

REVIEW

MiR-92a – a key player in cardiovascular remodeling

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Small non-coding, highly conserved microRNAs (miRs) play a crucial role in gene regulation, especially in post-transcriptional gene silencing, and are important for vascular homeostasis as well as during pathophysiological vascular remodeling processes. MiR-92a is known to attenuate endothelial cell proliferation, and angiogenesis. Conversely, down regulation of miR-92a improves these endothelial cell-dependent processes. We recently showed that inhibition of miR-92a also accelerates the re-endothelialization process and thus prevents neointima formation following wire-induced injury of murine femoral arteries. Thus, inhibition of miR-92a may represent a promising therapeutic strategy for the treatment of vascular diseases.

Keywords: microRNAs; cardiovascular remodeling; re-endothelialization; endothelial cells

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Percutaneous coronary interventions for the treatment of coronary atherosclerosis count to the most frequently performed therapeutic procedures in medicine [1]. The inevitable endovascular injury triggers a healing process of the arterial wall resulting in neointimal hyperplasia and vessel remodeling [2]. Drug-eluting stents with local delivery of anti-proliferative agents are one of the most important achievements of modern interventional cardiology. These stents sufficiently prevent vessel re-narrowing and thereby markedly reduce the rate of repeat revascularization. However, the substances currently used on drug-eluting stent platforms often impair endothelial coverage of stent struts thus initiating a chronic inflammatory process, delaying arterial healing, and increasing the risk of thrombotic events [3]. Hence, the investigation of molecular strategies targeting specifically the function of distinct cell types i.e. smooth muscle cell proliferation without affecting endothelial cell regenerative capacity are coming in the focus of novel treatment approaches. In this context, selective enhancement of endothelial regeneration after vascular injury has recently been shown to prevent neointimal lesion formation [4].

Small non-coding microRNAs (miRs) involved in post-transcriptional gene silencing are known to control several physiological and pathophysiological processes in the vascular wall [5,6]. MiR-92a is a member of the miR-17-92a cluster comprising six mature miRs, which are involved in the regulation of cell proliferation, development, immunity and tumorigenesis. Specifically, miR-92a has been shown to inhibit EC proliferation, angiogenesis, and vascular repair by an attenuation of the expression of validated target genes, i.e. the class III histone deacetylase sirtuin (Sirt)-1, integrin $\alpha 5$ (Itga5), and the flow-induced atheroprotective transcription factors Krüppel-like factor (Klf)-2 and Klf4 [7-10].

In initial observations, we detected miR-92a expression primarily in EC of uninjured murine vessels. Consecutively, we evaluated the spatiotemporal expression of miR-92a in a mouse model of wire-induced injury of the mouse femoral artery and found miR-92a levels significantly up-regulated in endothelial cells adjacent to the vascular injury site [11]. Following the overexpression of miR-92a in EC in vitro, we observed a significantly reduced proliferation and migration in ECs but not in SMCs, suggesting that the functional

impact of miR-92a is predominantly restricted to EC. Neither ECs nor SMCs showed changed apoptotic rates following sole overexpression of miR-92a^[11]. We then abrogated miR-92a expression following vascular injury by the use of two different strategies. Both, systemic injection of locked nucleic acid-based (LNA)-antimiRs and specific deletion of endothelial miR-92a using Tie2-Cre; miR-92a (fl/fl)-mice accelerated the re-endothelialization process. Furthermore, we found a reduced number of CD68⁺ monocytes/macrophages accumulating in the lesions as well as a reduced number of proliferating Ki67⁺ SMCs within the vessel wall, and an impairment of neointima lesion development. As expected, the expression of the pro-angiogenic miR-92a target genes Sirt1 and Itga5 was strongly increased at 2 weeks after wire-induced injury^[11]. Itga5 interacts with fibronectin, which represents the major component of the early extracellular matrix, and its expression has been shown to be an important prerequisite for vascular regeneration^[12]. The histone deacetylase Sirt1 regulates the expression and activity of numerous pro-angiogenic proteins and has been shown to have an inhibitory effect on neointima formation^[13]. Both have a critical impact on EC migration and proliferation, indicating that therapeutic inhibition of miR-92a to stimulate re-endothelialization involves at least in part the de-repression of these factors^[14].

In addition to neointima formation, miR92a has been shown to promote an atheroprone EC phenotype *inter alia* by suppression of the endothelial nitric oxide synthase in response to locally disturbed blood flow^[6, 9]. Consistently, specific blockade of miR-92a in LDLR^{-/-} mice reduced endothelial inflammation and decreased atherosclerotic plaque burden^[15]. Interestingly, circulating levels of miR-92a are significantly downregulated in patients with coronary artery disease, which might represent a compensatory mechanism. Selective analysis of these patients for vasculoprotective drug therapies revealed a trend towards lower levels of miR-92a in patients with statin therapy compared with patients without statin therapy^[16, 17]. Thus, low circulating levels of miR-92a likely represent a compensatory protective mechanism that might be boosted in response to statin therapy.

Expression of miR-92a is under control of several transcription factors^[18, 19]. Most of them are known to be critically involved in vascular remodeling even before miRs came to the focus of research interest^[11, 20, 21]. Inhibition of their transcriptional activity or targeting the respective downstream signaling pathways have been shown to prevent neointima formation. As mentioned above and in contrast to the expression of these transcription factors, miR-92a seems to be predominantly expressed in ECs, so that clinical inhibition of miR-92a might exert higher cell specificity than

inhibition of the respective transcription factors.

Regarding a possible translational approach using miR-inhibitors, a LNA-based therapy targeting miR-122 using a modified DNA phosphorothioate antisense oligonucleotide that binds miR-122 in a stable heteroduplex, thereby inhibiting its function, was demonstrated to be safe and efficient in a first-in-man phase II trial in patients suffering from chronic hepatitis C^[22]. However, miR-based therapeutics have not yet entered the stage of clinical trials for cardiovascular disorders. But given the very recent successful inhibition of miR-92a in a large-animal model of cardiac ischemia/reperfusion which resulted in a significant reduction of infarct size on the one hand and the pivotal role of miR-92a in vascular diseases on the other hand suggest that inhibition of miR-92a might emerge as a novel, promising therapeutic approach for the treatment of cardiovascular diseases^[23].

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