to significant induction of miR-1 expression and inhibition of SMC proliferation by targeting Pim-1, a serine/threonine kinase [32].

What's more, the damaged endothelial cells also could secret miRNAs to promote the SMC phenomenon switching via vesicles mediated intercellular communication [33,34]. Vesicle-mediated miRNAs has been proved in atherosclerosis while the research is very few in PAH, and it will become a new research hotspot. MiR-126 is an endothelial cell-restricted microRNA and highly expressed in endothelial cells [35]. Targeted deletion of miR-126 in mice causes leaky vessels, hemorrhaging and partial embryonic lethality, due to loss of vascular integrity and defects in endothelial cell proliferation, migration and angiogenesis [36]. Apoptotic endothelial cells at atherosclerotic plaques release microvesicles known as apoptotic bodies which are enrich in miR-126 into the circulation, and these microvesicles shuttle miR-126 to recipient neighboring vascular cells, their abundance correlates with negative indicators of the disease [37], suggesting possible intercellular communication or intercellular signal transduction mediated by miR-126 between EC and SMC. So we believe that in pulmonary hypertension, vesicles mediated miR-126 from ECs may also stimulate

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the proliferation of SMC. Besides, extracellular vesicles secreted by KLF2-transduced or shear-stress-stimulated HUVECs are enriched in miR-143/145 and control target gene expression in co-cultured SMCs [34]. Several reports suggested that miR-143 and miR-145 play critical roles in phenotype remodeling of VSMCs. Deficiency of miR-143 and miR-145 leads to VSMCs phenotypic switching from a contractile to synthetic phenotype [38], MiR-145 is down-regulated in PAH mouse models which can protect against the development of PAH. Besides, miR-145 is expressed in remodeled vessels in patient samples of heritable PAH and idiopathic PAH [39].

Apart from vesicle mediated microRNAs, recently Zhou et al. demonstrated that EC-secreted miR-126 and RNA-protein complexes (miRNAs and Ago2) regulate SMC gene expression (Forkhead Box O3, B cell Lymphoma 2 and Insulin Receptor substrate 1) and cellular functions via paracrine effects [40]. They also detected the association between Ago2 and miR-21, miR-221, miR-155, miR-143 and 145 and the results supporting the hypothesis that Ago-mediated miRNAs transmission is a general mechanism regulating intercellular communications [34].

Chronic hypoxia causes pulmonary vascular remodeling and leads to Pulmonary Hypertension (PAH) and right ventricle hypertrophy [41,42]. The remodeling process encompasses concentric medial thickening of small arterioles, muscularization of previously capillary-like vessels, and structural wall changes in larger pulmonary arteries [43]. The pulmonary arterial muscularization is characterized by the proliferation and phenotypic switching of smooth muscle cells. In hypoxic pulmonary hypertension, misexpression of miRNAs has been implicated in the pathologies.

Nuclear factor of activated T cells (NFAT) signaling pathway is linked to PASMC proliferation and phenotypic modulation in hypoxia. Down-regulation of miR-124 in hypoxia-treated PASMC is consistent with the activation of NFAT signaling pathway in hypoxia by targeting NFATc1, CAMTA1 and PTBP1 genes [44]. Fhl-1 is a member of the LIM family and acts as an early key protein in the mechanism of PAH [45]. It is regulated by HIF-1 α in a feedback loop that serves to limit HIF-1 α activity under conditions of prolonged hypoxia [46,47]. Hypoxia-induced down-regulation of miR-206 promotes PAH by targeting the HIF-1 α /Fhl-1 pathway in PASMCs [46]. MiR-210 plays an anti-apoptotic role in HPASMC via interaction with transcription factor E2F3 [48]. MiR-138 has the similar effects in PAH by interaction with serine/threonine kinase Mst1 and preventing caspase activation and Bcl-2 signaling [4]. Hypoxia also could produce a significant inhibition of miRNA-328 expression, which is involved in PA vasoconstriction and remodeling by targeting at insulin growth factor 1 receptor and L-type calcium channel- α 1C [49]. MiR-24 overexpression has detrimental effects on the SMC functional capacity inducing apoptosis, migration defects, enhanced autophagy and loss of contractile marker genes by targeting heme oxygenase 1 [50]. MiR-21 plays a significant role in hypoxia-mediated SMC phenotype by targeting PDCD4, SPRY2 and PPAR α [51]. These miRNAs are potential regulators of hypoxia-mediated proliferation, apoptosis and differentiation of PASMCs. They are therefore recognized as novel treatment strategies in PAH [52].

Conclusion

MicroRNAs play an important role in the SMC phenotypic switching in pulmonary hypertension in response to different stimulus and they may become potential novel therapeutic agents in the cardiovascular diseases. However it still has a far way to go because of the little data in vivo in patients. The stability and safety of miRNA and targeted miRNA delivery should draw more attention in the future.

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